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OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 04:27:56 ; Search time 504 Seconds
(without alignments)
9801.046 Million cell updates/sec

Title: US-10-783-519-1
Perfect score: 2640
Sequence: 1 cggcgtgcggagcggcag.....gcaaaaaaaaaaaaaaaaaa 2640

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /EMC Celerra_SID33/ptodata/2/ina/1 COMB.seq.*
- 2: /EMC Celerra_SID33/ptodata/2/ina/5 COMB.seq.*
- 3: /EMC Celerra_SID33/ptodata/2/ina/6A COMB.seq.*
- 4: /EMC Celerra_SID33/ptodata/2/ina/6B COMB.seq.*
- 5: /EMC Celerra_SID33/ptodata/2/ina/7 COMB.seq.*
- 6: /EMC Celerra_SID33/ptodata/2/ina/7 COMB.seq.*
- 7: /EMC Celerra_SID33/ptodata/2/ina/7 COMB.seq.*
- 8: /EMC Celerra_SID33/ptodata/2/ina/7 COMB.seq.*
- 9: /EMC Celerra_SID33/ptodata/2/ina/7 COMB.seq.*
- 10: /EMC Celerra_SID33/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2640	100.0	2640	3	US-08-684-932A-37
2	2640	100.0	2640	3	US-09-618-304B-1
3	2640	100.0	2655	3	US-09-016-434-1094
4	2640	100.0	2655	4	US-09-023-655-916
5	2640	100.0	2655	4	US-09-880-107-3363
6	2580	97.7	2654	3	US-09-949-016-2404
7	2580	97.7	2654	3	US-09-949-016-2405
8	2553.4	96.7	2706	3	US-09-949-016-2975
9	2553.4	96.7	2706	3	US-09-949-016-2976
10	2051	77.7	2457	3	US-09-949-016-1330
11	2051	77.7	2457	3	US-09-949-016-1331
12	741.2	28.1	2945	10	5196526-2
13	740.8	28.1	2568	10	5196526-3
14	618.6	23.4	3062	3	US-09-799-451-895
15	554.6	21.0	4132	3	US-09-566-921-83
16	553	20.9	3033	3	US-09-016-434-1162
17	502.2	19.0	2339	3	US-09-495-050A-26
18	486.6	18.4	493	4	US-09-880-107-1291
19	301.6	11.4	1724	3	US-09-270-767-1291
20	247.8	9.4	11917	3	US-09-949-016-13072
21	247.8	9.4	11917	3	US-09-949-016-13073
22	247.8	9.4	15061	3	US-09-949-016-14717
23	247.8	9.4	15061	3	US-09-949-016-14718

24	247.8	9.4	15859	3	US-09-949-016-14146
25	247.8	9.4	15859	3	US-09-949-016-14147
c 26	239.2	9.1	1145	3	US-09-270-767-12941
c 27	223.2	8.5	847	3	US-09-270-767-28814
28	221.8	8.4	601	3	US-09-949-016-83496
29	221.8	8.4	601	3	US-09-949-016-83505
30	221.8	8.4	601	3	US-09-949-016-83505
31	221.8	8.4	601	3	US-09-949-016-107576
32	214.2	8.1	2037	4	US-10-094-749-572
33	214.2	8.1	601	3	US-09-949-016-46215
34	214.2	8.1	601	3	US-09-949-016-46222
35	214.2	8.1	601	3	US-09-949-016-83501
36	214.2	8.1	601	3	US-09-949-016-83510
37	214.2	8.1	601	3	US-09-949-016-107581
38	214.2	8.1	601	3	US-09-949-016-107590
c 39	166.6	6.3	762	3	US-09-270-767-11453
40	164.8	6.2	1351	3	US-09-270-767-1513
41	164.8	6.2	1351	3	US-09-270-767-1513
42	164.4	6.2	601	3	US-09-949-016-46216
43	164.4	6.2	601	3	US-09-949-016-46223
44	164.4	6.2	601	3	US-09-949-016-83502
45	164.4	6.2	601	3	US-09-949-016-83511

ALIGNMENTS

RESULT 1
US-08-684-932A-37
Sequence 37, Application US/08684932A
Patent No. 6403304
GENERAL INFORMATION:
APPLICANT: Stashenko, Philip
APPLICANT: Li, Yi-Ping
TITLE OF INVENTION: HUMAN OSTEOCLAST-SPECIFIC AND -RELATED
TITLE OF INVENTION: DNA SEQUENCES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,932A
FILING DATE: 19-JUL-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: PDC92-02FM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 2640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 58..2523
US-08-684-932A-37

Query Match 100.0%; Score 2640; DB 3; Length 2640;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	CGGCGTGC	CGGAGCGG	CAGCAG	CAGCAG	CGGAGCGG	CAGCAG	CGGAGCGG	CGGAGCGG
DB	1	CGGCGTGC	CGGAGCGG	CAGCAG	CAGCAG	CGGAGCGG	CAGCAG	CGGAGCGG	CGGAGCGG
QY	61	GGCTCCAT	TTCCGAGCGG	AGGAGG	TTGGGCTT	GGTCCAGCT	TTTTCG	CCACAGCGGCT	120
DB	61	GGCTCCAT	TTCCGAGCGG	AGGAGG	TTGGGCTT	GGTCCAGCT	TTTTCG	CCACAGCGGCT	120
QY	121	GGCTACAC	CTGGCTGAG	CTGGGCTG	GGGCTG	GGGCTG	GGGCTG	GGGCTG	180
DB	121	GGCTACAC	CTGGCTGAG	CTGGGCTG	GGGCTG	GGGCTG	GGGCTG	GGGCTG	180
QY	181	GGCTCGGT	GAGCGCTT	CCAGAG	CGCTTT	GTGGTT	GTGAT	TTGGCGCT	240
DB	181	GGCTCGGT	GAGCGCTT	CCAGAG	CGCTTT	GTGGTT	GTGAT	TTGGCGCT	240
QY	241	GAGAGAC	CTTCCAC	CTTCCG	AGGAGG	TTGGGCTT	GGGCTT	GGGCTT	300
DB	241	GAGAGAC	CTTCCAC	CTTCCG	AGGAGG	TTGGGCTT	GGGCTT	GGGCTT	300
QY	301	CCAAAGGG	AGGAGG	CTGCGG	CAACCC	CCCGGAC	CTGCGG	CAACCC	360
DB	301	CCAAAGGG	AGGAGG	CTGCGG	CAACCC	CCCGGAC	CTGCGG	CAACCC	360
QY	361	GAGCGCT	GGCCAG	AGCTGG	GGATGT	GGGGCA	CCAGCG	CCCTGG	420
DB	361	GAGCGCT	GGCCAG	AGCTGG	GGATGT	GGGGCA	CCAGCG	CCCTGG	420
QY	421	CTGCAAC	AGCTGAG	CTTCC	CGCGG	CTTCC	CGCGG	CTTCC	480
DB	421	CTGCAAC	AGCTGAG	CTTCC	CGCGG	CTTCC	CGCGG	CTTCC	480
QY	481	GC CGCC	CAACAG	ATGAGG	CGCCCT	CTGCGG	CAACAG	ATGAGG	540
DB	481	GC CGCC	CAACAG	ATGAGG	CGCCCT	CTGCGG	CAACAG	ATGAGG	540
QY	541	CAACAGG	AGCTGAGG	CTTCA	CTTGTG	GCGG	AGCTGAGG	CTTCA	600
DB	541	CAACAGG	AGCTGAGG	CTTCA	CTTGTG	GCGG	AGCTGAGG	CTTCA	600
QY	601	CTAGAGC	CGCTGCT	CGAGG	CGCTG	CGGCTT	CGCTG	CGGCTT	660
DB	601	CTAGAGC	CGCTGCT	CGAGG	CGCTG	CGGCTT	CGCTG	CGGCTT	660
QY	661	GAGCAGC	CGCTGAG	CAACCC	CGGAG	CGGAG	CGGAG	CGGAG	720
DB	661	GAGCAGC	CGCTGAG	CAACCC	CGGAG	CGGAG	CGGAG	CGGAG	720
QY	721	TCCTACT	GGGGT	GAGCAG	ATCGG	AGATTC	CGGAG	ATCGG	780
DB	721	TCCTACT	GGGGT	GAGCAG	ATCGG	AGATTC	CGGAG	ATCGG	780
QY	781	CAGCTT	CTTCCG	TTCTG	CAGCAG	AGGAGG	CGCCCT	CGGCGG	840
DB	781	CAGCTT	CTTCCG	TTCTG	CAGCAG	AGGAGG	CGCCCT	CGGCGG	840
QY	841	CAGCAGC	AGGAGG	CTGAGG	AGGCTT	CGGGAG	AGGAGG	CTGAGG	900
DB	841	CAGCAGC	AGGAGG	CTGAGG	AGGCTT	CGGGAG	AGGAGG	CTGAGG	900
QY	901	CTAGGCG	GGGTG	CTGAGT	GTGCG	CCAGG	CGAGG	CGAGG	960
DB	901	CTAGGCG	GGGTG	CTGAGT	GTGCG	CCAGG	CGAGG	CGAGG	960
QY	961	GTGTACT	GGCCCT	GAA	CCAGT	GAGCGT	GAGC	CAACAG	1020
DB	961	GTGTACT	GGCCCT	GAA	CCAGT	GAGCGT	GAGC	CAACAG	1020
QY	1021	GCCTGGT	GCTCT	GTGCG	AGACCT	CGCCCT	GTGCG	AGAGG	1080
DB	1021	GCCTGGT	GCTCT	GTGCG	AGACCT	CGCCCT	GTGCG	AGAGG	1080

Qy	61	GGCTCCATGTTCCGGAGCGAGAGGTGGCCCTGGTCCAGCTCTTTCTGCCCCACAGCGGCT	120
Db	61	GGCTCCATGTTTCCGGAGCGAGAGAGGTGGCCCTGGTCCAGCTCTTTCTGCCACACAGCGCT	120
Qy	121	GCCTACACCTCGCTGAGTCGGCTGGCGGAGCTGGGCCCTCGTGGAGTTTCAGAGACCTCAAC	180
Db	121	GCCTACACCTCGGTGAGTCGGCTGGCGGAGCTGGGCCCTCGTGGAGTTTCAGAGACCTCAAC	180
Qy	181	GCCTCGGTGAGCGGCTTCCAGAGACGCTTTCTGTGTTGATGTTTGGCGCTGTGAGGAGCTG	240
Db	181	GCCTCGGTGAGCGGCTTCCAGAGACGCTTTCTGTGTTGATGTTTGGCGCTGTGAGGAGCTG	240
Qy	241	GAGAGAGCTTTCACCTTCCTGCAGGAGAGAGTGGCGGGCTGGGCTGGTCTCTGCCCCCG	300
Db	241	GAGAAGACCTTTCACCTTCTGCAGGAGAGAGTGGCGGGCTGGGCTGGTCTCTGCCCCCG	300
Qy	301	CCAAAGGGGAGGCTCCGGCACCCGCCACCCCGGGACCTGCTGCCATCCACGAGGAGACG	360
Db	301	CCAAAGGGGAGGCTGCCGGCACCCCCACCCCGGACCTGCTGCCATCCACGAGGAGAGCG	360
Qy	361	GAGCGCTGGCCCAAGAGCTCGGGATGTGCGGGCAACACAGCAGGCCCTGCGGGCCGAG	420
Db	361	GAGCGCTGGCCCAAGAGCTCGGGATGTGCGGGCAACACAGCAGGCCCTGCGGGCCGAG	420
Qy	421	CTGCACACAGCTGCAGCTCCACGCCCGCGTGTACGCCAGGGGCCATGAACCTCAGCTGGCA	480
Db	421	CTGCACACAGCTGCAGCTCCACGCCCGCGTGTACGCCAGGGGCCATGAACCTCAGCTGGCA	480
Qy	481	GCCGCCCAACAGATGGGGCTCAGAGAGACGCCCTGCTCCAGGCCCCCCGGGGGGCGG	540
Db	481	GCCGCCCAACAGATGGGGCTCAGAGAGAGCGCCCTGCTCCAGGCCCCCCGGGGGGCGG	540
Qy	541	CACAGAGCTGAGGGTCAACTTTTGTGGCAGGTGCCGTGGAGCCCCCAAGAGCCCTTGCC	600
Db	541	CACCAGGACCTGAGGGTCAACTTTTGTGGCAGGTGCCGTGGAGCCCCCAAGAGCCCTTGCC	600
Qy	601	CTAGAGCGCTGCTCGAGGGCTCGCGGGCTTCTCATTTGCCAGCTTCAGGAGAGCTG	660
Db	601	CTAGAGCGCTGCTCTCGAGGGCTCGCGGGCTTCTCATTTGCCAGCTTCAGGAGAGCTG	660
Qy	661	GAGCAGCGCTGGAGCACCCCGTGACGGGGGAGCAGCCAGCTGGATGACTTCTCCTCATC	720
Db	661	GAGCAGCGCTGGAGCACCCCGTGACGGGGGAGCAGCCAGCTGGATGACTTCTCCTCATC	720
Qy	721	TCCTACTGGGGTAGCAGATCGGACAGAGATCCGCAAGATCAAGGACTGTGTTCCATGCTC	780
Db	721	TCCTACTGGGGTAGCAGATCGGACAGAGATCCGCAAGATCAAGGACTGTGTTCCATGCTC	780
Qy	781	CACGTCTTCGGTTTCTGACAGAGGAGGAGCGCCGCTCGGGGCCCTGACGAGCTGCAA	840
Db	781	CACGTCTTCGGTTTCTGACAGAGGAGGAGCGCCGCTCGGGGCCCTGACGAGCTGCAA	840
Qy	841	CAGCAGAGCCAGGAGCTGCAGGAGGTCCTCGGGGAGACAGAGCGGTTCTTGAGCCAGGTG	900
Db	841	CAGCAGAGCCAGGAGCTGCAGGAGGTCCTCGGGGAGACAGAGCGGTTCTTGAGCCAGGTG	900
Qy	901	CTAGGCCGGGTGTGCACTGCTGCCGCCAGGGCAGGTGCAAGGTCCACAAGATGAAGGCC	960
Db	901	CTAGGCCGGGTGTGCACTGCTGCCGCCAGGGCAGGTGCAAGGTCCACAAGATGAAGGCC	960
Qy	961	GTGTACTGTGCCCTGAACACAGTCAGAGTCAGACACACGACAGTGCCTCATTTGCCGAG	1020
Db	961	GTGTACTGTGCCCTGAACACAGTCAGAGTCAGACACACGACAGTGCCTCATTTGCCGAG	1020
Qy	1021	GCCTGGTGTCTGTGCGAGACTTGCGCCCGCTGACGAGGCGCTTGCGGGACAGCTCGATG	1080
Db	1021	GCCTGGTGTCTGTGCGAGACTTGCGCCCGCTGACGAGGCGCTTGCGGGACAGCTCGATG	1080
Qy	1081	GAGGAGGAGTAGTGCGGTGGTTCACCGCATCCCTTGCGGGACATGCCCCCACAATC	1140
Db	1081	GAGGAGGAGTAGTGCGGTGGTTCACCGCATCCCTTGCGGGACATGCCCCCACAATC	1140

QY	1141	ATCCGCAACACCGCTTCA	CGGCAGAGCTTCCAGGGCATCTGTGAT	CGCTACGGCGTGGGC	1200
DB	1141	ATCCGCAACACCGCTTCA	CGGCAGAGCTTCCAGGGCATCTGTGAT	CGCTACGGCGTGGGC	1200
QY	1201	CGCTACCAAGGAGTCAAC	CCCGCTCCCTACACCATCATCACTTCCCTT	CCCTGTTTGTCT	1260
DB	1201	CGCTACCAAGGAGTCAAC	CCCGCTCCCTACACCATCATCACTTCCCTT	CCCTGTTTGTCT	1260
QY	1261	GTGATGTTGGGGATGTGGG	CCAGGGCTGCTCATGTTCCTTCCTCGGCCCTGGCCATGGTC	1320	
DB	1261	GTGATGTTGGGGATGTGGG	CCAGGGCTGCTCATGTTCCTTCCTCGGCCCTGGCCATGGTC	1320	
QY	1321	CTTGGGGAACCCAGCCGGCTGTGA	AAGCCGCGAGAAACGAGATCTGGCAGACTTCTTTC	1380	
DB	1321	CTTGGGGAACCCAGCCGGCTGTGA	AAGCCGCGAGAAACGAGATCTGGCAGACTTCTTCTTC	1380	
QY	1381	AGGGCCGCTACCTGCTCCTGCTTAT	TGGGCTGTTCATCTPACACCGGCTTCATCTAC	1440	
DB	1381	AGGGCCGCTACCTGCTCCTGCTTAT	TGGGCTGTTCATCTPACACCGGCTTCATCTAC	1440	
QY	1441	AACGAGTGCTTCACTCGCGCCAC	CAGCATCTTCCCTCGGGCTGGAGTGTGGCCGCATG	1500	
DB	1441	AACGAGTGCTTCACTCGCGCCAC	CAGCATCTTCCCTCGGGCTGGAGTGTGGCCGCATG	1500	
QY	1501	GCCAAACAGTCTGGCTGGAGTGATG	CATCTTCTCGGCCAGCACAGATCTTACCTTGGAT	1560	
DB	1501	GCCAAACAGTCTGGCTGGAGTGATG	CATCTTCTCGGCCAGCACAGATCTTACCTTGGAT	1560	
QY	1561	CCCAACGTCACCGGTGCTTCTCGG	AGACCTACCCCTTTGGCATCGATCTTATTTGGAGC	1620	
DB	1561	CCCAACGTCACCGGTGCTTCTCGG	AGACCTACCCCTTTGGCATCGATCTTATTTGGAGC	1620	
QY	1621	CTGGCTGCACCAACTTGAAGTCTCT	CAACTCTTCAAGATGAAGATGTCCGTCATCTCTG	1680	
DB	1621	CTGGCTGCACCAACTTGAAGTCTCT	CAACTCTTCAAGATGAAGATGTCCGTCATCTCTG	1680	
QY	1681	GGCTGTGTGCACATGGCCTTTGGG	TGGTCTTGGAGTCTTCAACACCGTGCACTTTGGC	1740	
DB	1681	GGCTGTGTGCACATGGCCTTTGGG	TGGTCTTGGAGTCTTCAACACCGTGCACTTTGGC	1740	
QY	1741	CAGAGGCACCGGCTGTGTGGAGAG	CGCTGCGGAGCTCACTTCTGCTGGGACTTCTTC	1800	
DB	1741	CAGAGGCACCGGCTGTGTGGAGAG	CGCTGCGGAGCTCACTTCTGCTGGGACTTCTTC	1800	
QY	1801	GGTTACCTCTGTTCCTAGTCACTA	CAAGTGCTGTGTCTGGGCTGCGAGGGCGGC	1860	
DB	1801	GGTTACCTCTGTTCCTAGTCACTA	CAAGTGCTGTGTCTGGGCTGCGAGGGCGGC	1860	
QY	1861	TCGCCCCAGCATCTCATCTCATCT	CAACATGTTCTTCTCCACAGCCCGCAGCAAC	1920	
DB	1861	TCGCCCCAGCATCTCATCTCATCT	CAACATGTTCTTCTCCACAGCCCGCAGCAAC	1920	
QY	1921	AGGCTGCTTACCCCGGCAAGGAGTG	GTGTCCAGGCCACCGTGTGTCTGGGCTTGGGC	1980	
DB	1921	AGGCTGCTTACCCCGGCAAGGAGTG	GTGTCCAGGCCACCGTGTGTCTGGGCTTGGGC	1980	
QY	1981	ATGTGTCCCATCTGTGCTTGTGCA	CACCCCTGCACCTGTGTGCA	CGCCGCGC	2040
DB	1981	ATGTGTCCCATCTGTGCTTGTGCA	CACCCCTGCACCTGTGTGCA	CGCCGCGC	2040
QY	2041	CTCGGAGGAGGCCCGTGACCGAG	AGGAAAAAAGGGGCGCTGTGACCTTGGCCT	2100	
DB	2041	CTCGGAGGAGGCCCGTGACCGAG	AGGAAAAAAGGGGCGCTGTGACCTTGGCCT	2100	
QY	2101	GAGGCATCTGTGAATGGCTGGAG	ACTCGATGAGGAAAGCGGGGCTGTGATGAA	2160	
DB	2101	GAGGCATCTGTGAATGGCTGGAG	ACTCGATGAGGAAAGCGGGGCTGTGATGAA	2160	
QY	2161	GAGGAGCCGAGCTCGTCCCTCCG	AGGTGCTCATGCCAGGCCATCCACACCTCGAG	2220	
DB	2161	GAGGAGCCGAGCTCGTCCCTCCG	AGGTGCTCATGCCAGGCCATCCACACCTCGAG	2220	
QY	2221	TTCTGCTCGGGCTCGTCTCCAA	ACCGGCTCTTACTGCGGCTGTGGGCTCTGAGGCTG	2280	

2221 TTCTGCTGGGCTGGCTCTCCAAACACCGCTCTCTACCTGGGCTGTGGCCCTGAGCCTG 2280
2281 GCCACGCGCCAGCTGTCCGAGGTTCTGTGGCCATGATGCGCATAGGCTGTGGCCTG 2340
2281 GCCACGCGCCAGCTGTCCGAGGTTCTGTGGCCATGATGCGCATAGGCTGTGGCCTG 2340
2341 GSCCGGGAGGTGGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 2400
2341 GSCCGGGAGGTGGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 2400
2401 ATGACCGTGGCTATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460
2401 ATGACCGTGGCTATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460
2461 CTGCACTGGGTGGATTCAGAACAAAGTTCTACTCAGGCAAGGCTTCAAGCTGAGTCCC 2520
2461 CTGCACTGGGTGGATTCAGAACAAAGTTCTACTCAGGCAAGGCTTCAAGCTGAGTCCC 2520
2521 TTACCTCTCGCTGCCACAGATGACTAGGCGCCACTGCGAGTCTCTGCCAGACCTCTCT 2580
2521 TTACCTCTCGCTGCCACAGATGACTAGGCGCCACTGCGAGTCTCTGCCAGACCTCTCT 2580
2581 GACCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
2581 GACCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640

RESULT 4

US-09-023-655-916
Sequence 916, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 916:
SEQUENCE CHARACTERISTICS:
LENGTH: 2655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

LIBRARY: GENBANK
CLONE: g1245045
US-09-023-655-916
Query Match 100.0%; Score 2640; DB 3; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGCTGCGCGAGCGGGCAGCAGCAGCGGAGGCGCGCGAGCACAACCCGGGGAGCCATG 60
Db 1 CGCGCTGCGCGAGCGGGCAGCAGCAGCGGAGGCGCGCGAGCACAACCCGGGGAGCCATG 60
QY 61 GGCCTCAATGTTCCCGAGCGAGGAGGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 120
Db 61 GGCCTCAATGTTCCCGAGCGAGGAGGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 120
QY 121 GCCTACACCTCGT 180
Db 121 GCCTACACCTCGT 180
QY 181 GCCTCGT 240
Db 181 GCCTCGT 240
QY 241 GAGAGACCTTCACTTCTCTGAGGAGGAGGTGGGCGGCTGTGGCTGTGGCTGTGGCTGTGG 300
Db 241 GAGAGACCTTCACTTCTCTGAGGAGGAGGTGGGCGGCTGTGGCTGTGGCTGTGGCTGTGG 300
QY 301 CCAAGGGAGGAGGCTGCGCGCACCCCGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
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QY 361 GAGCGCTGTGGCCAGAGAGCTGTGGGATGTGGGGGCAACAGAGAGGCGCTGTGGGGCCAG 420
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QY 421 CTGACACAGCTGTGAGCTTCCAGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db 421 CTGACACAGCTGTGAGCTTCCAGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY 481 GCGCGCCACACAGATGTGGGCTCTGAGAGGAGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGT 540
Db 481 GCGCGCCACACAGATGTGGGCTCTGAGAGGAGCGCGCTGTGTGTGTGTGTGTGTGTGTGT 540
QY 541 CACAGAGACCTGTGAGGCTCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db 541 CACAGAGACCTGTGAGGCTCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 601 CTAGAGCGCTGTCTGTGAGGCGCTGTGGCGGCTGTGGCGGCTGTGGCGGCTGTGGCGG 660
Db 601 CTAGAGCGCTGTCTGTGAGGCGCTGTGGCGGCTGTGGCGGCTGTGGCGGCTGTGGCGG 660
QY 661 GAGCAGCGCTGTGAGGAGCACCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 661 GAGCAGCGCTGTGAGGAGCACCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
QY 721 TCCTACTGT 780
Db 721 TCCTACTGT 780
QY 781 CACGTCTTCCCGTTTGTGACAGAGGAGGCGCGCTGTGGGGCGCTGTGGGGCGCTGTGGAA 840
Db 781 CACGTCTTCCCGTTTGTGACAGAGGAGGAGGCGCGCTGTGGGGCGCTGTGGGGCGCTGT 840
QY 841 CAGCAGAGCCAGGAGCTGTGAGAGGTCTCTGGGAGAGCAGAGCGGTCTCTGAGCCAGGTG 900
Db 841 CAGCAGAGCCAGGAGCTGTGAGAGGTCTCTGGGAGAGCAGAGCGGTCTCTGAGCCAGGTG 900
QY 901 CTAGGCGGGGT 960
Db 901 CTAGGCGGGGT 960
QY 961 GTGTACCTGGGCGCTGAAACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020

Db 961 GTGTACCTGGCCCTGAACAGTGTGAGGTGAGCAGCAGCAAGTGTCTCTATTTGCCGAG 1020
QY 1021 GCCTGTGTCTGTGCGAGACCTGCGCCCTGCGAGAGGCTTGCAGGAGCAGCTCGATG 1080
Db 1021 GCCTGTGTCTGTGCGAGACCTGCGCCCTGCGAGAGGCTTGCAGGAGCAGCTCGATG 1080
QY 1081 GAGGAGGAGTGTGAGTGTGCGGTCTACGCGATCCCTGCGGAGCAGTCCGCCACATC 1140
Db 1081 GAGGAGGAGTGTGAGTGTGCGGTCTACGCGATCCCTGCGGAGCAGTCCGCCACATC 1140
QY 1141 ATCCGACCAACCGCTTTCAGGCGCAGCTTCCAGGCGATCGTGGATCGTACGGCGTGGC 1200
Db 1141 ATCCGACCAACCGCTTTCAGGCGCAGCTTCCAGGCGATCGTGGATCGTACGGCGTGGC 1200
QY 1201 CGCTACGAGAGGTCAACCCCGCTTCTCAACCATCATCACTTCCCTCTCTCTGTCTGCT 1260
Db 1201 CGCTACGAGAGGTCAACCCCGCTTCTCAACCATCATCACTTCCCTCTCTCTGTCTGCT 1260
QY 1261 GTGATGTTCCGGGATGTGGGCGCAGGCGCTCTCATGTTCTCTTCGCGCTGGCCATGGTC 1320
Db 1261 GTGATGTTCCGGGATGTGGGCGCAGGCGCTCTCATGTTCTCTTCGCGCTGGCCATGGTC 1320
QY 1321 CTTGCGGAGAACCGACCGCTGTGAAGCCGCGCAGAACGAGATCTCGCAGACTTCTTC 1380
Db 1321 CTTGCGGAGAACCGACCGCTGTGAAGCCGCGCAGAACGAGATCTCGCAGACTTCTTC 1380
QY 1381 AGGGCGCGCTACCTGCTCTCTGTATGGGCTGTCTCCATCTACACCGGCTTCATCTAC 1440
Db 1381 AGGGCGCGCTACCTGCTCTCTGTATGGGCTGTCTCCATCTACACCGGCTTCATCTAC 1440
QY 1441 AAGAGTGTCTAGTCCGCGCACAGCATCTTCCCTCGGGCTGGAGTGGCGCCATG 1500
Db 1441 AAGAGTGTCTAGTCCGCGCACAGCATCTTCCCTCGGGCTGGAGTGGCGCCATG 1500
QY 1501 GCCAACAGTCTGCGTGGAGTGTGATCTTCTGCGCCAGCACAGATCTTACCTGTGGAT 1560
Db 1501 GCCAACAGTCTGCGTGGAGTGTGATCTTCTGCGCCAGCACAGATCTTACCTGTGGAT 1560
QY 1561 CCCAACGTCAACCGTGTCTTCTGGGACCTTCCCTTGGCATCGATCTTATTTGGAGC 1620
Db 1561 CCCAACGTCAACCGTGTCTTCTGGGACCTTCCCTTGGCATCGATCTTATTTGGAGC 1620
QY 1621 CTGGCTGCCAACCATGAGCTTCTCAACTCTTCAAGATGAAGATGTCGCTCATCTG 1680
Db 1621 CTGGCTGCCAACCATGAGCTTCTCAACTCTTCAAGATGAAGATGTCGCTCATCTG 1680
QY 1681 GCGGTGTGCACATGCGCTTGGGTTGGTCTCGGAGTCTTCAACACGTCGACTTTGGC 1740
Db 1681 GCGGTGTGCACATGCGCTTGGGTTGGTCTCGGAGTCTTCAACACGTCGACTTTGGC 1740
QY 1741 CAGAGGCAACCGGCTGTCTGGAGACGCTGCCGAGCTCACCTTCTCTGCTGGGACTTTC 1800
Db 1741 CAGAGGCAACCGGCTGTCTGGAGACGCTGCCGAGCTCACCTTCTCTGCTGGGACTTTC 1800
QY 1801 GGTACTCTGTGTCTTAGTCATCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860
Db 1801 GGTACTCTGTGTCTTAGTCATCTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860
QY 1861 TCGCCGAGCATCTCACTTCAATCAATGTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1920
Db 1861 TCGCCGAGCATCTCACTTCAATCAATGTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1920
QY 1921 AGGCTGTCTTACCCCGGCGAGGAGTGGTCCAGGCCACGCTGGTGGTCTTGGCTTGGCC 1980
Db 1921 AGGCTGTCTTACCCCGGCGAGGAGTGGTCCAGGCCACGCTGGTGGTCTTGGCTTGGCC 1980
QY 1981 ATGGTGGCATCTGT 2040
Db 1981 ATGGTGGCATCTGT 2040
QY 2041 CTTGCGGAGAGGCGCTGTGACGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100

Db 2041 CTTGCGGAGAGGCGCTGTGACGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100
QY 2101 GACGCATCTGTGAATGGCTGGAGCTCCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160
Db 2101 GACGCATCTGTGAATGGCTGGAGCTCCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160
QY 2161 GAGGAGGCGAGCTGTCTCCCTCCGAGGCTCTCATGACACGAGGAGGAGGAGGAGGAGG 2220
Db 2161 GAGGAGGCGAGCTGTCTCCCTCCGAGGCTCTCATGACACGAGGAGGAGGAGGAGGAGG 2220
QY 2221 TTCTGCTGTGGCTGTGGCTTCCAAACACCGCTTCTTACCTGCGCCCTGCGGCGCTG 2280
Db 2221 TTCTGCTGTGGCTGTGGCTTCCAAACACCGCTTCTTACCTGCGCCCTGCGGCGCTG 2280
QY 2281 GCCACGCGCAGCTGTCTCGAGGTTCTGTGGGCGATGTGATGCGCATAGGCTTGGGCTG 2340
Db 2281 GCCACGCGCAGCTGTCTCGAGGTTCTGTGGGCGATGTGATGCGCATAGGCTTGGGCTG 2340
QY 2341 GCGCGGAGGAGTGGGCGCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
Db 2341 GCGCGGAGGAGTGGGCGCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2400
QY 2401 ATGACCGTGTGTATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460
Db 2401 ATGACCGTGTGTATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460
QY 2461 CTTGACCTGTGGTGAATTTCCAGAACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2520
Db 2461 CTTGACCTGTGGTGAATTTCCAGAACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2520
QY 2521 TTCACTTCTGCTGCCACAGATGACTAGGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2580
Db 2521 TTCACTTCTGCTGCCACAGATGACTAGGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2580
QY 2581 GACCTCTGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
Db 2581 GACCTCTGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640

RESULT 5

US-09-880-107-3363
Sequence 3363, Application US/09880107
Patent No. 6974667
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3363
LENGTH: 2655
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. 6974667 U45285
US-09-880-107-3363

Query Match 100.0%; Score 2640; DB 4; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGGTGCGCGGACGGGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
Db 1 CGCGGTGCGCGGACGGGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60

QY 61 GGTCCATGTTCCGGAGCGAGGAGTGGCCCTGGTCCAGCTCTTTCTGCCCAAGGGCT 120
DB 61 GGTCCATGTTCCGGAGCGAGGAGTGGCCCTGGTCCAGCTCTTTCTGCCCAAGGGCT 120
QY 121 GCTACACCTGCGTAGTGGCTGGCGAGCTGGGCTCGTGGAGTTTCAGAGACCTCAAC 180
DB 121 GCTACACCTGCGTAGTGGCTGGCGAGCTGGGCTCGTGGAGTTTCAGAGACCTCAAC 180
QY 181 GCTCGGTGAGCGCTTCAGAGACGCTTTGTGGTTGATGTTTGGCGCTGTGAGAGCTG 240
DB 181 GCTCGGTGAGCGCTTCAGAGACGCTTTGTGGTTGATGTTTGGCGCTGTGAGAGCTG 240
QY 241 GAGAAGACCTTCACCTTCCTGTCAGAGAGGAGTGGCGGGCTGGGCTGGTCCGCCCG 300
DB 241 GAGAAGACCTTCACCTTCCTGTCAGAGAGGAGTGGCGGGCTGGGCTGGTCCGCCCG 300
QY 301 CCAAGGGAGGCTGCCGGCACCCCAACCCCGGACCTGCTGCGCATCCAGGAGGAGCG 360
DB 301 CCAAGGGAGGCTGCCGGCACCCCAACCCCGGACCTGCTGCGCATCCAGGAGGAGCG 360
QY 361 GAGCGCTGGCCAGAGCTGGGGATGTGGGGGCAACAGAGGCGCTGGCGGCCAG 420
DB 361 GAGCGCTGGCCAGAGCTGGGGATGTGGGGGCAACAGAGGCGCTGGCGGCCAG 420
QY 421 CTGCAACAGCTGAGCTCCAGCGCCGCTGCTAGCGGAGGAGGAGGAGGAGGAGGAG 480
DB 421 CTGCAACAGCTGAGCTCCAGCGCCGCTGCTAGCGGAGGAGGAGGAGGAGGAGGAG 480
QY 481 GCGGCCACACAGATGGGGCTCAGAGAGGAGCGCCCTGCTCCAGGCGCCCGGGGGCG 540
DB 481 GCGGCCACACAGATGGGGCTCAGAGAGGAGCGCCCTGCTCCAGGCGCCCGGGGGCG 540
QY 541 CACAGGACCTGAGGGTCAACTTTGTGGAGGAGTGGCGGTGGAGGCGCCCAAGGCGCTGCC 600
DB 541 CACAGGACCTGAGGGTCAACTTTGTGGAGGAGTGGCGGTGGAGGCGCCCAAGGCGCTGCC 600
QY 601 CTAGAGCGCTGCTGAGAGGCGTCCCGCGCTTCTCATTTGCGAGCTTCAGGAGGCTG 660
DB 601 CTAGAGCGCTGCTGAGAGGCGTCCCGCGCTTCTCATTTGCGAGCTTCAGGAGGCTG 660
QY 661 GAGCAGCGCTGAGACACCCCGTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
DB 661 GAGCAGCGCTGAGACACCCCGTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 721 TCTTACTGGGTGAGCAGATCGGACGAGATCGGACGAGGAGGAGGAGGAGGAGGAGGAG 780
DB 721 TCTTACTGGGTGAGCAGATCGGACGAGATCGGACGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 CAGCTCTTCCGTTCTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB 781 CAGCTCTTCCGTTCTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 CAGCAGAGCAGGAGCTGAGGAGTCTCGGGGAGACAGAGCGGTTCTGAGCAGGAGGAG 900
DB 841 CAGCAGAGCAGGAGCTGAGGAGTCTCGGGGAGACAGAGCGGTTCTGAGCAGGAGGAG 900
QY 901 CTAGGCGGGTCTGAGCTGCTGCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
DB 901 CTAGGCGGGTCTGAGCTGCTGCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 961 GTGTACTGGCTGAAACAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
DB 961 GTGTACTGGCTGAAACAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
QY 1021 GCTGCTGCTGTGGAGACCTGCGCCCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
DB 1021 GCTGCTGCTGTGGAGACCTGCGCCCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1081 GAGGAGGAGGAGTGAAGTGGCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
DB 1081 GAGGAGGAGGAGTGAAGTGGCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140

QY 1141 ATCCGACCAACCGCTTCAAGGCGAGCTTCAAGGCGATCGTGATCGCTACGCGTGGCG 1200
DB 1141 ATCCGACCAACCGCTTCAAGGCGAGCTTCAAGGCGATCGTGATCGCTACGCGTGGCG 1200
QY 1201 CGCTACCAAGGAGTCAACCGCTTCAACCATCATCATCATCATCATCATCATCATCAT 1260
DB 1201 CGCTACCAAGGAGTCAACCGCTTCAACCATCATCATCATCATCATCATCATCATCAT 1260
QY 1261 GTGATGTTGGGGATGTGGGCAAGGCTGTCTCTTTCCTTTCCTTTCCTTTCCTTTCCT 1320
DB 1261 GTGATGTTGGGGATGTGGGCAAGGCTGTCTCTTTCCTTTCCTTTCCTTTCCTTTCCT 1320
QY 1321 CTTGCGGAGAACCGAGCGCTGTGAAGCGCGGAGAGAGATCTGGCAGACTTCTTC 1380
DB 1321 CTTGCGGAGAACCGAGCGCTGTGAAGCGCGGAGAGAGATCTGGCAGACTTCTTC 1380
QY 1381 AGGGCGCGCTACT 1440
DB 1381 AGGGCGCGCTACT 1440
QY 1441 AACGAGTGTTCAGTGGGCGCACAGATCTTCCCTCGGGCTGGAGTGTGGCGCGCATG 1500
DB 1441 AACGAGTGTTCAGTGGGCGCACAGATCTTCCCTCGGGCTGGAGTGTGGCGCGCATG 1500
QY 1501 GCCAACCAAGTGTGGGCTGTGAGTGTGATCTTCTGGGCGCACAGATCTTCCCTCGGG 1560
DB 1501 GCCAACCAAGTGTGGGCTGTGAGTGTGATCTTCTGGGCGCACAGATCTTCCCTCGGG 1560
QY 1561 CCAACAGTCAAGGCTGTCTCTCTGGGAGGCTTACCCCTTTGGCATCGATCTTATTTGGAG 1620
DB 1561 CCAACAGTCAAGGCTGTCTCTGGGAGGCTTACCCCTTTGGCATCGATCTTATTTGGAG 1620
QY 1621 CTGGCTGGCAACCACTGAGCTTCTCAATCTCTTCAAGATGAAGATGTCCGTCTCTG 1680
DB 1621 CTGGCTGGCAACCACTGAGCTTCTCAATCTCTTCAAGATGAAGATGTCCGTCTCTG 1680
QY 1681 GCGCTGCTGACATGGGCTTTGGGCTGTCTCGAGTCTTCAACAGTGCACCTTGGC 1740
DB 1681 GCGCTGCTGACATGGGCTTTGGGCTGTCTCGAGTCTTCAACAGTGCACCTTGGC 1740
QY 1741 CAGAGGCAACCGCTGCTCTGAGAGCGCTCGGAGCTCACCTTCTCTCTCTCTCTCTCTCT 1800
DB 1741 CAGAGGCAACCGCTGCTCTGAGAGCGCTCGGAGCTCACCTTCTCTCTCTCTCTCTCTCT 1800
QY 1801 GGTACTCTGCTTCTCTAGTCTCTCAAGTGGCTGTGTGTCTGGCTGCGAGGCGCGC 1860
DB 1801 GGTACTCTGCTTCTCTAGTCTCTCAAGTGGCTGTGTGTCTGGCTGCGAGGCGCGC 1860
QY 1861 TCGCCAGACCTCTCATCTTCAATCAACATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920
DB 1861 TCGCCAGACCTCTCATCTTCAATCAACATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920
QY 1921 AGGTGCTCTACCCCGGAGGAGTGTTCAGAGGCAAGCTGTGTGTGTGTGTGTGTGTGTGT 1980
DB 1921 AGGTGCTCTACCCCGGAGGAGTGTTCAGAGGCAAGCTGTGTGTGTGTGTGTGTGTGTGT 1980
QY 1981 ATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
DB 1981 ATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
QY 2041 CTTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
DB 2041 CTTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
QY 2101 GACGATCTGTGAATGGCTGGAGTCTCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
DB 2101 GACGATCTGTGAATGGCTGGAGTCTCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
QY 2161 GAG 2220
DB 2161 GAG 2220
QY 2221 TTCTGCTGGGCTGCTGCTCTCAACACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2280

1381 GCAGAACGAGATCTGGCAGACTTTCTTCAAGGGCCGCTACCTGCTCTCTTATGGCCT 1440
1413 GTTCTCCATCTACACGGCTTCTCATCTACAAAGAGTGTCTTCACTGCGGCCACACGATCTT 1472
1441 GTTCTCCATCTACACGGCTTCTCATCTACAAAGAGTGTCTTCACTGCGGCCACACGATCTT 1500
1473 CCCTCGGCTGAGTGTGGCCGATGCGCCATGCGCAACAGTCTGGCTGGAGTGATGCAATCCT 1532
1501 CCCTCGGCTGAGTGTGGCCGATGCGCCATGCGCAACAGTCTGGCTGGAGTGATGCAATCCT 1560
1533 GCGCCAGCACAAGATCTTACCTGGATCCCAACGTCACCGGTGTCTTCTCGGACCTTA 1592
1561 GCGCCAGCACAAGATCTTACCTGGATCCCAACGTCACCGGTGTCTTCTCGGACCTTA 1620
1593 CCGCTTGGCATGATCTTATTTGGAGCTTGGCTGCCAACCCTTGGAGCTTCTCACTC 1652
1621 CCGCTTGGCATGATCTTATTTGGAGCTTGGCTGCCAACCCTTGGAGCTTCTCACTC 1680
1653 CTTCAAGATGAAGATGTCGTCATCTGGGCGTCTGTGCAATGGCCCTTTGGGTGTCTCT 1712
1681 CTTCAAGATGAAGATGTCGTCATCTGGGCGTCTGTGCAATGGCCCTTTGGGTGTCTCT 1740
1713 CGAGTCTTCAACCAAGTCTTGGCCAGAGGCAACCGCTGTCTGGAGACGCTGCC 1772
1741 CGAGTCTTCAACCAAGTCTTGGCCAGAGGCAACCGCTGTCTGGAGACGCTGCC 1800
1773 GAGTCTCACTTCTGCTGGATCTTCTGGTTACCTGCTGTCTTCTAGTATCTACAGTG 1832
1801 GAGTCTCACTTCTGCTGGATCTTCTGGTTACCTGCTGTCTTCTAGTATCTACAGTG 1860
1833 GCTGTGTCTGGCTGTCAGAGCGCGCTCG--CCAGCATCTCTCATCTCATCA 1889
1861 GCTGTGTCTGGCTGTCAGAGCGCGCTCGCGCCCGCCAGCATCTCTCATCTCATCA 1920
1890 CATGTTCTCTTCTCCACAGCCCCAGAAAGGCTCTTACCCCGGACGAGGTGT 1949
1921 CATGTTCTCTTCTCCACAGCCCCAGAAAGGCTCTTACCCCGGACGAGGTGT 1980
1950 CAGGCGACGCTGTGTCTTCTGGCTTGGCCATGTGTCCTCTGCTGTGGCCAC 2009
1981 CAGGCGACGCTGTGTCTTCTGGCTTGGCCATGTGTCCTCTGCTGTGGCCAC 2040
2010 CTGCACTGTCTGACCGCGCACCGCGCTGTGGAGGAGCGCGCTGACCGACGAG 2069
2041 CTGCACTGTCTGACCGCGCACCGCGCTGTGGAGGAGCGCGCTGACCGACGAG 2100
2070 GGAACAAAGGCGGCTTCTGACCTGTCTGACGATCTGTGAATGGCTGGAGCTCGA 2129
2101 GGAACAAAGGCGGCTTCTGACCTGTCTGACGATCTGTGAATGGCTGGAGCTCGA 2160
2130 TGAGGAAAGGAGGCGGCTTCTGATGATGAAGAGGCGAGCTGTCTCCCTCGAGGT 2189
2161 TGAGGAAAGGAGGCGGCTTCTGATGATGAAGAGGCGAGCTGTCTCCCTCGAGGT 2220
2190 GCTCATGACACAGGCGATCCACACCTGAGTTCTGCTGGCTGTCTCCACACCG 2249
2221 GCTCATGACACAGGCGATCCACACCTGAGTTCTGCTGGCTGTCTCCACACCG 2280
2250 CTCTCATGCGCTGTGGGCTTCTGAGCTGTGCGCCACGCTGTCTCGAGGTTCTGTG 2309
2281 CTCTCATGCGCTGTGGGCTTCTGAGCTGTGCGCCACGCTGTCTCGAGGTTCTGTG 2340
2310 GGCATGATGATGCGCATAGGCTTGGCTTGGCGGAGGAGTGGGCTGGCTGTGT 2369
2341 GGCATGATGATGCGCATAGGCTTGGCTTGGCGGAGGAGTGGGCTGGCTGTGT 2400
2370 GCTGTCTCCCATCTTGTGCGCTTGTGCGTGTATGACCGGTGTCTCTCTGATGA 2429
2401 GCTGTCTCCCATCTTGTGCGCTTGTGCGTGTATGACCGGTGTCTCTCTGATGA 2460
2430 GGCATCTCAGGCTTCTGCAAGCGCTGTGCGCTGTGCACTGGGTGGAATTCAGAA 2489

2461 GGGACTCTCAGCTTCTGACGCGCTGCGCTGCACTGGGTGGAATTCAGAA 2520
2490 CTACTCAGCAGCGGCTACAGCTGAGTCCCTTCACTTCTGCTGCCACAGATGACTAGGG 2549
2521 CTACTCAGCAGCGGCTACAGCTGAGTCCCTTCACTTCTGCTGCCACAGATGACTAGGG 2580
2550 CCCTCTGAGGCTCTGCGCAGACCTCTTCTGCACTCTGAGGACGAGAGGAATAAGAC 2609
2581 CCCTCTGAGGCTCTGCGCAGACCTCTTCTGCACTCTGAGGACGAGAGGAATAAGAC 2640
2610 GGTCCGCGCTGGCA 2623
2641 GGTCCGCGCTGGCA 2654

RESULT 7

US-09-949-016-2405
; Sequence 2405, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2405
; LENGTH: 2654
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2405

Query Match 97.7%; Score 2580; DB 3; Length 2654;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2585; Conservative 0; Mismatches 6; Indels 3; Gaps 1;
QY 33 GCGCGCGCAGCACACCGCGGACCATGGGCTCCATGTTCGAGGAGGAGGTGGCCCT 92
DB 61 GCGCGCGCAGCACACCGCGGACCATGGGCTCCATGTTCGAGGAGGAGGTGGCCCT 120
QY 93 GGTCCAGCTCTTTCTGCCCAACAGCGGCTGTACACCTGCGTGAGTGGGCTGGGAGCT 152
DB 121 GGTCCAGCTCTTTCTGCCCAACAGCGGCTGTACACCTGCGTGAGTGGGCTGGGAGCT 180
QY 153 GGGCTCTGTGGAGTTTCAAGACCTCAACGCTCTCGTGAGCGCTTCCAGAGACGCTTTGT 212
DB 181 GGGCTCTGTGGAGTTTCAAGACCTCAACGCTCTCGTGAGCGCTTCCAGAGACGCTTTGT 240
QY 213 GGTTCATGTTTGGCGCTGTGAGGAGCTGAGAGACCTTCACTTCTCTGACAGAGAGT 272
DB 241 GGTTCATGTTTGGCGCTGTGAGGAGCTGAGAGACCTTCACTTCTCTGACAGAGAGT 300
QY 273 GCGGCGGCTGGGCTGTCTTCCCGCCGCGGAGGCTGCGGACACCCCGCCCG 332
DB 301 GCGGCGGCTGGGCTGTCTTCCCGCCGCGGAGGCTGCGGACACCCCGCCCG 360
QY 333 GGAACCTGTGCGCATCCAGAGAGAGAGAGCGCTGCGCCAGAGAGCTGCGGATGTGG 392
DB 361 GGAACCTGTGCGCATCCAGAGAGAGAGAGCGCTGCGCCAGAGAGCTGCGGATGTGG 420
QY 393 GGGCAACCAAGAGGCTTGGGCGGCTGTGACAGCTGACAGCTTCCAGCGCGCTGTCT 452
DB 421 GGGCAACCAAGAGGCTTGGGCGGCTGTGACAGCTGACAGCTTCCAGCGCGCTGTCT 480
QY 453 AGCCAGGCGCATGAACCTTCAGCTGGCAGCGCGCCCAACAGATGGGCGCTCAGAGAGGAC 512

RESULT 8

US-09-949-016-2975
; Sequence 2975, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2975
; LENGTH: 2706
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2975

Query Match 96.7%; Score 2553.4; DB 3; Length 2706;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2573; Conservative 0; Mismatches 11; Indels 3; Gaps 1;
QY 40 GCAGCACACCCGGGACCATGGCTCCATGTTCCGGAGCGAGGAGTGGCCCTGGTCCAG 99
DB 120 GGAGCCAGCCACAGGACCATGGCTCCATGTTCCGGAGCGAGGAGTGGCCCTGGTCCAG 179
QY 100 CTCCTTTGCCCCACAGCGCTGCTTACCTCGCTGAGTCGCTGGGAGTGGGCCCTC 159
DB 180 CTCCTTTGCCCCACAGCGCTGCTTACCTCGCTGAGTCGCTGGGAGTGGGCCCTC 239
QY 160 GTGGAGTTTCAGAGACTCAACGCTCGGTGAGCGCTTCCAGAGAGCTTGTGTTGAT 219
DB 240 GTGGAGTTTCAGAGACTCAACGCTCGGTGAGCGCTTCCAGAGAGCTTGTGTTGAT 299
QY 220 GTTTGGCGCTGTGAGGAGCTGAGAGAGACTTTCACCTTCCAGAGGAGGAGTGGCGGG 279
DB 300 GTTTCGGCGCTGTGAGGAGCTGAGAGAGACTTTCACCTTCCAGAGGAGGAGTGGCGGG 359
QY 280 GCTGGGCTGGTCTGCCCCCGCCAAAGGGGAGGCTGCGGACACCCCAACCCCGGGA 339
DB 360 GCTGGGCTGGTCTGCCCCCGCCAAAGGGGAGGCTGCGGACACCCCAACCCCGGGA 419
QY 340 CTGCGCATCCAGAGGAGAGCGAGCGCTGCGGCCAGGAGCTCGGGGATGTGGGGGCAAC 399
DB 420 CTGCGCATCCAGAGGAGAGCGAGCGCTGCGGCCAGGAGCTCGGGGATGTGGGGGCAAC 479
QY 400 CAGCAGGCGCTGCGGGCCAGCTGCACCAAGCTGCGAGCTCCAGCGCGCGCTGTACGCCAG 459
DB 480 CAGCAGGCGCTGCGGGCCAGCTGCACCAAGCTGCGAGCTCCAGCGCGCGCTGTACGCCAG 539
QY 460 GGCATGAACTCAGCTGGCAGCGCGCCACACAGATGGGGCTCAGAGAGAGCGCCCTG 519
DB 540 GGCATGAACTCAGCTGGCAGCGCGCCACACAGATGGGGCTCAGAGAGAGCGCCCTG 599
QY 520 CTCACAGGCGCGGGGGCGCCACAGGAGCTGAGGCTCACTTGTGGCAGGTGCGGTG 579
DB 600 CTCACAGGCGCGGGGGCGCCACAGGAGCTGAGGCTCACTTGTGGCAGGTGCGGTG 659
QY 580 GAGCCCCACAGGCGCCCTGAGAGCGCTGCTCTGAGGAGCGCTGCGCGGCTTCTC 639
DB 660 GAGCCCCACAGGCGCCCTGAGAGCGCTGCTCTGAGGAGCGCTGCGCGGCTTCTC 719
QY 640 ATTGCCAGCTTACGGAGCTGAGAGAGCGCGCTGAGAGAGCGCGCTGAGCGGCGAGCAGCG 699

DB 720 ATTGCCAGCTTACGGAGCTGAGAGAGCGCGCTGAGAGACCCCGTGACGGGCGAGCAGCG 779
QY 700 ACGTGGATGACCTTCTCTCATCTCTACTGGGGTGGAGAGATCGGACAGAGATCCGCAAG 759
DB 780 ACGTGGATGACCTTCTCTCATCTCTACTGGGGTGGAGAGATCGGACAGAGATCCGCAAG 839
QY 760 ATCAGGAGTCTTCTCACTGCGACGCTCTTCCGCTTCTGACAGCAGGAGAGGAGCCGCGCTC 819
DB 840 ATCAGGAGTCTTCTCACTGCGACGCTCTTCCGCTTCTGACAGCAGGAGAGGAGCCGCGCTC 899
QY 820 GGGGCGCTTGCAGCAGCTGCAACAGCAGAGCAGGAGCTGACAGAGGTCCTCGGGAGACA 879
DB 900 GGGGCGCTTGCAGCAGCTGCAACAGCAGAGCAGGAGCTGACAGAGGTCCTCGGGAGACA 959
QY 880 GAGCGGTTCTGAGCAGGCTGCTAGGCGGGTGTGACAGCTGCTGCGCCAGGCGAGGTG 939
DB 960 GAGCGGTTCTGAGCAGGCTGCTAGGCGGGTGTGACAGCTGCTGCGCCAGGCGAGGTG 1019
QY 940 CAGGTCCACAAAGATGAAGGCGGTGACCTGGCCCTGAACACCAAGTCAGGCTGAGACCAAG 999
DB 1020 CAGGTCCACAAAGATGAAGGCGGTGACCTGGCCCTGAACACCAAGTCAGGCTGAGACCAAG 1079
QY 1000 CACAAAGTCTCATTTGCCGAGGCTGTGCTGTGTCAGAGACTGCGCGCCCTGACGAGAG 1059
DB 1080 CACAAAGTCTCATTTGCCGAGGCTGTGCTGTGTCAGAGACTGCGCGCCCTGACGAGAG 1139
QY 1060 GCCCTGCGGGACAGCTCGATGGAGGAGGAGTGTGAGTGGCGCTGACCGCATCCCGCTG 1119
DB 1140 GCCCTGCGGGACAGCTCGATGGAGGAGGAGTGTGAGTGGCGCTGACCGCATCCCGCTG 1199
QY 1120 CGGACATGCCCCCACCACACTCATCCGACCAACCGCTTCAAGCGCCAGCTTCCAGGGCATC 1179
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QY 1897 CTCTTCTCCACAGCCCCAGCAACAGGCTGCTTACCCCGGCGAGGAGTGTTCAGGGCC 1956
Db 1980 CTCTTCTCCACAGCCCCAGCAACAGGCTGCTTACCCCGGCGAGGAGTGTTCAGGGCC 2039
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QY 1957 ACGTGTGTGCTCTGGCCTTGGCCATGTGTGCCCATCTCTGCTTGGGACACCCCTGCAC 2016
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Db 2100 TTGTGTCAACCGCACCGCCGCTTGGAGAGGAGCCGCTGACCGACAGGAGGAAAC 2159
QY 2077 AAGGCGGGTTGCTGTGACCTGTGATCGCATCTGTGAATGGCTGAGCTCCGATGAGAA 2136
Db 2160 AAGGCGGGTTGCTGTGACCTGTGATCGCATCTGTGAATGGCTGAGCTCCGATGAGAA 2219
QY 2137 AAGGCGAGGGGCTGATGATGAAGAGGAGGCGGAGCTGCTCCCTCGAGGTGCTCATG 2196
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QY 2197 CACAGGGCCATCCACACCATCGAGTTCTGCTTGGGCTGCGTCTCACAACCGCCTCTTAC 2256
Db 2280 CACAGGGCCATCCACACCATCGAGTTCTGCTTGGGCTGCGTCTCACAACCGCCTCTTAC 2339
QY 2257 CTGCGCTGTGTGGCCCTGAGCCTGCGCCACCGCCACAGCTGTGCGAGGTTCTGTGGCCATG 2316
Db 2340 CTGCGCTGTGTGGCCCTGAGCCTGCGCCACCGCCACAGCTGTGCGAGGTTCTGTGGCCATG 2399
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Db 2580 GGCACGGGCTACAAGCTGAGTCCCTTCACTTCTGCTGCGCACAGATGACTAGGGCCCACTG 2639
QY 2557 CAGGTCTGTGCGACAGCTCTTCTGATCTTGTGAGGCAAGAGGAGTAAGACGCTCCGC 2616
Db 2640 CAGGTCTGTGCGACAGCTCTTCTGATCTTGTGAGGCAAGAGGAGTAAGACGCTCCGC 2699
QY 2617 CCGTGGCA 2623
Db 2700 CCGTGGCA 2706
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RESULT 10

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US-09-949-016-1330
; Sequence 1330, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1330
; LENGTH: 2457
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1330
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Query Match				77.7%; Score 2051; DB 3; Length 2457;			
Best Local Similarity				98.0%; Pred. No. 0;			
Matches 2088; Conservative				0; Mismatches 40; Indels 3; Gaps 1;			
QY	496	GGGGCTTCAGAGGACGCGCCCTGCTCCAGGCCCCCGGGGGCGCGACACAGGACCTGAGG	555	1516	TTGAGTGTATGATTCCTTGGGCCGAGCACGATGCTTACCTTGGATCCCAAGCTCACCGGT	1575	
DB	327	GGGGGCTGTGGGGGAGGAGGGGAGGAGGTGGAGCAGCCCTGCCACGCCGCTGGCC	386	1347	TTGAGTGTATGATTCCTTGGGCCGAGCACGATGCTTACCTTGGATCCCAAGCTCACCGGT	1406	
QY	556	GTCAACTTTGTGAGGTGCGGTGGAGCCCAAGGCCCTGCGCTAGAGCGCTGCTC	615	1576	GTCTTCTGAGGACCTTACCCCTTTGGCATCGATCTTATTTTGGAGCTTGGCTGCCAACAC	1635	
DB	387	GCCAGCTTTGTGAGGTGCGGTGGAGCCCAAGGCCCTGCGCTAGAGCGCTGCTC	446	1407	GTCTTCTGAGGACCTTACCCCTTTGGCATCGATCTTATTTTGGAGCTTGGCTGCCAACAC	1466	
QY	616	TTGAGGGCTTGC CGCGCTTCTCATTTGCCAGCTTCAGGAGCTTGGAGCAGCGCTGGAG	675	1636	TTGAGCTTCTCAACTCTCTTCAAGATGTAAGATGTCCGTTCATCTTGGGCGCTGTGCAATG	1695	
DB	447	TTGAGGGCTTGC CGCGCTTCTCATTTGCCAGCTTCAGGAGCTTGGAGCAGCGCTGGAG	506	1467	TTGAGCTTCTCAACTCTCTTCAAGATGTAAGATGTCCGTTCATCTTGGGCGCTGTGCAATG	1526	
QY	676	CACCCGCTGACGGGCGAGCCAGCACGCTGATGACCTTCTCTCATCTCTACTTGGGGTGAG	735	1696	GCCTTTGGGGTGTCTCTGGAGTCTTCAACCAAGTGCACCTTTGGCCAGAGGACCGCGCTG	1755	
DB	507	CACCCGCTGACGGGCGAGCCAGCACGCTGATGACCTTCTCTCATCTCTACTTGGGGTGAG	566	1527	GCCTTTGGGGTGTCTCTGGAGTCTTCAACCAAGTGCACCTTTGGCCAGAGGACCGCGCTG	1586	
QY	736	CAGATCGGACAGAGATTCGCAAGATCA CGGACTGTCTTCCACTGCCACGCTTCCCGTTT	795	1756	CTCTGAGAGACGCTGCGGAGCTCACCTTCTCTGCTGGGACTTTCGGTTCACCTGCTGTTTC	1815	
DB	567	CAGATCGGACAGAGATTCGCAAGATCA CGGACTGTCTTCCACTGCCACGCTTCCCGTTT	626	1587	CTCTGAGAGACGCTGCGGAGCTCACCTTCTCTGCTGGGACTTTCGGTTCACCTGCTGTTTC	1646	
QY	796	CTGACGAGGAGGCGCGCTCGGGCCCTGCGAGCTGCAAGAGTGCACAGCAGCAGGAG	855	1816	CTAGTCAATTAAGTGGCTGTGTCTTGGGCTGCGAGGGCCGCTTCG---CCAGCATC	1872	
DB	627	CTGACGAGGAGGCGCGCTCGGGCCCTGCGAGCTGCAAGAGTGCACAGCAGCAGGAG	686	1647	CTAGTCAATTAAGTGGCTGTGTCTTGGGCTGCGAGGGCCGCTTCGGCCCGCAGCATC	1706	
QY	856	CTGACGAGGCTCTCGGGGAGACAGACGCGGTTCTGAGCCAGGTGCTTAGGCCGGGTCTG	915	1873	CTCATCACTTCACTCAACATGTTCTTCTTCCACAGCCCCAGCAACAGGCTGCTCTAC	1932	
DB	687	CTGACGAGGCTCTCGGGGAGACAGACGCGGTTCTGAGCCAGGTGCTTAGGCCGGGTCTG	746	1707	CTCATCACTTCACTCAACATGTTCTTCTTCCACAGCCCCAGCAACAGGCTGCTCTAC	1766	
QY	916	CAGCTGCTGCCCGCAGGCGAGTGCAGGTCCACAAGATGAAGCCGCTGTACCTTGGCCCTG	975	1933	CCCCGGCAGAGGTGCTCAGGCGCAGCTGCTGGTCTCTGCTTGGCCATGCTGGCCCATC	1992	
DB	747	CAGCTGCTGCCCGCAGGCGAGTGCAGGTCCACAAGATGAAGCCGCTGTACCTTGGCCCTG	806	1767	CCCCGGCAGAGGTGCTCAGGCGCAGCTGCTGGTCTCTGCTTGGCCATGCTGGCCCATC	1826	
QY	976	AACCACTGACGTGAGCACCA CGCAAGTGTCTCATTTGCCAGGCGCTGCTCTGTG	1035	1993	CTGCTCTTGGCACACCCCTTGCACTGCTGCAACCGCCACCGCCCGCTTGCAGAGGAGG	2052	
DB	807	AACCACTGACGTGAGCACCA CGCAAGTGTCTCATTTGCCAGGCGCTGCTCTGTG	866	1827	CTGCTCTTGGCACACCCCTTGCACTGCTGCAACCGCCACCGCCCGCTTGCAGAGGAGG	1886	
QY	1036	CGAGACTGCGCCCTGAGGAGGCGCTCGGGACAGCTCGATGGAGGAGGAGTGAGT	1095	2053	CCGCTGACCGCAGAGGAGGAGGAGGCGGCTTCTGCAACCTGCTGCAAGCATCTGTG	2112	
DB	867	CGAGACTGCGCCCTGAGGAGGCGCTCGGGACAGCTCGATGGAGGAGGAGTGAGT	926	1887	CCGCTGACCGCAGAGGAGGAGGAGGCGGCTTCTGCAACCTGCTGCAAGCATCTGTG	1946	
QY	1096	GCGGTGGCTCACCGCATCCCTGCGGGACATGCCCCCACAACCTATCCGACCAACCGC	1155	2113	AATGGCTGGAGCTCCGATGAGGAGGAGGAGGCGGCTCGATGATGAAGAGGAGGCGCAG	2172	
DB	927	GCGGTGGCTCACCGCATCCCTGCGGGACATGCCCCCACAACCTATCCGACCAACCGC	986	1947	AATGGCTGGAGCTCCGATGAGGAGGAGGAGGCGGCTCGATGATGAAGAGGAGGCGCAG	2006	
QY	1156	TTACCGGCGAGCTTCAGGGGATCGTGATCGCTACGGGCGGCGCTTACAGGAGGTC	1215	2173	CTGCTCCCTTCCAGAGTGTCTATGCAACAGGCGCATCCACCATCGAGTTCTGCTGGGC	2232	
DB	987	TTACCGGCGAGCTTCAGGGGATCGTGATCGCTACGGGCGGCGCTTACAGGAGGTC	1046	2007	CTGCTCCCTTCCAGAGTGTCTATGCAACAGGCGCATCCACCATCGAGTTCTGCTGGGC	2066	
QY	1216	AACCCGCTCCCTACACCATCATCTTCCCTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG	1275	2233	TGCGTCTCCAAACCGGCTTCTACCTTGGGCTGTGGGCGCTTGGGCGGCGGCGCAG	2292	
DB	1047	AACCCGCTCCCTACACCATCATCTTCCCTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG	1106	2067	TGCGTCTCCAAACCGGCTTCTACCTTGGGCTGTGGGCGCTTGGGCGGCGGCGCAG	2126	
QY	1276	GTGGGCGACGGGCTGTCTGTTCTCTTCTGCGCCCTGCGCATGTTCTTGGGAGAACCGA	1335	2293	CTGTCCGAGGCTTCTGTGGGCGATGTCGATAGGCGCTTGGGCGCTTGGGCGGAGGTC	2352	
DB	1107	GTGGGCGACGGGCTGTCTGTTCTCTTCTGCGCCCTGCGCATGTTCTTGGGAGAACCGA	1166	2127	CTGTCCGAGGCTTCTGTGGGCGATGTCGATAGGCGCTTGGGCGCTTGGGCGGAGGTC	2186	
QY	1336	CGGGCTGTGAAGCGCGGAGAGAGATCTGAGACTTTCTTCAAGGCGCGCTTACCTG	1395	2353	GGCGTGGCGGCTGTGTGTGTCCTTCTTGGCGGCTTTCGCGTGTATGACCTGGCT	2412	
DB	1167	CGGGCTGTGAAGCGCGGAGAGAGATCTGAGACTTTCTTCAAGGCGCGCTTACCTG	1226	2187	GGCGTGGCGGCTGTGTGTGTCCTTCTTGGCGGCTTTCGCGTGTATGACCTGGCT	2246	
QY	1396	CTCTCTCTTATGGGCTGTCTTCTTCTTCAACCGGCTTCTTCAACAGAGTCTTCACT	1455	2413	ATCTCTCTGTGTATGAGGAGCTTCTCAGCTTCTTCTGCAAGGCTTGGGCTGTGCTG	2472	
DB	1227	CTCTCTCTTATGGGCTGTCTTCTTCTTCAACCGGCTTCTTCAACAGAGTCTTCACT	1286	2247	ATCTCTCTGTGTATGAGGAGCTTCTCAGCTTCTTCTGCAAGGCTTGGGCTGTGCTG	2306	
QY	1456	CGCGCCACAGCATCTTCCCTCGGGGCTGGAGTGTGGCGCCCATGGCCACACAGTCTG	1515	2473	GAATTCAGAAAGTTCCTACTCAGGACCGGGCTTCAAGCTGTAGTCCCTTCACTTCGCT	2532	
DB	1287	CGCGCCACAGCATCTTCCCTCGGGGCTGGAGTGTGGCGCCCATGGCCACACAGTCTG	1346	2307	GAATTCAGAAAGTTCCTACTCAGGACCGGGCTTCAAGCTGTAGTCCCTTCACTTCGCT	2366	
				2533	GCCACAGATGACTAGGGCCCATGCGAGGCTCTGCCAGACCTCTTCTGACCTCTGAGGC	2592	
				2367	GCCACAGATGACTAGGGCCCATGCGAGGCTCTGCCAGACCTCTTCTGACCTCTGAGGC	2426	
				2593	AGGAGGAGGAATAAAGACGGTCCGCCCTGGCA	2623	

Qy	820	GGGGCCCTGCAGCAGCTCCAAACAGCAGACCGCAGAGGCTCTCGGGGAGACA	879
Db	781	GAGATTCAGGAGGGGCTCAATACTCGGATCCAAGACCTTTACACGGTGTCTGCACAAACG	840
Qy	880	GAGCGGTTCTGAGCCAGGTGCTAGGCCGGGTGTGCAGCTCTGCCCGCAGAGGCGAGTG	939
Db	841	GAGGACTATCTCGCGCAAGTGTCTGCAAACTGCCGAGTCCGTGTGCGACCGTGTGGTC	900
Qy	940	CAGGTCCAAGATGAAGCCCGTGTACTGTGCCCTCTGAACCAAGTGCAGCTGCAGCACCAG	999
Db	901	CAGGTGAGGAAGATGAAGGCCCATCTTACCACATGTCTCAACATGTGCAGCTTTGACGTCA	960
Qy	1000	CACAAGTGCCTCATTTGCCGAGCCCTGGTCTCTGTGTGAGACCTTCCCGCCCTCGCAGAG	1059
Db	961	AACAAGTGCCTCATAGCTGAGGTCTGTGTGCCCGAGGTGGACCTGCCAGGGCTTGCAGAG	1020
Qy	1060	GCCCTGCGGGACAGCTCGATCGAGGAGGGAG-----TGAGTGCCTGTGGCTCACCGCATC	1113
Db	1021	GCACTGGAGGAAGGCTCGAGAGAGAGCGGAGCTACATCCCTCGTTTCATGAACACATC	1080
Qy	1114	CCCTGCCGGGACATGCCCCCCACACTCATCTCGCAACCAACCGCTTCAAGGCGAGTTCCAG	1173
Db	1081	CCTACGAAGAAGAACACCCCCACTCTGATCCGCAACCAAAATCTACTGAAGGTTTCCAG	1140
Qy	1174	GGCATCTGGATCGCTACGGCGTGGCGCGCTTACAGGAGGTCAACCCGGCTTCCCTACACC	1233
Db	1141	AACATCGTGGATGCTATGGAGTGGGAGCTTACAGAGGTGAACCCAGCTCTCTTTACC	1200
Qy	1234	ATCATCACCTTCCCCTTCTGTTTGTGTGATGTTTCGGGGATGTGGGCAACGGCTGCTC	1293
Db	1201	ATCATCACCTTCCCGTTCCTGTTTGTGTGATGTTTGGGACTTGGGCAACGGCTTGTCTC	1260
Qy	1294	ATGTTCTCTTTCGCCCTGGCCGATGGTCTTTCGGGAGAACCGACCGGCTGTGAAGCCGCG	1353
Db	1261	ATGTTCTCTGTTTGGCCCTTACTTGGTGTAAATGAGAAATCACCCAGACTAAGCCAGTCA	1320
Qy	1354	CAGAAACGAGATCTGGCAGACTTTCCTCAGGGGCGCTACCTGCTCTCTGCTTATGGGCTG	1413
Db	1321	CAG---GAGATCTTTAGATGTTCTTTGACGGCCGGTATATCTCTGCTGTGTATGGGCTG	1377
Qy	1414	TTCTCCCATCTACCCGGCTTCATCTACAAACAGTGTCTTCAGTTCGGCGCACACAGCATCTC	1473
Db	1378	TTCTCTGTGTACACGGGCTCATCTACACGACTGCTTCTCCAAGTCTGTGTAACCTCTTT	1437
Qy	1474	CCCTCGGGCTGAGTGTGGCCGATGGCCGATGGCCAAACAGTCTGGC-----1515	1515
Db	1438	GGTTCTGGGTGGAAACGTAATGTGCCATGTACAGCTCCAGCCACTCTCCAGGAGGACAGAG	1497
Qy	1516	-----TGAGTGTATGCATTCTCTGGCCACGACACGATCTTACCTTGGATCCC	1563
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Qy	1564	AACGTCAACCGGTGTCTTCTCTGGGACCTTACCCCTTTTGGGATCGATCTCTATTTGGAGCTG	1623
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Qy	1624	GCTGCCAAACCATTTGAGGTTCTCTCACTCTTCAAGATGAAGATGTCCTGATCTCTGGCG	1683
Db	1618	GCCACAAACCGCCTCACGTTCTCTCACTCTTCAAGATGAATAATGTCTGTGATTTAGGA	1677
Qy	1684	GTGTGCACATGGCTTTTGGGGTGGTCTCTCGGAGTCTTCAACCAACGTCACCTTTGGCCAG	1743
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Db	1738	AAGTTCAACGCTTACCTTGGTCTCGGTGCTCGAGATCTGTTTCAATGCTCTGCATCTTTGGG	1797
Qy	1804	TACCTCGTGTCTTAGTCATCTACAAGTGGGTGTGTGTCTGGGCTG---CGAGGCGCCG	1860
Db	1798	TACCTGATTTTCAATGATCATTTTACAAGTGGCTGGCATCTCTGGCAGAGACTCTCGAGAG	1857

	Qy	1861	TGCCCCAGCATCTTCATCCACTTCAACAACATGTTCTCTTCCCACAGGCCCGCAGAAC	1920
	Db	1858	GCCCCGAGCATCTCTGATTCGAGTTTCATTAAACATGTCTCTGTTCCCAACCAGACAGACAC	1917
	Qy	1921	AGGCTGCTCTACCCCGGACGGAGGTGGTCCAGGCCACGCCTGTGTGTCTCTGGCCTTGCGC	1980
	Db	1918	GGG---CTCTACCCAGGGCAGGCACAGCTCCAGAGAGTGTGTGTGCTCTCACGGTGTCTG	1974
	Qy	1981	ATGFTGCCCATCTCTGTCTTGGGAACCCCTTGCACTGTGTGACCGGCCAOCGCCCGCC	2040
	Db	1975	GCTGTCCCGCTGCTCTTCTTAGGAAAAGCCGCTTTTTCTGTGTGGTGTGCACAACAGCGCGC	2034
	Qy	2041	CTGG-----GAGGAGSCCGCTGACCGACAGAGGAAACAAGGCCGGTTCGTCTG	2091
	Db	2035	AATTGCTTTGGCATGAGCCGACGGTTACACTGTGAGGAGGACAGCGHGAAGAG	2094
	Qy	2092	GACCTGCTGACGCATCTGTGAATGBCTGGAGCTCCGATGAGGAAAGGACGGGGCCTG	2151
	Db	2095	GTGTCTCTTCTGGGCAACACGACATAGAAGAGGGCAAACAGCCGATGGAAGAAGCTGC	2154
	Qy	2152	GATGATCAAGAGGCGGAGCTGTCGCCCTCCGAGGTCTCATGACACGAGGCCATCCAC	2211
	Db	2155	GGAGAATGACGTGTGAGGAGTTTACTTCGGGGAGATCTGTATGACGACGAGGCATCCAC	2214
	Qy	2212	ACCATGAGTTCTCCCTGGCTCGCTCTCCAACACCGCCTCTTACTTGCGCCCTGTGGGCG	2271
	Db	2215	TCCATTGATTACTGCCTCGGCTGCATCTCCAACACCGCCTCTTACTCTGAGGCTCTGGGCA	2274
	Qy	2272	CTGAGCCTGGCCCCACGCCACGCTGTCCGAGGTTCTGTGGGCCCATGTGTATGCGCATAGC	2331
	Db	2275	CTACGCTGGCCCCATGCACAGCTCTCTGATGTGCTGTGGGCCCATGTGTATGCGGTGGGG	2334
	Qy	2332	CTGGGCTGGGCGGAGGTGGCGTGGCGGCTGTGGTGTGGTCCCATCTTTGCGCGC	2391
	Db	2335	CTG-----CGTGTGGACACCACTATGGGGTCTTGTCTGCTGCTCTCATGGCTTTC	2385
	Qy	2392	TTTGCGGTGATGACCGTGGCTATCTCTGTGTGTGATGAGGAGACTCTCAGCCTTCTGTGAC	2451
	Db	2386	TTTGCAGTTTGTGACCAATTTTATCTCTGTGGTCAITGAGGGGTCTTTCTGCATTCTCTCCAC	2445
	Qy	2452	GCCCTGGCGGTGCACCTGGGTGGAAATTCAGAACAAAGTTCTACTCAGGCAACGGCTACAAG	2511
	Db	2446	GCCATAAGGCTTCACTGGGTGAGAAATTTTCAGAACAAATTTCTACGTTGGTCGAGCCACAAG	2505
	Qy	2512	CTGAGTCCCTTCACCTTC	2529
	Db	2506	TTTGTTCCTCTCTCTTC	2523

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RESULT 14
US-09-799-451-895
; Sequence 895, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqiang
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Dmanac, Radjoje T.
; TITLE OF INVENTION: No. 6783969el

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/ TITLE OF INVENTION: Polypeptides
/ FILE REFERENCE: 803
/ CURRENT APPLICATION NUMBER: US/09/799,451
/ CURRENT FILING DATE: 2001-03-05
/ NUMBER OF SEQ ID NOS: 948
/ SOFTWARE: pt_FL_genes Version 2.0
/ SEQ ID NO 895-
/ LENGTH: 3062
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: CDS
/ LOCATION: (196)..(2715)
US-09-799-451-895

Query Match 23.4%; Score 618.6; DB 3; Length 3062;

Best Local Similarity 55.3%; Pred. No. 3.1e-103;

Matches 1410; Conservative 0; Mismatches 1099; Indels 42; Gaps 9;

QY	8	CGCGGACGGGACGACGAGCGGAGCGGCGGCGCAGCACACCCGGGACCATGGGCTCCA	67
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QY	68	TGTTCCGGAGCAGGAGGTGGCCCTGGTCCAGCTCTTTCTGCCCCACAGCGGCTGCCCTACA	127
DB	206	TGTTTCGAAGGAGGAGATGTGTTGTCACAACTGTTTCTCCAGGTGGAGCTGCATATT	265
QY	128	CTGCGGTAGTGCGCTGGGAGCTGGGCTCTGGTGGAGTTCAAGACCTCAACGCTCGG	187
DB	266	GCTGTGGCTGAGCTCGGAGAGCTCGGATGGTTGCTTCAAGATTTAAATATGAATG	325
QY	188	TGAGCGCCTTCCAGAGACCTTTGTGTTGATGTTTGGCGCTGTGAGAGCTGGAGAAGA	247
DB	326	TGAACAGCTTTCAGAGAAATTTGTGAATGAAGTCAGAAAGGTGTGAATCACTGGAGAGAA	385
QY	248	CCTTCACTTCTCTGACGAGGAGGTGCGGCGGCGCTGGGCTGGTCTGCTGCCCGCCAAAGG	307
DB	386	TCTCTCGTTTCTGGAAGACGAGAT--GCATAATGAGATTGTAGTTCAAGTTGCTCGAGA	442
QY	308	GGAGGTGCGGACACCCACCCCGGAGCTGTGTCGGCATCCAGGAGGAGAGCGAGCGCC	367
DB	443	AAAGCCCACTGACCCCGCTCCCAACGGGAAATGATTACCCCTGGAGACTGTTCTAGAAAAAC	502
QY	368	TGSCCCAGGAGCTGCGGGATGTGCGGGCAACACGACAGCCCTCGCGGCGCCAGCTGCACC	427
DB	503	TGAAGGAGAGTTACAGGAGCCACACAGAACACAGACGCGCTTGAAACAAAGCTTCTTAG	562
QY	428	AGCTGACGTCCACGCCCGCTGTCTACGCCAGGGCCATGAACCTCAGCTGGCAGCGCGCC	487
DB	563	AACTGACAGAACTGAAATACCTCTCGAAGAAACCCAGAGCTTCTTTGAGACGGAAACCA	622
QY	488	ACACAGATGGGCGCT-----CAGAGAGACGCCCTGTCTCAGGCCCCCGGGGGCCGC	541
DB	623	ATTAGCTGATGATTTCTTTACTGAGGACACTTCTGGCCCTCTGGAGTTGAAAGCAGTGCC	682
QY	542	ACCAGGACCTGAGGGTCAACTTTGTGCGAGGTGCGGTGGAGCCGCCAACAGGC-----CC	595
DB	683	CTGCATATATGACCGGAAGTTGGGTTTCATAGCCGGTGTGATCAACAGGAGAGATGG	742
QY	596	CTGCCCTAGAGCGCTGTCTGAGGGCCCTGCGCGGCTTTCCTCAATGGCAGCTTCAGGG	655
DB	743	CTTCTCTTGGCGGTACTGTGGCGAATCTGCGGAGAAACGTGTACTTTGAAGTTTCAGTG	802
QY	656	AGCTGGAGCAGCGCTGGAGCACCCCGTGACGGGCGAGCCAGCCAGCTGGATGACCTTCC	715
DB	803	AGATGGACGCCCTCTGGAGGATCTCTGTGACGGAAGAAATTCAGAAAGACATATTCA	862
QY	716	TCACTCTCTACTGGGGTGAGCAGATCGGACAGAAATCCGCAAGATCAAGACTGCTTCC	775
DB	863	TCAATATTTACCAAGAGAGCAGCTCAGGCAGAAATCAAGAGATCTGTGATGGGTTTC	922
QY	776	ACTGCCAGCTTCTCCGTTTCTGACGAGAGAGGCCCGCTTCGGGGCCCTGCGACGAGC	835

DB	923	GAGCCACTGTCTACCTTTGCCAGAGCCTCGGTTGGAGCGCAGAGATGTTGGAGCG	982
QY	836	TGCAACAGCAGAGCCAGGAGCTGACGAGGTCTCTCGGGGAGACAGAGCGGTTCTTGAGCC	895
DB	983	TCAATGTGAGGCTGGAAGATTTAATCAACGCTCATAAACACAAACAGAGTCTCACCGCCAGC	1042
QY	896	AGGTCTAGGCGGGTGTGACGCTGCTGCGGCGCAGGCGAGGTGAGGTCCACAAGATCA	955
DB	1043	GCCTGCTGAGGAAGCCGCTGCCAACTCTGCTCATCAAGGTGCAAGATGA	1102
QY	956	AGGCGGTGTACCTGGCCCTTGAAACCAAGTGCAGGTGAGCACACACGACCAAGTGCCTATTG	1015
DB	1103	AACTGCTTACCAACATCTGAAACATGTGCAACATCGACGTCAACCCAGCAGTGTGTCATCG	1162
QY	1016	CCGAGGCTGTGTGCTGTGCGAGACCTGCGCCGCTGCGAGGAGCCCTGCGGGACAGCT	1075
DB	1163	CCGAGATCTGTGTTCCGGTGGCAGATGCCACACGTATCAAGAGGCGACTGGAGCAAGG-	1221
QY	1076	CGATGAGGAGGAGTGTGCGGTGCTCACCGCATCCCTGCGCGGA-----CA	1126
DB	1222	--ATGGAACCTAAGTGGCTCTCCATGGCCCCCATCATGACACAGTGCATATAAACAG	1279
QY	1127	TGCCCCCCACACTCATCCGCGACCAACCGCTTCAACGCGCAGCTTCCAGGGCATCTGGATC	1186
DB	1280	CCCTCCACATTTAAACAGGACCAATAAATTCACAGCTGGCTTCCAGAAATATTGTTGATG	1339
QY	1187	GCTACGGGTGGGCGCTACACAGGAGTCAACCCGCTCCCTACACCAATCATCCTTCC	1246
DB	1340	CTATGTGTGCGGACGTACCGGAGATAAACCCAGCCCTTACACCATCATCCTTCC	1399
QY	1247	CTTCTCTGTTGCTGTGATGTTGCGGGATGTGGGCGACGGGCTGCTCATGTTCTCTTCG	1306
DB	1400	CTTCTCTGTTGCTGTGATGTTTGGAGACTGTGGTCAATGGAACCGTGTGCTCTGGCTG	1459
QY	1307	CCCTGGCCATGCTCTTGGGAGAAACCGACCGGCTGTGAAAGCCCGCAGAACGAGATCT	1366
DB	1460	CACTTTGGATGATTTCTGAATGAGAGCGCTGCTCTCCAGAGACAGACATAGATTT	1519
QY	1367	GGCAGACTTTCTTACGGGCGCTACCTGCTCTGCTTATGGGCTGTGTTCTCATCTACA	1426
DB	1520	GGAAACACCTTCTTCCACGGGCGCTATCTGATCTACTTATGGGCTATCTTCCCATCTACA	1579
QY	1427	CGGCTTCTCATCTACAAACGAGTGTCTTCACTCGCGCCACACAGCATCTTCCCTCGGCTGA	1486
DB	1580	CGGTTTGTATCTACAACTGATGCTTCTCAAGTCTCTGAACTCTTTGGCTCTTCTTGA	1639
QY	1487	GTGTGGCCGCTATGGCCAAACCAAGTGTGGTGTGAGTGTGCAATCTCTGCGCCAGCACGA	1546
DB	1640	GTGTCCAAACCCATGTTTCAGAAACCGCACATGGAATACTCATGTAATGGAGGAAAGTCTAT	1699
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DB	1760	TTGATCCGATTTGGAACTTGGCTTCAACAAACTCACTTCTGAATCTGTATAAATGA	1819
QY	1664	AGATGTCGTTCATCTGGGCGTGTGTCACATGGCCCTTTGGGGTGTCTCTCGAGTCTTCA	1723
DB	1820	AGATGTCGTGTATCTCGGAAATGTCAGATGGTTTGTGTCATCTCTCAGCCTTTTCA	1879
QY	1724	ACCAGTGCATTTTGGCCAGAGGACCCGGCTGCTGAGAGCGTTCGCGGAGCTCACCT	1783
DB	1880	ATCATACTATCTCAGAAAGAACTCTCAACATCATTTCTGCAATTTTATCTCTGAGATGATTT	1939
QY	1784	TCTCTCTGGGACTTTCGTTTACCTCGTGTCTCTAGTCACTTACAAAGTGGCTGTG---TG	1840
DB	1940	TTATCTGTGTCTGTTTGGATACCTGGTTTTCATGATCATTTTCAAATGGTCTGCTTTG	1999
QY	1841	TCGTGGGTGCCAGGGCGCGCTGCGCCAGCATCTCTCATCTCATCAATCAACATGTCTCT	1900
DB	2000	ACGTCCAGTATCTCAGACCGCCCCCAGCATCTCTCATCCACTTTCATCAACATGTTTCTGT	2059


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QY 1901 TCTCCACAG---CCCAGCAACAGGCTGCTTACCCCGGAGGAGGTGCTCAGGCCA 1957
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QY 1958 CGCTGTGTGTCTTGGGCTTGGCCATGTGTCCTGCTGCTTGGCAGCACCCTGCACC 2017
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QY 2120 TCTTTGTGTATGCTTGTATTTCTGTGCGTGGATGCTTCTGATTAAGCGTTTATTC 2179
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QY 2018 TGCTGCACCGCACCGCGCGCTGCGGAGGAGGCCGCTGACCGACGAGAGGAAACA 2077
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QY 2180 TTAGAGCCAGTCACTCGGAAATCCAGCTGCGAGGCATCCAGATCCAAAGAAGTCCCACTG 2239
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RESULT 15

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US-09-566-921-83
; Sequence 83, Application US/09566921
; Patent No. 668288
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne P.
; APPLICANT: Tingley, Debra W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 83
; LENGTH: 4132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 251826.7
US-09-566-921-83
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Query Match      21.0%; Score 554.6; DB 3; Length 4132;
Best Local Similarity 53.7%; Pred. No. 1.4e-91;
Matches 1345; Conservative 0; Mismatches 1119; Indels 39; Gaps 8;
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QY 215 TTTCTACAGTCAGAGGCTGCTTATTTGTTGTGCTAGTGAATTTAGGAGAACTTTGGAAGGTT 274
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QY 163 GAGTTACAGACCTCAACGCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTGATGTT 222
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QY 1114 CCCTGCGGAGCATGCGCCCGCCCACTCATCCGACCAACCGGTTTCAAGGCGGAGCTTCCAG 1173
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Db	1295	AACATAGTAGTGTATGGAATTTGGAACCTTACGAGAGATAAATCAGACTCCGTATACT	1354
Qy	1234	ATCATCACTTCGCCCTTCCTGTGTGTGTGATGTTCGGGATGTGGGCCACGGCTGCTC	1293
Db	1355	ATTATCACGTTCCCTTTTCTATTGTCTGATGTTTGGAGACTTCGGTCAATGCAITTTTA	1414
Qy	1294	ATGTTCTCTTCGCCCTGGCCATGGTCTTTCGGGAGAACCGACGGGCTGTGAAGACGGCG	1353
Db	1415	ATGACCCCTTTTGTGTGTGGATGGTACTGAGGGAGAGCCGGATCTCTTCCAGAGAAT	1474
Qy	1354	CAGAAACAGATCTGGCAGACTTTCTTCAGGGGCGCTACCTGCTCTCTGCTTATAGGCGCTG	1413
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Qy	1414	TTCTCCATCTACACCGGCTTCATCTACAACGAGTGTCTTCAAGTCGGCCACAGCATCTTC	1473
Db	1535	TTCTCCATGTACACTGGCCCTCATCTACAATGATTTGCTTTTCCAAGTCTCTTAATATCTTT	1594
Qy	1474	CCCTCGGGCTGGAGTGTGGCGCCATGGCCAAACGAGTCTGGCTGGAGTGAATTCCTG	1533
Db	1595	GGGTCACTCTGGAGTGTACGGCCGATGTTTAA---CTTATAATTTGGACTGAAGAGACGCTT	1651
Qy	1534	GCCAGACACAGATGCTTTACCTTGGATCCCAACGTCAACCGGTGCTTCTCTGGACACCTAC	1593
Db	1652	CGGGGAAACCTGTTCTACAGCTGAACCCAGCCCTCCTCGAGTGTGTGGTGACCAATAC	1711
Qy	1594	CCCTTTGGCATCGATCCTATTGAGAGCTGGCTGCCAACACACTTGAGTCTTCCTCAAGTCC	1653
Db	1712	CCTTTGGCATTGATCCAAITTTGGAACATTTGCTACCAATAAATCTGAGTTCCTTGAAGTCC	1771
Qy	1654	TTCAAGATGAAGATGTCCTGATCTCTGGGCGTGTGACATGCGCTTTTGGGTGGTCTTC	1713
Db	1772	TTTAAAGATGAAGATGTCTGTATCTTGTGTATCATCTCATATGCTGTTTGGAGTCAGCCTG	1831
Qy	1714	GGAGTCTTCAACACGTGCACTTTGGCCAGAGCAACGGCTGCTGTGGAGACGCTGCCG	1773
Db	1832	AGTCTGTTCAACCAATATCTATTTCAAGAGCCCTGAAATCTACTTTGGATTTATTCCT	1891
Qy	1774	GAGCTCACCTTCCTGCTGGGACTCTTCGGTTTACCTCGTGTTCCTAGTCACTCAAGTGG	1833
Db	1892	GAAATAATCTTCATGACCTCTTGTGTGGCTATTTGGTTATCCTATTTTTTACAGTGG	1951
Qy	1834	CTG---TGTGTCTGGGTGTCAGGGCGGCTCGGCCAGCATTCCTCATCTCACTTCATCAAC	1890
Db	1952	ACGGCCCTATGATGCTCATACCTCTGAGAAATGCAACCAAGCCTTCGTATCCATTTTATAAAC	2011
Qy	1891	ATGTTCTCTTCTCCAC---AGCCCCAGCAACAGGCTGCTCTACCCCGGAGGAGGTG	1947
Db	2012	ATGTTCTCTTCTTCCACCAAGTCTGTTTATTCATATGTGTATTCATGAGAGAAAGGA	2071
Qy	1948	GTCCAGGCCACGCTGTGTGTCTGGCCCTTGGCCATGTGTGCCATCTCTGCTGTGGCACA	2007
Db	2072	ATTTCAGTGTTCCTGTGTAGTGTGCACTACTGTGTGTACTCTTGGATGCTGCTGTTTAA	2131
Qy	2008	CCCTGTGACCTGTGCAACGCCACCGCCCGGCTCGGAGGAGGCGCGCTGACCCAGCAG	2067
Db	2132	CCATGGTCTCT-----TCGCCGTCAAGTATTTGAGGAGAAAGCAATTTGGGAACTCTC	2182
Qy	2068	GAGGAAACAAAGCCGGTGTGCACTCGCTGACGCATCTGTGAATGTGCTGGAGCTCC	2127
Db	2183	AATCTTGTGGGATCAGGGTGGGCAACGGACCGACAGAGAGGATGCTGAGATTTATTCAG	2242
Qy	2128	GATGAGGAAAGGAGGGGCGCTGGATGATGAAGAGGAGGCGGAGCTCGTCCCTCCGAG	2187
Db	2243	CATGACCAAGTCTCCACCACTCAGAGAACGCAGACGAGTTGACTTTGGGAGACCAATG	2302
Qy	2188	GTGCTCATGCAACAGGCCATCCACAACATCGAGTTCCTGCTGGGCTCGCTCTCCAAACACC	2247

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
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2	2640	100.0	2640	2	AR577091	AR577091	Sequence
3	2640	100.0	2655	2	AR270531	AR270531	Sequence
4	2640	100.0	2855	2	AR380371	AR380371	Sequence
5	2640	100.0	2855	2	AX332228	AX332228	Sequence
6	2640	100.0	2855	2	AX336173	AX336173	Sequence
7	2640	100.0	2655	2	AX410717	AX410717	Sequence
8	2640	100.0	2655	5	HSU45285	HSU45285	Human speci
9	2597	98.4	2722	5	BC032465	BC032465	Homo sapi
10	2594	98.3	2691	5	BC018133	BC018133	Homo sapi
11	2550.2	96.6	2582	2	CQ718250	CQ718250	Sequence 1
12	2068	78.3	2488	2	A98501	A98501	Sequence 1
13	2068	78.3	2488	2	AX320850	AX320850	Sequence
14	2068	78.3	2488	2	ED080989	ED080989	Novel T c
15	2068	78.3	2488	5	AF025374	AF025374	Homo sapi
16	2066.4	78.3	2488	2	A98512	A98512	Sequence 12
17	2066.4	78.3	2488	2	AX320861	AX320861	Sequence 12
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QY 241 GAGAGACCTTACCTTCTGACGAGGAGGTGCGCGGCTGGGTGGTCTCTGCCCGG 300
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QY 301 CAAAGGGAGGCTGCGGCA CCCCCA CCGCGGACCTGCTGCGCATCCAGGAGGAGCG 360
DB 301 CAAAGGGAGGCTGCGGCA CCCCCA CCGCGGACCTGCTGCGCATCCAGGAGGAGCG 360
QY 361 GAGCGCTCGCCAGAGCTGGGATGTCGGGCA CCGAGGAGGCTGCGGCGGCG 420
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DB 841 GAGCAGCGAGGCTGAGAGGTCTCGGGGAGACAGAGGCTTCTGAGCAGGTG 900
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DEFINITION Sequence 1 from patent US 677537.
ACCESSION AR577091
VERSION AR577091.1 GI:56579543
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2640)
AUTHORS Stashenko, P. and Li, Y.-P.
TITLE Osteoclast proton pump subunit
JOURNAL Patent: US 677537-A 1 17-AUG-2004;
Forsyth Dental Infirmary for Children; Boston, MA;
WOX;

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VERSION	AR270531.1	GI:29701765							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 2655)								
AUTHORS	Au-Young, J. and Seilhamer, J.J.								
TITLE	Composition for the detection of signaling pathway gene expression								
JOURNAL	Patent: US 6500938-A 1094 31-DEC-2002;								
	Incyte Genomics, Inc.; Palo Alto, CA;								
	WOX;								
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ACCESSION AX410717
VERSION AX410717.1 GI:21443422
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominoidea; Homo.
1
REFERENCE
AUTHORS Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J. G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 3364 11-APR-2002;
GENE LOGIC INC (US)
FEATURES
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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Homnidae; Homo.
REFERENCE
1 (bases 1 to 2655)
Li, Y.-P., Chen, W. and Stashenko, P.
Molecular cloning and characterization of a putative novel human
osteoclast-specific 116-kDa vacuolar proton pump subunit
Biochem. Biophys. Res. Commun. 218 (3), 813-821 (1996).
2 (bases 1 to 2655)
Li, Y.-P., Chen, W. and Stashenko, P.
Direct Submission
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Dental Center, 140 Fenway, Boston, MA 02115, USA
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FEATURES
source
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Query Match 100.0%; Score 2640; DB 5; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 10

LOCUS BC018133

DEFINITION Homo sapiens T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3, transcript variant 1, mRNA (cDNA clone MGC:9307 IMAGE:3905446), complete cds.

ACCESSION BC018133

VERSION BC018133.1 GI:17390297

KEYWORDS MGC.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 2691)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D., Altschul,S.F., Zebberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Scapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schreitz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullah,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Mammalian Gene Collection Program Team

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2691)

NIH MGC Project

Direct Submission

Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps-x@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: <http://image.llnl.gov>

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19924144.

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ORIGIN

Query Match 98.3%; Score 2594; DB 5; Length 2691;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2599; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

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VERSION CO718250.1 GI:42279107
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
human exons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 4184 06-SEP-2002; /
PE Corporation (NY) (US)
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ORIGIN
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 2568; Conservative 0; Mismatches 8; Indels 3; Gaps 1;
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ORIGIN

Query Match 78.3%; Score 2068; DB 2; Length 2488;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2105; Conservative 0; Mismatches 40; Indels 3; Gaps 1;

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Qy	556	GTCAACTTTGTGGCAGGTGCGTGGAGCCCAACAGGCCCTGCGCCCTAGAGCGCTGCTC	615
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Qy	736	CAGATCGGACAGAGATCCGACAGATCACGGACGTCTTCCACTTGCACAGCTTTCCTGGTTT	795
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Qy	796	CTGCAGCAGGAGGAGGCCCGCTCGGGGCCCTGCAGCAGCTTGCAACAGCAGAGCCAGGAG	855
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Qy	1036	CGAGACTTGCCTGCCCTGCAAGAGAGCCCTCGGGGACAGCTCGATGAGAGGGAGTGAAT	1095
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QY	2533	GCCACAGATGACTAGGGCCCACTGCAAGTCTTCCAGACCTCTTCTGACCTCTGAGGC	2592
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RESULT 14			
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LOCUS		Novel T cell membrane protein (TIRC7), peptide, antibody	
DEFINITION		originating therein and utilization thereof.	
ACCESSION	BD080989		
VERSION	BD080989.1	GI:22626592	
KEYWORDS	JP 2001514852-A/1.		
SOURCE	unidentified		
ORGANISM	unclassified sequences.		
REFERENCE	1 (bases 1 to 2488)		
AUTHORS	Utku.N., Gullans.S.R. and Milford.E.L.		
TITLE	Novel T cell membrane protein (TIRC7), peptide, antibody		
JOURNAL	originating therein and utilization thereof		
COMMENT	Patent: JP 2001514852-A 1.18-SEP-2001: NALLAN UTUKU, BRIGHAM AND WOMEN'S HOSPITAL INC OS Unidentified PN JP 2001514852-A/1 PD 18-SEP-2001 PF 28-AUG-1998 JP 2000508792 PR 29-AUG-1997 DE 197 38 710.1.12-FEB-1998 DE 298 02 653.8 PI NALLAN UTUKU, STEVEN R GULLANS, EDGAR L MILFORD PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61K48/00, PC A61P31/00,A61P35/00,A61P37/04,A61P37/06,A61P37/08,C07K14/705, PC C07K16/28, PC C12N5/10,G01N33/15,G01N33/50,C12N15/00,A61K37/02,C12N5/00 CC Strandedness: Single; CC Topology: linear; CC Novel T cell membrane protein (TIRC7), peptide, antibody CC originating CC therein and utilization thereof FH Key Location/Qualifiers FT CDS 537..2378. Location/Qualifiers 1..2488 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"		
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ORIGIN			
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Best Local Similarity	98.0%;	Pred. No. 0;	Indels 3; Gaps 1;
Matches 2105;	Conservative	0; Mismatches	40;
QY	496	GGGGCCCTCAGAGAGGACGGCCCTGCTCCAGGCCCCCGGGGGCCGACACGACCTGAGG	555
Db	327	GGGGCCCTGCTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	386
QY	556	GTCAACTTTGTGGCAGGTGCGTGGAGCCCCCAAGCGCCCTGCGCTTAGAGCGCTGCTC	615
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QY	616	TGGAGGGCTTGGCGGGCTTCTCATTTGCCAGTTTTCAGGAGCTGGAGCGGCTGGAG	675
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QY	676	CAACCCCGTGACGGGGCGAGCCACCGCTGGATGACCTTCTCATCTCTCTTCTGGGGTGAG	735

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CC is used in an example of the present invention, which describes isolated
CC osteoclast specific or related DNA sequences. The present invention also
CC describes; a DNA construct capable of replicating and optionally
CC expressing, in a host cell, osteoclast specific or related DNA,
CC comprising an osteoclast specific or related DNA sequence and sequences
CC necessary for transforming or transfecting a host cell, and for
CC replicating and optionally expressing an osteoclast specific or related
CC DNA sequence in a host cell; and a cell stably transformed or transfected
CC with the DNA construct. The osteoclast specific or related DNA sequence
CC can be used as a probe to screen a genomic DNA or cDNA library for
CC osteoclast specific or related DNA sequences, or as an osteoclast cell
CC surface marker
XX

SQL Sequence 2640 BP; 445 A; 885 C; 824 G; 486 T; 0 U; 0 Other;

	Query Match	100.0%;	Score 2640;	DB 2;	Length 2640;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2640;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CGGCGTGGCGGACGGGACGAGCGAGCGCGCGGCGGAGCACACCGGGGACCATG	60		
DB	1	CGGCGTGGCGGACGGGACGAGCGAGCGCGGCGGCGGAGCACACCGGGGACCATG	60		
QY	61	GGCTCCATGTTCCGAGCGAGGAGTGGCCCTGGTCCAGCTCTTTCTGCCACAGCGGT	120		
DB	61	GGCTCCATGTTCCGAGCGAGGAGTGGCCCTGGTCCAGCTCTTTCTGCCACAGCGGT	120		
QY	121	GGCTACACCTGGTGGTGGCGGAGCTGGGCTCGTGGAGTTGAGAGCTCAAC	180		
DB	121	GGCTACACCTGGTGGTGGCGGAGCTGGGCTCGTGGAGTTGAGAGCTCAAC	180		
QY	181	GGCTCGGTGAGGCGCTTCAGAGACGCTTTGTGTGTGATGTTGGCGTGTGAGGAGTG	240		
DB	181	GGCTCGGTGAGGCGCTTCAGAGACGCTTTGTGTGTGATGTTGGCGTGTGAGGAGTG	240		
QY	241	GAGAGACCTTCACTTCTGAGGAGGAGTGGCGCGGCTGGTGGTCTCTGCCCGG	300		
DB	241	GAGAGACCTTCACTTCTGAGGAGGAGTGGCGCGGCTGGTGGTCTCTGCCCGG	300		
QY	301	CCAAAGGGGAGGCTGGCGGACCCCAACCCCGGACCTGCTGGCATCCAGGAGGAGCG	360		
DB	301	CCAAAGGGGAGGCTGGCGGACCCCAACCCCGGACCTGCTGGCATCCAGGAGGAGCG	360		
QY	361	GAGCGCTCGGCGCAGGAGCTGGGAGTGTGGGGCAACAGCAGGCGCTGGGGGCCAG	420		
DB	361	GAGCGCTCGGCGCAGGAGCTGGGAGTGTGGGGCAACAGCAGGCGCTGGGGGCCAG	420		
QY	421	CTGCAACAGCTGAGCTCAACGCGCGCTGCTACGCAAGGCGCATGAACCTCAGCTGGCA	480		
DB	421	CTGCAACAGCTGAGCTCAACGCGCGCTGCTACGCAAGGCGCATGAACCTCAGCTGGCA	480		
QY	481	GCGGCCACACAGATGGGCGCTCAGAGAGCGCCCTGCTCCAGGCGCCCGGGGGCGG	540		
DB	481	GCGGCCACACAGATGGGCGCTCAGAGAGCGCCCTGCTCCAGGCGCCCGGGGGCGG	540		
QY	541	CACGAGGACCTGAGGCTCAACTTTGTGGCAGTGGCGTGGAGCCCGCACAGGCGCTGCC	600		
DB	541	CACGAGGACCTGAGGCTCAACTTTGTGGCAGTGGCGTGGAGCCCGCACAGGCGCTGCC	600		
QY	601	CTAGAGCGCTGCTCTGAGAGGCGTGGCGCGCTTCTCATTCGCAAGTTCAGGAGCTG	660		
DB	601	CTAGAGCGCTGCTCTGAGAGGCGTGGCGCGCTTCTCATTCGCAAGTTCAGGAGCTG	660		
QY	661	GAGGAGCGCTGGAGCACCCCTGACGGGCGAGCGCCCTGCTCCAGGCGCCCGGGGGCGG	720		
DB	661	GAGGAGCGCTGGAGCACCCCTGACGGGCGAGCGCCCTGCTCCAGGCGCCCGGGGGCGG	720		
QY	721	TCTTACTGGGGTGAGCAGATCGGACAGAGAGATCCGCAAGATCAACGAGCTGCTTCCACTGC	780		
DB	721	TCTTACTGGGGTGAGCAGATCGGACAGAGAGATCCGCAAGATCAACGAGCTGCTTCCACTGC	780		
QY	781	CAGCTCTTCCGTTCTGAGAGGAGGCGCGCTCGGGCGCTCGAGGAGCTGCA	840		

DB	781	CACGTCTTCCCGCTTTCGACAGCAGGAGGAGCGCGCTCGGGCGCTCGAGCAGCTGCAA	840
QY	841	CAGCAGGCCAGGAGCTGACAGAGCTCTCGGGGAGACAGAGCGGTTCTTGAGCCAGGTG	900
DB	841	CAGCAGGCCAGGAGCTGACAGAGCTCTCGGGGAGACAGAGCGGTTCTTGAGCCAGGTG	900
QY	901	CTAGGCGGGGTGCTGCTGAGCTGCTGCCCGCAGGCGAGTGCAGTCCACAAGATGAAGGCC	960
DB	901	CTAGGCGGGGTGCTGCTGAGCTGCTGCCCGCAGGCGAGTGCAGTCCACAAGATGAAGGCC	960
QY	961	GTGTACTTGGCCCTGAACAGTGCAGCTGACGACACCAAGTGCCTCATTTGCCGAG	1020
DB	961	GTGTACTTGGCCCTGAACAGTGCAGCTGACGACACCAAGTGCCTCATTTGCCGAG	1020
QY	1021	GGCTGGTCTCTGTGGGAGACCTGCGCGCTGCGAGGAGCGCTCGGGGACAGCTCGATG	1080
DB	1021	GGCTGGTCTCTGTGGGAGACCTGCGCGCTGCGAGGAGCGCTCGGGGACAGCTCGATG	1080
QY	1081	GAGGAGGAGTGTGAGTGGCTGCTCACCGCATCCCTGCGGGGACATGCCCCCACACTC	1140
DB	1081	GAGGAGGAGTGTGAGTGGCTGCTCACCGCATCCCTGCGGGGACATGCCCCCACACTC	1140
QY	1141	ATCCGACCAACCCGCTTCAOGGCCAGCTTCCAGGGCATCGTGGATCGCTACGCGGTGGC	1200
DB	1141	ATCCGACCAACCCGCTTCAOGGCCAGCTTCCAGGGCATCGTGGATCGCTACGCGGTGGC	1200
QY	1201	CGCTACCAAGGAGTCAACCCCGCTCCCTACACCATCATCCTTCCCTTCTGTTGCT	1260
DB	1201	CGCTACCAAGGAGTCAACCCCGCTCCCTACACCATCATCCTTCCCTTCTGTTGCT	1260
QY	1261	GTGATGTTCCGGGATGTGGGCGCACGGGCTGCTCATGTTCTCTTGCCCTGGCCATGGTC	1320
DB	1261	GTGATGTTCCGGGATGTGGGCGCACGGGCTGCTCATGTTCTCTTGCCCTGGCCATGGTC	1320
QY	1321	CTTGGCGAGAACCGACCGGCTGTGAAAGCGCGGAGAGAGATCTGGCAGACTTTCTTC	1380
DB	1321	CTTGGCGAGAACCGACCGGCTGTGAAAGCGCGGAGAGAGATCTGGCAGACTTTCTTC	1380
QY	1381	AGGGGCGCTACCTGCTCTGCTTATGGGCGCTGTTCTCATCTACACGGCTTCTATCTAC	1440
DB	1381	AGGGGCGCTACCTGCTCTGCTTATGGGCGCTGTTCTCATCTACACGGCTTCTATCTAC	1440
QY	1441	AACGAGTGTCTCAGTGGCGCACACGAGCATCTTCCCTCGGGCTGGAGTGTGGCGGCATG	1500
DB	1441	AACGAGTGTCTCAGTGGCGCACACGAGCATCTTCCCTCGGGCTGGAGTGTGGCGGCATG	1500
QY	1501	GCACCAAGTGTGGCTGGAGTGTGATTTCTGGGCGGAGCACAGATGTTCACCTGGAT	1560
DB	1501	GCACCAAGTGTGGCTGGAGTGTGATTTCTGGGCGGAGCACAGATGTTCACCTGGAT	1560
QY	1561	CCCAAGCTCACCGGCTCTTCTGGGAGCGCTACCCCTTGGGATCGATCTTATTTGGAGC	1620
DB	1561	CCCAAGCTCACCGGCTCTTCTGGGAGCGCTACCCCTTGGGATCGATCTTATTTGGAGC	1620
QY	1621	CTGGCTGCCAACCACTTGAAGTCTTCAAGTGAAGATGTCCGCTCATCTG	1680
DB	1621	CTGGCTGCCAACCACTTGAAGTCTTCAAGTGAAGATGTCCGCTCATCTG	1680
QY	1681	GGCTGTGTCACAGCGCTTTGGGCTGTGCTCGAGTCTTCAACAGGTGCACTTTGGC	1740
DB	1681	GGCTGTGTCACAGCGCTTTGGGCTGTGCTCGAGTCTTCAACAGGTGCACTTTGGC	1740
QY	1741	CAGAGGACCGGCTGCTGCTGGAGCGCTGCGGAGCTCACCTTCTGCTGGGACTCTTC	1800
DB	1741	CAGAGGACCGGCTGCTGCTGGAGCGCTGCGGAGCTCACCTTCTGCTGGGACTCTTC	1800
QY	1801	GGTTACCTCGTGTCTTAGTCACTTCAAGTGGCTGTGCTGGGCTGCCAGGCGCGCC	1860
DB	1801	GGTTACCTCGTGTCTTAGTCACTTCAAGTGGCTGTGCTGGGCTGCCAGGCGCGCC	1860
QY	1861	TGCCCCAGGATCTCATCACTTCAACAGTGTCTCTTCTCCACAGCCCCAGCAAC	1920
DB	1861	TGCCCCAGGATCTCATCACTTCAACAGTGTCTCTTCTCCACAGCCCCAGCAAC	1920

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QY 1921 AGGCTGCTTACCCCGGCGAGAGGTGTTCCAGGCGACGCTGTTGCTTGGCTTGGCC 1980
DB 1921 AGGCTGCTTACCCCGGCGAGAGGTGTTCCAGGCGACGCTGTTGCTTGGCTTGGCC 1980
QY 1981 ATGGTCCCATCTGCTGTTGGCACACCCCTGCTGCTGACCGCCACCGCCGCGCCG 2040
DB 1981 ATGGTCCCATCTGCTGTTGGCACACCCCTGCTGCTGACCGCCACCGCCGCGCCG 2040
QY 2041 CTGCGGAGGAGGCGGCTGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100
DB 2041 CTGCGGAGGAGGCGGCTGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100
QY 2101 GAGCGATCTGTGAATGGCTGGAGCTCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160
DB 2101 GAGCGATCTGTGAATGGCTGGAGCTCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160
QY 2161 GAGGAGGCGGAGCTGCTCCCTCCGAGGCTCTCATGACGAGGAGGAGGAGGAGGAGG 2220
DB 2161 GAGGAGGCGGAGCTGCTCCCTCCGAGGCTCTCATGACGAGGAGGAGGAGGAGGAGG 2220
QY 2221 TTCTGCTGGGCTGCTCTCAACACCGGCTCTTACCTGCGGCTGTGGGCTCTGAGCCTG 2280
DB 2221 TTCTGCTGGGCTGCTCTCAACACCGGCTCTTACCTGCGGCTGTGGGCTCTGAGCCTG 2280
QY 2281 GCGCAGCCGAGCTGTCGAGGTTCTGTGGGCTCATGATGCGATGAGGCTGTGGGCTG 2340
DB 2281 GCGCAGCCGAGCTGTCGAGGTTCTGTGGGCTCATGATGCGATGAGGCTGTGGGCTG 2340
QY 2341 GCGCGGAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTG 2400
DB 2341 GCGCGGAGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTG 2400
QY 2401 ATGACCGTGGCTATCTGCTGTTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2460
DB 2401 ATGACCGTGGCTATCTGCTGTTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2460
QY 2461 CTGCACTGGGTGAATTCAGAAACAAATTCATCTAGGCAAGGCTCTAGGCTAGTCCC 2520
DB 2461 CTGCACTGGGTGAATTCAGAAACAAATTCATCTAGGCAAGGCTCTAGGCTAGTCCC 2520
QY 2521 TTCACTTCTGCTGCCACAGATGATAGGCGCCACTGCGCTCTGCGAGCTCTTCTTCT 2580
DB 2521 TTCACTTCTGCTGCCACAGATGATAGGCGCCACTGCGCTCTGCGAGCTCTTCTTCT 2580
QY 2581 GACCTCTGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
DB 2581 GACCTCTGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
```

RESULT 2

ABN86735

ID ABN86735 standard; cDNA; 2640 BP.

XX AC ABN86735;

XX DT 16-SEP-2002 (first entry)

XX DE Human OC-116KDa cDNA.

KW Human; osteoclast; gene therapy; aberrant bone resorption; OC-116KDa;

XX KW gene; ss.

XX OS Homo sapiens.

XX EH Key

XX FT CDS

XX FT 58..2523

XX FT /tag= a

XX FT /product= "OC-116KDa"

XX FT /note= "No stop codon given"

XX PN US6403304-B1.

PD 11-JUN-2002.

XX 19-JUL-1996; 96US-00684932.

XX 06-APR-1993; 93US-00045270.

XX 23-FEB-1995; 95US-00392678.

XX 20-JUL-1995; 95US-0001292P.

XX 22-FEB-1996; 96US-000605378.

XX (FORS-) FORSYTH DENTAL INFIRMARY FOR CHILDREN.

XX Strashenko P, Li Y, Wucherpfennig AL;

XX WPI; 2002-536031/57.

XX P-PSDB; AB881811.

XX Novel isolated osteoclast-specific or -related DNA sequence, useful for

XX producing gene products useful in the therapeutic treatment or diagnosis

XX of disorders involving aberrant bone resorption.

XX Example 8; Fig 3; 34pp; English.

XX The invention relates to novel human osteoclast-specific or -related cDNA

XX sequences. The sequence encodes human osteoclast 116KDa (OC-116KDa). The

XX sequences may have a use in gene therapy. The sequences of the invention

XX are useful in the production of gene products useful in the therapeutic

XX treatment or diagnosis of disorders involving aberrant bone resorption,

XX for generating peptides which are useful for producing antibodies for

XX identifying osteoclast-specific or -related peptides or gene products

XX Sequence 2640 BP; 445 A; 885 C; 824 G; 486 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 2640; DB 6; Length 2640;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCTGCGCGGACGCGGACGCGGAGCGGAGCGGCGGCGGAGCGGCGGCGGAGCGG 60

DB 1 CGCGCTGCGCGGACGCGGACGCGGAGCGGAGCGGCGGCGGAGCGGCGGCGGAGCGG 60

QY 61 GGTCTCATGTTCCGAGAGCGAGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

DB 61 GGTCTCATGTTCCGAGAGCGAGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY 121 GCTTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

DB 121 GCTTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

QY 181 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

DB 181 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

QY 241 GAGAGACCTTACCTTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300

DB 241 GAGAGACCTTACCTTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300

QY 301 CCAAGGGGAGGCTGCGGCGACCCCGGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

DB 301 CCAAGGGGAGGCTGCGGCGACCCCGGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 361 GAGCGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420

DB 361 GAGCGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420

QY 421 GTGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

DB 421 GTGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

QY 481 GCGCGCCACACAGATGCGGCGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540

DB 481 GCGCGCCACACAGATGCGGCGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540

QY 541 CACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600

[illegible]

Db	1621	CTGGCTGCCAACACATTGAGCTTCTCAAATCTCTTCAAGATGAAGATGTCGCGTCATCCTCG	1680
Qy	1681	GGCGTCGTGCACATGGCCCTTTGGGGTGGTCTCTCGAGTCTTCAACACACGTGCACTTTGGC	1740
Db	1681	GGCGTCGTGCACATGGCCCTTTGGGGTGGTCTCTCGAGTCTTCAACACACGTGCACTTTGGC	1740
Qy	1741	CAGAGGACCGGCTGTCTGTGAGAGACGCTGCCGGAGCTCACCTTCTGTCTGGAGACTCTTC	1800
Db	1741	CAGAGGACCGGCTGTCTGTGAGAGACGCTGCCGGAGCTCACCTTCTGTCTGGAGACTCTTC	1800
Qy	1801	GGTTACTCTGTGTTCCTAGTCACTCAAGTGGCTGTGTCTGGCTGCCAGGGCCGCC	1860
Db	1801	GGTTACTCTGTGTTCCTAGTCACTCAAGTGGCTGTGTCTGGCTGCCAGGGCCGCC	1860
Qy	1861	TCGCCCAGCATCTCATCCACTTTCATCAACATGTTCTCTTCTCCACAGCCCCAGCAAC	1920
Db	1861	TCGCCCAGCATCTCATCCACTTTCATCAACATGTTCTCTTCTCCACAGCCCCAGCAAC	1920
Qy	1921	AGGCTGCTTACCCCCGGACAGAGTGTTCAGGCCACCGCTGGTGTCTCTGGCCTTGGCC	1980
Db	1921	AGGCTGCTTACCCCCGGAGGAGTGTTCAGGCCACCGCTGGTGTCTCTGGCCTTGGCC	1980
Qy	1981	ATGGTGCCCATCTGTCTGTGTGGCACACCCCTGCACCTCTGTGCACCGCCACCGCCGCCG	2040
Db	1981	ATGGTGCCCATCTGTCTGTGTGGCACACCCCTGCACCTCTGTGCACCGCCACCGCCGCCG	2040
Qy	2041	CTCGGAGGAGGCCCTGCACCGACAGGAGGAAAAAAGGCGCGGGTGTGTGGACCTGCGCT	2100
Db	2041	CTCGGAGGAGGCCCTGCACCGACAGGAGGAAAAAAGGCGCGGGTGTGTGGACCTGCGCT	2100
Qy	2101	GAGCGATCTGTGAATGGCTGGAGCTCCGATGAGGAAAAAGGCAAGGGGCCCTGGATGATGA	2160
Db	2101	GAGCGATCTGTGAATGGCTGGAGCTCCGATGAGGAAAAAGGCAAGGGGCCCTGGATGATGA	2160
Qy	2161	GAGGAGCGGAGCTCGTCCCTCCGAGGTGCTCATGSCACAGGCCATCCACACCATCGAG	2220
Db	2161	GAGGAGCGGAGCTCGTCCCTCCGAGGTGCTCATGSCACAGGCCATCCACACCATCGAG	2220
Qy	2221	TTCTGCTCGGCTGGCTCTCCAAACACCGCTCTACCTGCGCTGTGGCCCTGAGCCCTG	2280
Db	2221	TTCTGCTCGGCTGGCTCTCCAAACACCGCTCTACCTGCGCTGTGGCCCTGAGCCCTG	2280
Qy	2281	GCCACGCGCAGCTGTCGAGGTTCTGTGGGCCATGGTGAATGGCNATAGGCTTGGCCCTG	2340
Db	2281	GCCACGCGCAGCTGTCGAGGTTCTGTGGGCCATGGTGAATGGCNATAGGCTTGGCCCTG	2340
Qy	2341	GGCGGGAGGTGGCGCTGTGGTGTGGTCTCCCATCTTTGCCGCCCTTGGCCCTG	2400
Db	2341	GGCGGGAGGTGGCGCTGTGGTGTGGTCTCCCATCTTTGCCGCCCTTGGCCCTG	2400
Qy	2401	ATGACCGTGGCTATCTCTGTGTGATGAGAGGACTCTCAGCCTTCTGTGACGCCCTGGG	2460
Db	2401	ATGACCGTGGCTATCTCTGTGTGATGAGAGGACTCTCAGCCTTCTGTGACGCCCTGGG	2460
Qy	2461	CTGCACCTGGGTGAAATTCAGAACAGTTCTACTCAGGCACCGGCTACAGCTGAGTCCC	2520
Db	2461	CTGCACCTGGGTGAAATTCAGAACAGTTCTACTCAGGCACCGGCTACAGCTGAGTCCC	2520
Qy	2521	TTCACTTCTGCTGCCACAGATGACTAGGGCCCACTGCAAGTCTCTGCGACCTCTTCTCT	2580
Db	2521	TTCACTTCTGCTGCCACAGATGACTAGGGCCCACTGCAAGTCTCTGCGACCTCTTCTCT	2580
Qy	2581	GACCTCTGAGGCAAGAGAGAAATAAGACGGTCCGCCCTGGCAAAAAAATAAAAAA	2640
Db	2581	GACCTCTGAGGCAAGAGAGAAATAAGACGGTCCGCCCTGGCAAAAAAATAAAAAA	2640

RESULT 3
ADR4118
ID ADR
XX
AC ADR
XX

AC ADR44118;

QY 241 GAGAGACCTTACCTTCTGCGAGGAGAGGTGCGGGGTGGGTGGTCTGTCGCCCGC 300
DB 241 GAGAGACCTTACCTTCTGCGAGGAGAGGTGCGGGGTGGGTGGTCTGTCGCCCGC 300
QY 301 CCAAGGGAGGCTGCGGACACCCACCCCGGAGCCTGTGCGCATCCAGAGGAGACG 360
DB 301 CCAAGGGAGGCTGCGGACACCCACCCCGGAGCCTGTGCGCATCCAGAGGAGACG 360
QY 361 GAGGCGCTGCCAGGAGCTGCGGATGTGCGGGGCAACAGCAGGCCCCCTGCGGGCCAG 420
DB 361 GAGGCGCTGCCAGGAGCTGCGGATGTGCGGGGCAACAGCAGGCCCCCTGCGGGCCAG 420
QY 421 CTGACACAGCTCAGCTCAGCGCGCGCTGTAGCCAGGCCCCATGAACCTCAGCTGGCA 480
DB 421 CTGACACAGCTCAGCTCAGCGCGCGCTGTAGCCAGGCCCCATGAACCTCAGCTGGCA 480
QY 481 GCGGCCACACAGATGGGGCTCAGAGAGGACGCCCCCTGTCTCAGGGCCCCCGGGGGCCG 540
DB 481 GCGGCCACACAGATGGGGCTCAGAGAGGACGCCCCCTGTCTCAGGGCCCCCGGGGGCCG 540
QY 541 CACAGGACCTGAGGGTCAACTTTGTGGCAGGTGCGGTGAGGCCCAAGGCCCTTGCC 600
DB 541 CACAGGACCTGAGGGTCAACTTTGTGGCAGGTGCGGTGAGGCCCAAGGCCCTTGCC 600
QY 601 CTAGAGGCGCTGCTGAGGGGCTGCGCGGCTTCTCATTTGCGCAGCTTCAGGAGCTG 660
DB 601 CTAGAGGCGCTGCTGAGGGGCTGCGCGGCTTCTCATTTGCGCAGCTTCAGGAGCTG 660
QY 661 GAGCAGCGCTGAGCACCCTGAGCGGGGAGCAGCCACGTCGATGACCTTCTTCATC 720
DB 661 GAGCAGCGCTGAGCACCCTGAGCGGGGAGCAGCCACGTCGATGACCTTCTTCATC 720
QY 721 TCCTACTGGGGTGAAGATCGGACAGAGATCCGCAAGATCAGCGACTGCTTCCACTGC 780
DB 721 TCCTACTGGGGTGAAGATCGGACAGAGATCCGCAAGATCAGCGACTGCTTCCACTGC 780
QY 781 CAGCTCTTCCGTTTCTGAGCAGGAGGAGGCGCGCTCGGGGCTTGCAGCAGCTGCA 840
DB 781 CAGCTCTTCCGTTTCTGAGCAGGAGGAGGCGCGCTCGGGGCTTGCAGCAGCTGCA 840
QY 841 CAGCAGGCGAGGCTGAGGAGGTCTCGGGGAGACAGCGGTTCCTGAGCAGGTG 900
DB 841 CAGCAGGCGAGGCTGAGGAGGTCTCGGGGAGACAGCGGTTCCTGAGCAGGTG 900
QY 901 CTAGGCGGGTCTGAGCTGCTGCGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
DB 901 CTAGGCGGGTCTGAGCTGCTGCGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
QY 961 GTGTACTGGCCCTGAACAGTGCAGGTGAGCAGCAGCAGCAGTGCCTCATTTGCCGAG 1020
DB 961 GTGTACTGGCCCTGAACAGTGCAGGTGAGCAGCAGCAGCAGTGCCTCATTTGCCGAG 1020
QY 1021 GCCTGTGTCTCTGCGAGACCTGCGCCCTGCGAGGAGGAGGAGGAGGAGGAGGAGG 1080
DB 1021 GCCTGTGTCTCTGCGAGACCTGCGCCCTGCGAGGAGGAGGAGGAGGAGGAGGAGG 1080
QY 1081 GAGGAGGAGTGAAGTGCCTGAGCTCAGCGCATCCCTGCGGAGCATGCCCCCAGCTC 1140
DB 1081 GAGGAGGAGTGAAGTGCCTGAGCTCAGCGCATCCCTGCGGAGCATGCCCCCAGCTC 1140
QY 1141 ATCCGACACACCGCTTACGGCAGCTTCCAGGGGATCGTGATCGCTACGCGGTGGG 1200
DB 1141 ATCCGACACACCGCTTACGGCAGCTTCCAGGGGATCGTGATCGCTACGCGGTGGG 1200
QY 1201 CGCTACAGGAGTCAACCCCGCTCCCTACCATCATCATCATCATCATCATCATCATCAT 1260
DB 1201 CGCTACAGGAGTCAACCCCGCTCCCTACCATCATCATCATCATCATCATCATCATCAT 1260
QY 1261 GTGATGTTGGGATGTGGGACAGGCTGCTCATGTTCTTCTGCGGCTGGGATGGT 1320
DB 1261 GTGATGTTGGGATGTGGGACAGGCTGCTCATGTTCTTCTGCGGCTGGGATGGT 1320

QY 1321 CTTGCGGAGAACCGACCGGCTGTGAAGCCGCGGAGAACGAGATCTGGCAGACTTCTTC 1380
DB 1321 CTTGCGGAGAACCGACCGGCTGTGAAGCCGCGGAGAACGAGATCTGGCAGACTTCTTC 1380
QY 1381 AGGGGCGCTTACCTGCTGCTTATGGGCTGTTCCTCATCTACACCGGCTTCATCTAC 1440
DB 1381 AGGGGCGCTTACCTGCTGCTTATGGGCTGTTCCTCATCTACACCGGCTTCATCTAC 1440
QY 1441 AACGAGTGTCTAGTCCGCGCACAGCATCTTCCCTCGGGCTGGAGTGTGGCCGCTG 1500
DB 1441 AACGAGTGTCTAGTCCGCGCACAGCATCTTCCCTCGGGCTGGAGTGTGGCCGCTG 1500
QY 1501 GCCAACGAGTCTGGCTGGAGTGAATCTTGGCCGACACAGCATGCTTACCTTCGAT 1560
DB 1501 GCCAACGAGTCTGGCTGGAGTGAATCTTGGCCGACACAGCATGCTTACCTTCGAT 1560
QY 1561 CCCAACGCTACCGGCTGTCTTCTGGGACCTTACCCCTTGGCATCGATCTTATTTGAGC 1620
DB 1561 CCCAACGCTACCGGCTGTCTTCTGGGACCTTACCCCTTGGCATCGATCTTATTTGAGC 1620
QY 1621 CTGGCTGCCAACCACTTGAAGTCTTCAAGTGAAGATGTCCGTCTCATCTG 1680
DB 1621 CTGGCTGCCAACCACTTGAAGTCTTCAAGTGAAGATGTCCGTCTCATCTG 1680
QY 1681 GCGCTGCTGACATGCGCTTGGGGTGTCTCGGAGTCTTCAACGAGCTGCTTGGC 1740
DB 1681 GCGCTGCTGACATGCGCTTGGGGTGTCTCGGAGTCTTCAACGAGCTGCTTGGC 1740
QY 1741 CAGAGCAGCGGCTGTCTGAGAGCGTCCGCGAGCTCACTTCTGCTGGGCTGCCAGGCGCC 1800
DB 1741 CAGAGCAGCGGCTGTCTGAGAGCGTCCGCGAGCTCACTTCTGCTGGGCTGCCAGGCGCC 1800
QY 1801 GGTACTCTGTTCTAGTCACTCAAGTGGCTGTGTCTGGGCTGCCAGGCGCGCC 1860
DB 1801 GGTACTCTGTTCTAGTCACTCAAGTGGCTGTGTCTGGGCTGCCAGGCGCGCC 1860
QY 1861 TCGCCAGCATCTCATCCACTTTCATCAATGTTCTTCTTCCACAGCCGCGGAGCAAC 1920
DB 1861 TCGCCAGCATCTCATCCACTTTCATCAATGTTCTTCTTCCACAGCCGCGGAGCAAC 1920
QY 1921 AGGCTGCTTACCCCCCGGAGAGGTGTCAGGCGACGCTGTGTGCTTCTGCTGGCTGCGCC 1980
DB 1921 AGGCTGCTTACCCCCCGGAGAGGTGTCAGGCGACGCTGTGTGCTTCTGCTGGCTGCGCC 1980
QY 1981 ATGGTCCCATCTGCTGTGTCACACCCCTGCACTGTGCAACCGCGCGCGCGC 2040
DB 1981 ATGGTCCCATCTGCTGTGTCACACCCCTGCACTGTGCAACCGCGCGCGCGC 2040
QY 2041 CTGCGGAGGAGGCGCGCTGACCGACAGGAGGAGAAACAGGCGGGTGTCTGGAGCTGCT 2100
DB 2041 CTGCGGAGGAGGCGCGCTGACCGACAGGAGGAGAAACAGGCGGGTGTCTGGAGCTGCT 2100
QY 2101 GAGCGATCTGTAAATGGCTGGAGCTCCGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
DB 2101 GAGCGATCTGTAAATGGCTGGAGCTCCGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
QY 2161 GAGGAGGCGAGCTGCTCCCTCCGAGGTGCTCATGCAACAGGAGGAGGAGGAGGAGGAG 2220
DB 2161 GAGGAGGCGAGCTGCTCCCTCCGAGGTGCTCATGCAACAGGAGGAGGAGGAGGAGGAG 2220
QY 2221 TTTCTGCTGGGCTGCTTCCAAACAGCGCTCTTCTGCGGCTGTGGGCGCTGAGGCTG 2280
DB 2221 TTTCTGCTGGGCTGCTTCCAAACAGCGCTCTTCTGCGGCTGTGGGCGCTGAGGCTG 2280
QY 2281 GCCCAGCGCAGCTGCTCCGAGGTTCCTGCGGCGATGCTGATGCGCATAGGCTGGGCTG 2340
DB 2281 GCCCAGCGCAGCTGCTCCGAGGTTCCTGCGGCGATGCTGATGCGCATAGGCTGGGCTG 2340
QY 2341 GCGCGGAGGAGTGGGCTGCGGCTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
DB 2341 GCGCGGAGGAGTGGGCTGCGGCTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
QY 2401 ATGACCGTGGCTATCTGCTGTGTGATGAGGAGTCTCTCAGCCTTCTGCAAGCGCTGCGG 2460

1741	Qy	CAGAGCACC	GGCTGCTGGAGAC	CGCTGCGGAGCTC	ACCTTCTCTGCTGGAC	CTTCTC	1800	
1741	Db	CAGAGGCAC	CGGCTGCTGCTGGAGAC	CGCTGCGGAGCTC	ACCTTCTCTGCTGGGAC	CTTCTC	1800	
1801	Qy	GGTTACCTC	GTGTTCTTAGTCA	TCTACAAGTGG	CTGTGCTCTGGGCTGC	CAGGCGGCC	1860	
1801	Db	GGTTACCTC	GTGTTCTTAGTCA	TCTACAAGTGG	CTGTGCTCTGGGCTGC	CAGGCGGCC	1860	
1861	Qy	TGCGCCAG	CATCTCTCATCTCA	CTTCAACAATGTT	TCCTTCTTCCCA	CAGCCCCAGCAAC	1920	
1861	Db	TGCGCCAG	CATCTCTCATCTCA	CTTCAACAATGTT	TCCTTCTTCCCA	CAGCCCCAGCAAC	1920	
1921	Qy	AGGCTGCTC	TACCCCGGCAGGAGT	GGTTCAGGSCAC	CGCTGGTGGTCT	TGGGCTGGGCC	1980	
1921	Db	AGGCTGCTC	TACCCCGGCAGGAGT	GGTTCAGGSCAC	CGCTGGTGGTCT	TGGGCTGGGCC	1980	
1981	Qy	ATGCTGCC	ATCTCTGCTGTGG	CACACCCCTG	CACTGTGCA	CCGCCACCCCGCCGC	2040	
1981	Db	ATGCTGCC	ATCTCTGCTGTGG	CACACCCCTG	CACTGTGCA	CCGCCACCCCGCCGC	2040	
2041	Qy	CTCGGAGG	AGGCCCGCTGAC	CGACAGGAGG	AAACAAGGCCGGT	TGCTGGACCTGCCT	2100	
2041	Db	CTCGGAGG	AGGCCCGCTGAC	CGACAGGAGG	AAACAAGGCCGGT	TGCTGGACCTGCCT	2100	
2101	Qy	GAGCCATCT	GTGAATGCTGAG	CTCCGATGAGG	AAAGGCAGGGG	CCCTTGGATGATGAA	2160	
2101	Db	GAGCCATCT	GTGAATGCTGAG	CTCCGATGAGG	AAAGGCAGGGG	CCCTTGGATGATGAA	2160	
2161	Qy	GAGGAGCC	AGCTGCTGCCCT	TCGAGGTGCT	ATGCAACAGG	GCATTCACACATCAG	2220	
2161	Db	GAGGAGCC	AGCTGCTGCCCT	TCGAGGTGCT	ATGCAACAGG	GCATTCACACATCAG	2220	
2221	Qy	TTCTGCTG	GGCTGCGTCTCAA	CACCGCTCTT	ACTCTGCGCTG	TGGGCGCTTGAGCCTG	2280	
2221	Db	TTCTGCTG	GGCTGCGTCTCAA	CACCGCTCTT	ACTCTGCGCTG	TGGGCGCTTGAGCCTG	2280	
2281	Qy	GCCCA	CGCCAGCTGTC	CGAGGTTCTGT	GGCCATATG	TGATGCGCATAGG	CCCTTGGGCTG	2340
2281	Db	GCCCA	CGCCAGCTGTC	CGAGGTTCTGT	GGCCATATG	TGATGCGCATAGG	CCCTTGGGCTG	2340
2341	Qy	GGCCGG	GAGGTGGCGGCTG	TGGTCTGGT	CCCCATCTT	TGCGCGCTTGGCGTG	2400	
2341	Db	GGCCGG	GAGGTGGCGGCTG	TGGTCTGGT	CCCCATCTT	TGCGCGCTTGGCGTG	2400	
2401	Qy	ATGAC	CGTGCTATCTCTG	CTGGTGA	TGGAGG	AGTCTCTCAG	CCCTTCCGCGG	2460
2401	Db	ATGAC	CGTGCTATCTCTG	CTGGTGA	TGGAGG	AGTCTCTCAG	CCCTTCCGCGG	2460
2461	Qy	CTGCA	CTGGGTGGAATTC	CAGAACAGT	TCTACTCAGG	CACGGGCTAC	AGCTGATGCC	2520
2461	Db	CTGCA	CTGGGTGGAATTC	CAGAACAGT	TCTACTCAGG	CACGGGCTAC	AGCTGATGCC	2520
2521	Qy	TTCA	CCCTTCGCTG	CCACAGATG	ACTAGGG	CGCCACTG	CAGAGCTCTTCTCT	2580
2521	Db	TTCA	CCCTTCGCTG	CCACAGATG	ACTAGGG	CGCCACTG	CAGAGCTCTTCTCT	2580
2581	Qy	GAC	CTCTGAGG	CAGGAGG	AAATAAG	ACGGTCCG	CCCTGGCAAAAA	2640
2581	Db	GAC	CTCTGAGG	CAGGAGG	AAATAAG	ACGGTCCG	CCCTGGCAAAAA	2640

RESULT 9
ACA56496
ID ACA56496 standard; cDNA; 2655 BP.

ACA56496:

DT 06-JUN-2003 (first entry)

DE Human signalling pathway polynucleotide probe SEQ ID NO 1094.

Human: probe: ss: array element: parkinson's disease:

human; probe; ss; array element; parkinson's disease;
signalling pathway population; cancer; adenocarcinoma; leukaemia;

KW	immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX	
OS	Homo sapiens.
XX	
PN	US6500938-B1.
XX	
PD	31-DEC-2002.
XX	
PP	30-JAN-1998; 98US-00016434.
XX	
PR	30-JAN-1998; 98US-00016434.
XX	
PA	(INCY-) INCYTE GENOMICS INC.
XX	
PI	Au-Young J, Seilhamer JJ;
XX	
WPI	2003-352189/33.
XX	
PT	Combination of polynucleotide probes, useful as array elements in a
PT	microarray for monitoring the expression of a number of target
PT	polynucleotides.
XX	
PS	Claim 1; SEQ ID NO 1094; 650p; English.

Query Match	100.0%	Score 2640;	DB 10;	Length 2655;
Best Local Similarity	100.0%;	Pred. NO. 0;		
Matches 2640;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

Qy	1	CGCGGTGCGCGGACGGCGAGCCAGCAGCAGGAGCGCGGCGCAGCA	CACCGGGGACCATG	60
Db	1	CGCGGTGCGCGGACGGCGAGCCAGCAGCAGGAGCGCGGCGCAGCA	CACCGGGGACCATG	60
Qy	61	GGCTCCATGTTCCGGAGCGAGGAGTGCCCTGGTCCAGCTCTTCTGCCACAGCGGCT		120
Db	61	GGCTCCATGTTCCGGAGCGAGGAGTGCCCTGGTCCAGCTCTTCTGCCACAGCGGCT		120
Qy	121	GCCTACACCTGCGTGAGTCGGCTGGGCGAGCTGGGCGCTCGTGGAGTTACAGAGACCTCAAC		180
Db	121	GCCTACACCTGCGTGAGTCGGCTGGGCGAGCTGGGCGCTCGTGGAGTTACAGAGACCTCAAC		180
Qy	181	GCCTCGGTGAGCCCTTTCAGAGACCGCTTTGTGGTTGATGTTTGGCGCTGTGAGGAGCTG		240
Db	181	GCCTCGGTGAGCCCTTTCAGAGACCGCTTTGTGGTTGATGTTTGGCGCTGTGAGGAGCTG		240
Qy	241	GAGAAGACCTTCACTTCTTCGACGAGGAGGTGCGCGGCGTGGCTGTGCTGCCCCCG		300
Db	241	GAGAAGACCTTCACTTCTTCGACGAGGAGGTGCGCGGCGTGGCTGTGCTGCCCCCG		300

QY 301 CCAAGGGAGGCTGCGGACCCCAACCCCGGACCTGCTGCGATCCAGGAGGAGCG 360
DB 301 CCAAGGGAGGCTGCGGACCCCAACCCCGGACCTGCTGCGATCCAGGAGGAGCG 360
QY 361 GAGCGCTGGGCCAGGAGCTGGGATGTCGGGATGTCGGGCAACCAAGCAGGCGCTGCGGCGCCAG 420
DB 361 GAGCGCTGGGCCAGGAGCTGGGATGTCGGGATGTCGGGCAACCAAGCAGGCGCTGCGGCGCCAG 420
QY 421 CTGCAACAGCTGACGCTCCAGCGCGCTGCTACGCCAGGGGCATGAACCTCAGCTGGCA 480
DB 421 CTGCAACAGCTGACGCTCCAGCGCGCTGCTACGCCAGGGGCATGAACCTCAGCTGGCA 480
QY 481 GCCGCCCAACAGATGGGGCTCAGAGAGGAGCGCCCTGCTCCAGGCGCCCGGGGGCGG 540
DB 481 GCCGCCCAACAGATGGGGCTCAGAGAGGAGCGCCCTGCTCCAGGCGCCCGGGGGCGG 540
QY 541 CACCAAGGACCTGAGGGTCACTTTGTGGAGGTGCGGTGGAGCCCAACAGGCGCCCTGCC 600
DB 541 CACCAAGGACCTGAGGGTCACTTTGTGGAGGTGCGGTGGAGCCCAACAGGCGCCCTGCC 600
QY 601 CTAGAGCGCTGCTCTGGAGGGCTGCGCGCGCTTCTCATTTGCGAGCTTCAGGAGCTG 660
DB 601 CTAGAGCGCTGCTCTGGAGGGCTGCGCGCGCTTCTCATTTGCGAGCTTCAGGAGCTG 660
QY 661 GAGCAGCGCTGGAGCAACCCGTGACGGGCGAGCCAGCCACGATGATGACCTTCTCATC 720
DB 661 GAGCAGCGCTGGAGCAACCCGTGACGGGCGAGCCAGCCACGATGATGACCTTCTCATC 720
QY 721 TCCTACTGGGTGAGCAGATCGGACAGAGATCCGCAAGATCCGCAAGATCCGCAAGATCCGCA 780
DB 721 TCCTACTGGGTGAGCAGATCGGACAGAGATCCGCAAGATCCGCAAGATCCGCAAGATCCGCA 780
QY 781 CAGGCTTCCGCTTCTGACAGAGGAGGCGCCGCTGCGGCGCTTCCAGGAGCTGCA 840
DB 781 CAGGCTTCCGCTTCTGACAGAGGAGGCGCCGCTGCGGCGCTTCCAGGAGCTGCA 840
QY 841 CAGCAGCGGAGCTGAGAGGTCTCTGGGGAGACAGAGCGGTCTCTGAGCCAGGTG 900
DB 841 CAGCAGCGGAGCTGAGAGGTCTCTGGGGAGACAGAGCGGTCTCTGAGCCAGGTG 900
QY 901 CTAGCGCGGTGCTGAGCTGTCGCGCAGGCGAGGTGCAAGATGAAGGCC 960
DB 901 CTAGCGCGGTGCTGAGCTGTCGCGCAGGCGAGGTGCAAGATGAAGGCC 960
QY 961 GTGTACCTGGCCCTGAAACAGTGCAGCTGAGCAGCAGCAAGTGCCTCATTTGCCGAG 1020
DB 961 GTGTACCTGGCCCTGAAACAGTGCAGCTGAGCAGCAGCAAGTGCCTCATTTGCCGAG 1020
QY 1021 GCCTGGTCTCTGTGCGAGACCTGCGCCGCTGCGAGAGGCGCTGCGGAGCAGCTCGATG 1080
DB 1021 GCCTGGTCTCTGTGCGAGACCTGCGCCGCTGCGAGAGGCGCTGCGGAGCAGCTCGATG 1080
QY 1081 GAGGAGGAGTGAAGTCCGCTGCTGCGGATGCTGCGGAGCAATGCGCCCGCACTC 1140
DB 1081 GAGGAGGAGTGAAGTCCGCTGCTGCGGATGCTGCGGAGCAATGCGCCCGCACTC 1140
QY 1141 ATCCGCAACACCGCTTCAAGGCGAGCTTCAAGGCGATGCTGAGTGCCTGAGGCGG 1200
DB 1141 ATCCGCAACACCGCTTCAAGGCGAGCTTCAAGGCGATGCTGAGTGCCTGAGGCGG 1200
QY 1201 CGCTACAGGAGGTCAACCCCGCTCCCTACACCATCATCCTTCCCTTCTGTTTGT 1260
DB 1201 CGCTACAGGAGGTCAACCCCGCTCCCTACACCATCATCCTTCCCTTCTGTTTGT 1260
QY 1261 GTGATGTTGGGGATGTTGGGCAACCGGCTGCTCATGTTCTTTCGCGCTGCGCATGTC 1320
DB 1261 GTGATGTTGGGGATGTTGGGCAACCGGCTGCTCATGTTCTTTCGCGCTGCGCATGTC 1320
QY 1321 CTTGGGAGAACCGACCGCTGTGAAGCGCGGAGAGAGATCTGCGAGCTTCTTC 1380
DB 1321 CTTGGGAGAACCGACCGCTGTGAAGCGCGGAGAGAGATCTGCGAGCTTCTTC 1380
QY 1381 AGGGCGCTACCTGCTCTGTTATGGGCGCTGTTCTCCATCTACACCGGCTTCATCTAC 1440

DB 1381 AGGGCGCTACCTGCTCTGTTATGGGCGCTGTTCTCATCTACACCGGCTTCATCTAC 1440
QY 1441 AACGAGTCTTCAAGTGCAGCAGCATCTTCCCTCGGCTGAGGTGTCGCCCGCATG 1500
DB 1441 AACGAGTCTTCAAGTGCAGCAGCATCTTCCCTCGGCTGAGGTGTCGCCCGCATG 1500
QY 1501 GCCAACAGTCTGGCTGGAGTGATGCAATCTTGGGCCAGCACAGATGCTTACCTGGAT 1560
DB 1501 GCCAACAGTCTGGCTGGAGTGATGCAATCTTGGGCCAGCACAGATGCTTACCTGGAT 1560
QY 1561 CCCAACGTCACCGGTGCTTCTTGGGACCTTACCCCTTGGCATCGATCTTATTTGGAGC 1620
DB 1561 CCCAACGTCACCGGTGCTTCTTGGGACCTTACCCCTTGGCATCGATCTTATTTGGAGC 1620
QY 1621 CTGGCTGCAACCACTTGAAGCTTCTCAACTCTTCAAGATGAAGATGCTCGTCACTG 1680
DB 1621 CTGGCTGCAACCACTTGAAGCTTCTCAACTCTTCAAGATGAAGATGCTCGTCACTG 1680
QY 1681 GGCGTCTGTCACATGGCCCTTGGGGTGTCTCGGAGTCTTCAACAGTGCACCTTTGGC 1740
DB 1681 GGCGTCTGTCACATGGCCCTTGGGGTGTCTCGGAGTCTTCAACAGTGCACCTTTGGC 1740
QY 1741 CAGAGGCAACCGCTGCTGTCGAGACGCTGCGGAGTCTCACCTTCTGCTGGGACTCTTC 1800
DB 1741 CAGAGGCAACCGCTGCTGTCGAGACGCTGCGGAGTCTCACCTTCTGCTGGGACTCTTC 1800
QY 1801 GGTTACTCTGTTCTTGAAGTCACTCAAGTGGTGTGTCTGGGCTGCGAGGCGCGC 1860
DB 1801 GGTTACTCTGTTCTTGAAGTCACTCAAGTGGTGTGTCTGGGCTGCGAGGCGCGC 1860
QY 1861 TCGCCGAGCATCTCATCCACTTCAACAGTGTCTTCTTCTCCACAGCCCGAGCAGC 1920
DB 1861 TCGCCGAGCATCTCATCCACTTCAACAGTGTCTTCTTCTCCACAGCCCGAGCAGC 1920
QY 1921 AGGCTGCTCTACCCCGGAGGAGTGTTCAGGCGACGCTGCTGGTCTTGGCTTTGGCC 1980
DB 1921 AGGCTGCTCTACCCCGGAGGAGTGTTCAGGCGACGCTGCTGGTCTTGGCTTTGGCC 1980
QY 1981 ATGTGCGCATCTCTGCTGTTGGACACCCCTGCACTGTGTGCAACCGCAGCGCGCGC 2040
DB 1981 ATGTGCGCATCTCTGCTGTTGGACACCCCTGCACTGTGTGCAACCGCAGCGCGCGC 2040
QY 2041 CTGCGGAGGCGCGCTGACCGAGAGGAGAAACAGGCGCGCTTCTGAGACCTGCT 2100
DB 2041 CTGCGGAGGCGCGCTGACCGAGAGGAGAAACAGGCGCGCTTCTGAGACCTGCT 2100
QY 2101 GACGATCTGTGAATGGCTGGAGCTTCCGATGAGGAAAGAGGCGGCTTGGATGATA 2160
DB 2101 GACGATCTGTGAATGGCTGGAGCTTCCGATGAGGAAAGAGGCGGCTTGGATGATA 2160
QY 2161 GAGGAGGCGGAGCTGCTCCCTCGAGTGTCTATGCAACAGGCGCATCCACACCTGAG 2220
DB 2161 GAGGAGGCGGAGCTGCTCCCTCGAGTGTCTATGCAACAGGCGCATCCACACCTGAG 2220
QY 2221 TTCTGCTGCGCTGCTGCTCAACACCGCTTCTTCTGCGCTGCGGCTTGGGCTTGG 2280
DB 2221 TTCTGCTGCGCTGCTGCTCAACACCGCTTCTTCTGCGCTGCGGCTTGGGCTTGG 2280
QY 2281 GCCACGCGCAGCTGCTCGAGGTTCTGTTGGGCCATGTTGATGCGCATAGGCGCTGG 2340
DB 2281 GCCACGCGCAGCTGCTCGAGGTTCTGTTGGGCCATGTTGATGCGCATAGGCGCTGG 2340
QY 2341 GCGCGGAGGTGGGCGTGTGGTGTGTTGTTGCTTCTTTCGCGCTTTCGCGCTG 2400
DB 2341 GCGCGGAGGTGGGCGTGTGGTGTGTTGTTGCTTCTTTCGCGCTTTCGCGCTG 2400
QY 2401 ATGACCGTGGCTATCTGCTGTGATGAGGAGTCTCAGGCTTCTCAGCGCTTGG 2460
DB 2401 ATGACCGTGGCTATCTGCTGTGATGAGGAGTCTCAGGCTTCTCAGCGCTTGG 2460
QY 2461 CTGCACTGGGTGGAATTCAGAAAGTTCTACTCAGGCGGCTTCAAGCTGAGTCCC 2520

901 CTAGCGGGGTGCTGAGCTGTGCGCCGAGGCGAGGTGCAGGTCCACAAGATGAAGGC 960
961 GTGTACTCTGCGCTGAACAGTGCAGCTGAGCACCACACCAAGTGCCTCATTTGCCGAG 1020
961 GTGTACTCTGCGCTGAACAGTGCAGCTGAGCACCACCAAGTGCCTCATTTGCCGAG 1020
1021 GCTGTGTCTGTGTGCGAGACCTTGCGCCGCGCTGCGAGGCGCTGCGGACAGCTCGATG 1080
1021 GCTGTGTCTGTGTGCGAGACCTTGCGCCGCGCTGCGAGGCGCTGCGGACAGCTCGATG 1080
1081 GAGGAGGAGTGTGTGCTGCGCTGACCGGATCCCTGCGGACATGCGCCGCCACACTC 1140
1081 GAGGAGGAGTGTGTGCTGCGCTGACCGGATCCCTGCGGACATGCGCCGCCACACTC 1140
1141 ATCCGACCAACCGCTTACGCGCAGCTTCCAGGCGCATGTCGATACGCGGTGGGC 1200
1141 ATCCGACCAACCGCTTACGCGCAGCTTCCAGGCGCATGTCGATACGCGGTGGGC 1200
1201 CGCTACGAGAGGTCAACCCCGCTCCCTACACCATCATCACCTTCCCTTCTGTTTGTCT 1260
1201 CGCTACGAGAGGTCAACCCCGCTCCCTACACCATCATCACCTTCCCTTCTGTTTGTCT 1260
1261 GTGATGTTCCGGGATGTGGGCGACCGGCTGCTCATGTTCTCTTGGCCCTGCGCATGCTC 1320
1261 GTGATGTTCCGGGATGTGGGCGACCGGCTGCTCATGTTCTCTTGGCCCTGCGCATGCTC 1320
1321 CTTGGGAGAACCGACCGGCTGTGAAGCGCGCAGAACGAGATCTGGCAGACTTCTTTC 1380
1321 CTTGGGAGAACCGACCGGCTGTGAAGCGCGCAGAACGAGATCTGGCAGACTTCTTTC 1380
1381 AGGGGCGCTACCTGCTCTGCTTATGAGGCGCTGTTCTCCATCTACACCGGCTTTCATCTAC 1440
1381 AGGGGCGCTACCTGCTCTGCTTATGAGGCGCTGTTCTCCATCTACACCGGCTTTCATCTAC 1440
1441 AACGAGTGTTCAGTGCAGGCGCAGCAGATCTTCCCTCGGGCTGAGTGTGGCGCGCATG 1500
1441 AACGAGTGTTCAGTGCAGGCGCAGCAGATCTTCCCTCGGGCTGAGTGTGGCGCGCATG 1500
1501 GCCAACCACTGTGGCTGAGTGTGATGATCTTCCGCGCCAGCAGATGCTTACCCCTGGAT 1560
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1561 CCCAACGTACCGGCTGTCTCTGAGGACCTTACCCCTTTGGCATCGATCTTATTTGGAGC 1620
1561 CCCAACGTACCGGCTGTCTCTGAGGACCTTACCCCTTTGGCATCGATCTTATTTGGAGC 1620
1621 CTGGGCTGCCAACCACTTGAAGTCTTCAACTGCTTCAAGATGAAGATGTCGATCTCTG 1680
1621 CTGGGCTGCCAACCACTTGAAGTCTTCAACTGCTTCAAGATGAAGATGTCGATCTCTG 1680
1681 GCGCTGTGTGCATGCGCTTTGGGCTGCTCGGAGTCTTCAACACGTCGACTTTGGC 1740
1681 GCGCTGTGTGCATGCGCTTTGGGCTGCTCGGAGTCTTCAACACGTCGACTTTGGC 1740
1741 CAGAGCACCGGCTGTCTGTGAGAGCGCTGCGGAGCTCACCTTCTGCTGGGACTCTTTC 1800
1741 CAGAGCACCGGCTGTCTGTGAGAGCGCTGCGGAGCTCACCTTCTGCTGGGACTCTTTC 1800
1801 GTTTACTCTGTGTTCTAGTGCATCTACAAAGTGGCTGTGTGCTGGGCTGCCAGGGCGGC 1860
1801 GTTTACTCTGTGTTCTAGTGCATCTACAAAGTGGCTGTGTGCTGGGCTGCCAGGGCGGC 1860
1861 TCGCCGAGCATCTCATCCACTTTCATCAACATGTTCTCTTCCACAGCCCGCAGCAC 1920
1861 TCGCCGAGCATCTCATCCACTTTCATCAACATGTTCTCTTCCACAGCCCGCAGCAC 1920
1921 AGGCTGCTTACCCCGGAGAGGTGGTCCAGGCGACCGCTGTGTGCTTGGCTTGGCC 1980
1921 AGGCTGCTTACCCCGGAGAGGTGGTCCAGGCGACCGCTGTGTGCTTGGCTTGGCC 1980
1981 ATGTGTGCCCATCTGTGCTTGGCAGACCCCTGCACTGCTGCAACCGCGCCGCGC 2040
1981 ATGTGTGCCCATCTGTGCTTGGCAGACCCCTGCACTGCTGCAACCGCGCCGCGC 2040

2041 CTGCGGAGAGGCGCGCTGACCGACGAGGAGGAACAAGCGCGGTTGCTGGACCTGCGCT 2100
2041 CTGCGGAGAGGCGCGCTGACCGACGAGGAGGAACAAGCGCGGTTGCTGGACCTGCGCT 2100
2101 GACGATCTGTGAATGGCTGGAGCTCCGATGAGGAGAAAAGCAGGGGCGCTGGATGATGAA 2160
2101 GACGATCTGTGAATGGCTGGAGCTCCGATGAGGAGAAAAGCAGGGGCGCTGGATGATGAA 2160
2161 GAGGAGGCGGAGCTGTCCTCCCTCCGAGTGTCTCATGACAGGCGCATCCACACCATCGAG 2220
2161 GAGGAGGCGGAGCTGTCCTCCCTCCGAGTGTCTCATGACAGGCGCATCCACACCATCGAG 2220
2221 TTCTGCTGGGCTGGGCTCTCCAAACCGCGCTCTTACCTGCGGCTGTGGGCGCTTGAGCCTG 2280
2221 TTCTGCTGGGCTGGGCTCTCCAAACCGCGCTCTTACCTGCGGCTGTGGGCGCTTGAGCCTG 2280
2281 GCCCAGCGCCAGCTGTCCGAGGTTCTGTGGGCGCATGTGTGATGCGATAGGCGCTGGGCGCTG 2340
2281 GCCCAGCGCCAGCTGTCCGAGGTTCTGTGGGCGCATGTGTGATGCGATAGGCGCTGGGCGCTG 2340
2341 GCGCGGAGGTGGGCGTGTGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2400
2341 GCGCGGAGGTGGGCGTGTGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2400
2401 ATGACCGTGGCTATCTGCTGTGTGATGAGGAGCTCTCAGCCCTTCTGCAAGCTGAGTCCC 2460
2401 ATGACCGTGGCTATCTGCTGTGTGATGAGGAGCTCTCAGCCCTTCTGCAAGCTGAGTCCC 2460
2461 CTGCACTGGGTGGAATTCAGAAACAAGTTCTACTCAGGCAAGGCTTACAGCTGAGTCCC 2520
2461 CTGCACTGGGTGGAATTCAGAAACAAGTTCTACTCAGGCAAGGCTTACAGCTGAGTCCC 2520
2521 TTCACTTCTGCTGCCACAGATGATAGGCGCCACTGAGGCTCTGCGAGACCTCTTCTCT 2580
2521 TTCACTTCTGCTGCCACAGATGATAGGCGCCACTGAGGCTCTGCGAGACCTCTTCTCT 2580
2581 GACCTCTGAGGCGAGGAGGAATAAAGACGGTCCGCTGGCAAAAAAAGGCTTCTGCGGCTTCTGCGG 2640
2581 GACCTCTGAGGCGAGGAGGAATAAAGACGGTCCGCTGGCAAAAAAAGGCTTCTGCGGCTTCTGCGG 2640

RESULT 11

ADIS6292

ID ADIS6292 standard; DNA; 2655 BP.

XX AC ADIS6292;

XX DT /22-APR-2004 (first entry)

XX Human polynucleotide probe #1094.

Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
effector-like polypeptide; cancer; immunopathology; neuropathology;
drug development; toxicology; carcinogenicity;
signalling pathway polypeptide; adrenal gland; bladder; bone;
bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
dementia; amnesia; epilepsy; Alzheimer's disease; depression.

OS Homo sapiens.

XX US2004010136-A1.

XX PD 15-JAN-2004.

XX PF 26-NOV-2002; 2002US-00305720.

XX PR 30-JAN-1998; 98US-00016434.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Au-Young J, Seilhamer JJ;

XX
DR WPI; 2004-090520/09.

PT New composition comprising polynucleotide probes, useful as array
PT elements in a microarray for monitoring the expression of target
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
PT fragments.

PS Claim 6; SEQ ID NO 1094; 73pp; English.

The invention relates to a composition of polynucleotide probes comprising first polynucleotide probes comprising at least a portion of a gene encoding a receptor-like polypeptide, second polynucleotide probes comprising at least a portion of a gene encoding a transducing polypeptide and third polynucleotide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polynucleotides. The microarray is useful in the diagnosis and treatment of cancer, an immunopathology or a neuropathology. It can also be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. Microarrays can also be used for monitoring the progression of diseases that may be associated with the altered expression of signalling pathway polypeptides. The composition can also be used to purify a subpopulation of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix, an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or ulcerative colitis, or a neuropathology, e.g. dementia, amnesia, epilepsy, Alzheimer's disease or depression. This sequence represents a human polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 2655 BP; 460 A; 885 C; 824 G; 486 T; 0 U; 0 Other;

Query Match	100.0%	Score 2640;	DB 12;	Length 2655;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2640;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

Qy	1	CGCGTTCGCGGACGGGACGACGACGCGGAGGCGCGCGCAGCACACCCGGGGACCATG	60
Db	1	CGCGTTCGCGGACGGGACGGGACGACGCGGAGGCGCGCGCAGCACACCCGGGGACCATG	60
Qy	61	GGCTCCATGTTCCGGAGCGAGGAGGTGGCCCTGCTGCTCCAGCTCTTCTTGCCACACGCGCT	120
Db	61	GGCTCCATGTTCCGGAGCGAGGAGGTGGCCCTGCTGCTCCAGCTCTTCTTGCCACACGCGCT	120
Qy	121	GCCTACACCTGCGTGAGTTCGGCTGGGGAGCTGGGGCTTCGTGGAGTTCAGAGACCTCAAC	180
Db	121	GCCTACACCTGCGTGAGTTCGGCTGGGGAGCTGGGGCTTCGTGGAGTTCAGAGACCTCAAC	180
Qy	181	GCCTCGGTGAGCGCCTTCCAGAGACGCTTGTGTGTTGATGTTTGGCGCTGTGAGAGCTG	240
Db	181	GCCTCGGTGAGCGCCTTCCAGAGACGCTTGTGTGTTGATGTTTGGCGCTGTGAGAGCTG	240
Qy	241	GAGAAGACCTTCACTTTCCTGCAGAGAGAGGTGCGGGGGCTGGGCTGGTCTGCCCCCG	300
Db	241	GAGAAGACCTTCACTTTCCTGCAGAGAGAGGTGCGGGGGCTGGGCTGGTCTGCCCCCG	300
Qy	301	CCAAAGGGGAGGTGTCGGGACCCCCACCCCGGACCTGTGTCGCATCCAGGAGGAGACG	360
Db	301	CCAAAGGGGAGGTGTCGGGACCCCCACCCCGGACCTGTGTCGCATCCAGGAGGAGACG	360
Qy	361	GAGCGCTGCGCCACAGGAGCTGCGGGATGTGCGGGGCAACACAGCAGGCCCTCGCGGGCCAG	420
Db	361	GAGCGCTGCGCCACAGGAGCTGCGGGATGTGCGGGGCAACACAGCAGGCCCTCGCGGGCCAG	420
Qy	421	CTGCAACAGCTGCAGCTTCCACGCCCGCGTGCTACGCCAGGGGCCATGAACCTCAGCTGSCA	480
Db	421	CTGCAACAGCTGCAGCTTCCACGCCCGCGTGCTACGCCAGGGGCCATGAACCTCAGCTGSCA	480

1561 CCAACGTCACCGTGTCTTCTGGGACCTTACCCCTTTGGCATCGATCTATTGGAGC 1620
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 1622 CTGGCTGCCAACAACCTTGAGCTTCTCAATCTCTTCAAGATGAAGATGTCGGTCAATCTG 1680
 1681 GGCGTCTGCACATGCGCTTGGGCTGCTCGGAGTCTTCAACCACTGCACTTTGGC 1740
 1682 GGCGTCTGCACATGCGCTTGGGCTGCTCGGAGTCTTCAACCACTGCACTTTGGC 1740
 1741 CAGAGCACCGGCTGCTGCTGAGAGCGCTGCCGAGCTCACCTTCTGCTGGGACTCTTC 1800
 1742 CAGAGCACCGGCTGCTGCTGAGAGCGCTGCCGAGCTCACCTTCTGCTGGGACTCTTC 1800
 1801 GGTACCTGCTGTCTAGTCTATCAAGAGTGTCTGCTGGCTGCTGGCTGCCAGGCGGC 1860
 1802 GGTACCTGCTGTCTAGTCTATCAAGAGTGTCTGCTGGCTGCTGGCTGCCAGGCGGC 1860
 1861 TCGCCGAGCATCTCATCTACCTTCAACATGTTCTCTTCCACAGCCCGAGCAAC 1920
 1862 TCGCCGAGCATCTCATCTACCTTCAACATGTTCTCTTCCACAGCCCGAGCAAC 1920
 1921 AGGCTGCTCTACCCCGGAGGAGTGTCTCGAGCCACGCTGTGTCTTGGCTTTGGCC 1980
 1922 AGGCTGCTCTACCCCGGAGGAGTGTCTCGAGCCACGCTGTGTCTTGGCTTTGGCC 1980
 1981 ATGGTCCCATCTGCTGTGGACACCCCTGCACTGCTGCAACCGCCGCGCCGC 2040
 1982 ATGGTCCCATCTGCTGTGGACACCCCTGCACTGCTGCAACCGCCGCGCCGC 2040
 2041 CTGGGAGAGGCGCGCTGACCGACAGGAGGAAACAGGCGGGTGTCTGACCTTGCCT 2100
 2042 CTGGGAGAGGCGCGCTGACCGACAGGAGGAAACAGGCGGGTGTCTGACCTTGCCT 2100
 2101 GACGATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGGAGGCGCTTGGATGATGAA 2160
 2102 GACGATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGGAGGCGCTTGGATGATGAA 2160
 2161 GAGGAGCGGAGCTGTCTCCCTCGAGGCTCATGACACAGGCGCATCACACCTATCGAG 2220
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 2281 GCCACGCGCCAGCTGTCCGAGGTTCTGTGGGCGATGCTGATGCGATAGGCTTGGGCTG 2340
 2282 GCCACGCGCCAGCTGTCCGAGGTTCTGTGGGCGATGCTGATGCGATAGGCTTGGGCTG 2340
 2341 GGCGGGAGGTGGCGTGGCGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 2400
 2342 GGCGGGAGGTGGCGTGGCGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 2400
 2401 ATGACCGTGGCTATCTGCTGTGTGATGAGGAGTCTTCAAGCTTCTGACGCTTGGCG 2460
 2402 ATGACCGTGGCTATCTGCTGTGTGATGAGGAGTCTTCAAGCTTCTGACGCTTGGCG 2460
 2461 CTGCACTGGGTGGAAATTCAGAACAGTTCTACTCAGGACCGGCTTCAAGCTTGGTCCC 2520
 2462 CTGCACTGGGTGGAAATTCAGAACAGTTCTACTCAGGACCGGCTTCAAGCTTGGTCCC 2520
 2521 TTCACTTCTGCTGCCACAGATGACTAGGCGCCACTGAGGTCTTGGCAGACCTTCTTCT 2580
 2522 TTCACTTCTGCTGCCACAGATGACTAGGCGCCACTGAGGTCTTGGCAGACCTTCTTCT 2580
 2581 GACCTCTGAGGAGGAGGAGTAAAGACGGTCCGCTTGGCAAAAAAAGGAGGAGGAGG 2640
 2582 GACCTCTGAGGAGGAGGAGTAAAGACGGTCCGCTTGGCAAAAAAAGGAGGAGGAGG 2640

ADS83657
 ID ADS83657 standard; cDNA; 2655 BP.
 AC ADS83657;
 DT 11-AUG-2005 (first entry)
 DE Human lymph node cDNA #916.
 KW ss; gene; human; immunological response; blood cell; cancer; immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis; bronchitis; ulcerative colitis; diabetes; multiple sclerosis; osteoporosis; pancreatitis; infection; arthritis; lymph node.
 OS Homo sapiens.
 PN US2004077003-A1.
 PD 22-APR-2004.
 PF 14-AUG-2003; 2003US-00641643.
 PR 09-FEB-1998; 98US-00023655.
 PA (INCV-) INCYTE CORP.
 PI Cocks BG, Stuart SG, Seilhamer JJ;
 DR WPI; 2004-387937/36.
 PT New compositions having a number of first, second and third polynucleotide probes, useful in research and diagnostic applications in cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and infections.
 PS Claim 15; SEQ ID NO 916; 16pp; English.
 CC The invention relates to polynucleotides which are used as probes to detect genes differentially expressed in an immunological response, abundantly expressed in an immunological response and/or coding for a polypeptide known to regulate blood cell biology. The polynucleotides are useful in research and diagnostic applications particularly in cancer and immunopathological conditions, such as AIDS, allergies, anaemia, asthma, atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple sclerosis, osteoporosis, pancreatitis, infections and arthritis. The present sequence represents a human lymph node cDNA used to detect blood cell and immunological response gene expression. Note: The present sequence does not appear in the printed specification but was obtained in electronic format from the USPTO web site (seqdata.uspto.gov/sequence.html?DocID=20040077003).
 SQ Sequence 2655 BP; 460 A; 885 C; 824 G; 486 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2640; DB 13; Length 2655;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGCTGCGCGAGCGGCGAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
 DB 1 CGGCTGCGCGAGCGGCGAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
 QY 61 GGCTCCATGTTCCGAGCGAGGAGTGGCTTCCAGCTCTTCTTCCACAGCGGCT 120
 DB 61 GGCTCCATGTTCCGAGCGAGGAGTGGCTTCCAGCTCTTCTTCCACAGCGGCT 120
 QY 121 GCCTACACCTGCTGAGTGGCTGGCGGAGCTGGGCTCTGTTGGAGTTTCAGAGACCTCAAC 180
 DB 121 GCCTACACCTGCTGAGTGGCTGGCGGAGCTGGGCTCTGTTGGAGTTTCAGAGACCTCAAC 180
 QY 181 GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTGTATGTTTGGCGCTGTGAGGAGCTG 240
 DB 181 GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTGTATGTTTGGCGCTGTGAGGAGCTG 240

QY 241 GAGAGACCTTACCTTCTCCAGGAGGAGGTGCGCGGGCTGGGTGGTCTGCCCCCG 300
DB 241 GAGAGACCTTACCTTCTCCAGGAGGAGGTGCGCGGGCTGGGTGGTCTGCCCCCG 300
QY 301 CCAAGGGAGGCTGCGGCACACCCACCCCGGAGCTGTGCGCATCCAGAGGAGACG 360
DB 301 CCAAGGGAGGCTGCGGCACACCCACCCCGGAGCTGTGCGCATCCAGAGGAGACG 360
QY 361 GAGGCTGCGCCAGAGCTGCGGGATGTGCGGGCAACACAGAGGCCCTGCGGGCCAG 420
DB 361 GAGGCTGCGCCAGAGCTGCGGGATGTGCGGGCAACACAGAGGCCCTGCGGGCCAG 420
QY 421 CTGACACAGCTGAGCTTCAAGCGCGCTGCTACGCGAGGGCCATGAACCTCAGCTGGCA 480
DB 421 CTGACACAGCTGAGCTTCAAGCGCGCTGCTACGCGAGGGCCATGAACCTCAGCTGGCA 480
QY 481 GCGGCCACACAGATGGGGCTCAGAGAGGACGCCCCCTGTCTCAGGCCCCCGGGGGCCG 540
DB 481 GCGGCCACACAGATGGGGCTCAGAGAGGACGCCCCCTGTCTCAGGCCCCCGGGGGCCG 540
QY 541 CACAGGACCTGAGGGTCAACTTTGTGGCAGGTGCCGTGAGGCCCAAGAGGCCCTGCC 600
DB 541 CACAGGACCTGAGGGTCAACTTTGTGGCAGGTGCCGTGAGGCCCAAGAGGCCCTGCC 600
QY 601 CTAGAGGCTGCTCTGAGGGCTGCGCGGGCTTCTCATTTGCCAGCTTACGGAGCTG 660
DB 601 CTAGAGGCTGCTCTGAGGGCTGCGCGGGCTTCTCATTTGCCAGCTTACGGAGCTG 660
QY 661 GAGCAGCGCTGAGGACACCCGTGACGGGCGAGCCAGCCAGCTGGATGACCTTCTCATC 720
DB 661 GAGCAGCGCTGAGGACACCCGTGACGGGCGAGCCAGCCAGCTGGATGACCTTCTCATC 720
QY 721 TCCTACTGCGGTGAGCAGATCGGACAGAGATCCGCAAGATCAAGCTGCTTCCACTGC 780
DB 721 TCCTACTGCGGTGAGCAGATCGGACAGAGATCCGCAAGATCAAGCTGCTTCCACTGC 780
QY 781 CAGCTTCTCCGTTCTGACAGAGGAGGCGCGCTCGGGCCCTGACAGCTGCA 840
DB 781 CAGCTTCTCCGTTCTGACAGAGGAGGCGCGCTCGGGCCCTGACAGCTGCA 840
QY 841 CAGCAGGCGAGGCTGACAGAGGTCTCTCGGGAGACAGAGCGTCTTGAGCCAGGTG 900
DB 841 CAGCAGGCGAGGCTGACAGAGGTCTCTCGGGAGACAGAGCGTCTTGAGCCAGGTG 900
QY 901 CTAGGCGGGTGTGAGCTGTGCGCCAGGCGAGGTGCAAGATGAAGGCC 960
DB 901 CTAGGCGGGTGTGAGCTGTGCGCCAGGCGAGGTGCAAGATGAAGGCC 960
QY 961 GTGTACTTGGCCCTGAACAGTGCAGGTGAGCACACGCAAGTGCCTCATTTGCCGAG 1020
DB 961 GTGTACTTGGCCCTGAACAGTGCAGGTGAGCACACGCAAGTGCCTCATTTGCCGAG 1020
QY 1021 GCCTGTGTCTGTGCGAGACTGCGCGCCCTGACAGAGGCCCTGCGGGACGCTCGATG 1080
DB 1021 GCCTGTGTCTGTGCGAGACTGCGCGCCCTGACAGAGGCCCTGCGGGACGCTCGATG 1080
QY 1081 GAGAGGGAGTGAAGTCCGCTGCTACCGCATCCCTGCGGGACATGCCCCCACTC 1140
DB 1081 GAGAGGGAGTGAAGTCCGCTGCTACCGCATCCCTGCGGGACATGCCCCCACTC 1140
QY 1141 ATCCGACCAACCGCTTCAAGGCGAGTTCAGGGGATCGTGGATCGTACGGCGTGGC 1200
DB 1141 ATCCGACCAACCGCTTCAAGGCGAGTTCAGGGGATCGTGGATCGTACGGCGTGGC 1200
QY 1201 CGCTACAGAGGTCAACCCGCTCCCTACACCATCATACCTTCCCTTCTGTTGCT 1260
DB 1201 CGCTACAGAGGTCAACCCGCTCCCTACACCATCATACCTTCCCTTCTGTTGCT 1260
QY 1261 GTGATGTTGGGATGTGGCCACCGGCTGCTCATGTTCTTTCGCGCTGGCCATGGTC 1320
DB 1261 GTGATGTTGGGATGTGGCCACCGGCTGCTCATGTTCTTTCGCGCTGGCCATGGTC 1320
QY 1321 CTTGCGGAGAACCGACCGGCTGTGAAGCGCGCAGAACGAGATCTGGCAGACTTCTTC 1380

DB 1321 CTTGCGGAGAACCGACCGGCTGTGAAGCGCGCAGAACGAGATCTGCGAGACTTCTTC 1380
QY 1381 AGGCGCGCTACCTGTCTCTGCTTATGGGCTGTCTTCTACATCTACACCGCTTCTATCTAC 1440
DB 1381 AGGCGCGCTACCTGTCTCTGCTTATGGGCTGTCTTCTACATCTACACCGCTTCTATCTAC 1440
QY 1441 AACGAGTGTCTAGTCCGCCACACAGATCTTCCCCTCGGGCTGGAGTGTGGCGCCCATG 1500
DB 1441 AACGAGTGTCTAGTCCGCCACACAGATCTTCCCCTCGGGCTGGAGTGTGGCGCCCATG 1500
QY 1501 GCCAACAGTCTGGCTGGAGTGAATCTTGGGCCAGCACAGATGCTTACCTCGAT 1560
DB 1501 GCCAACAGTCTGGCTGGAGTGAATCTTGGGCCAGCACAGATGCTTACCTCGAT 1560
QY 1561 CCCAAGCTCACCGGTGTCTTCTGGGACCTTACCCCTTGGCATCGATCTTATTTGGAGC 1620
DB 1561 CCCAAGCTCACCGGTGTCTTCTGGGACCTTACCCCTTGGCATCGATCTTATTTGGAGC 1620
QY 1621 CTGGCTGCCAACCACTTGAGCTTCTCAACTCTTCAAGATGAAGATGTCGTCATCTG 1680
DB 1621 CTGGCTGCCAACCACTTGAGCTTCTCAACTCTTCAAGATGAAGATGTCGTCATCTG 1680
QY 1681 GCGCTGCTGCACATGGCTTGGGGTGTCTCGGAGTCTTCAACAGCTGCACTTTGGC 1740
DB 1681 GCGCTGCTGCACATGGCTTGGGGTGTCTCGGAGTCTTCAACAGCTGCACTTTGGC 1740
QY 1741 CAGAGCACCGGCTGTCTGGAGACGCTGCCGGAGCTCACTTCTCTGCTGGGACTCTTC 1800
DB 1741 CAGAGCACCGGCTGTCTGGAGACGCTGCCGGAGCTCACTTCTCTGCTGGGACTCTTC 1800
QY 1801 GGTACTCTGTTTCTAGTCACTAAGTGGCTGTGTCTGGGCTGCCAGGGCGCC 1860
DB 1801 GGTACTCTGTTTCTAGTCACTAAGTGGCTGTGTCTGGGCTGCCAGGGCGCC 1860
QY 1861 TCGCCAGCATCTCTCACTTCACTCAACATGTTCTTCTTCCACAGCCGCCAGCAAC 1920
DB 1861 TCGCCAGCATCTCTCACTTCACTCAACATGTTCTTCTTCCACAGCCGCCAGCAAC 1920
QY 1921 AGGCTCTCTTACCCCCGCGAGGAGTGTCTCAGGCCACGCTGTGTCTTGGCTTGGCC 1980
DB 1921 AGGCTCTCTTACCCCCGCGAGGAGTGTCTCAGGCCACGCTGTGTCTTGGCTTGGCC 1980
QY 1981 ATGTTGCCATCTGTCTGTGGCACACCTGTGCACTGTGCAACCGCGCCG 2040
DB 1981 ATGTTGCCATCTGTCTGTGGCACACCTGTGCACTGTGCAACCGCGCGC 2040
QY 2041 CTGCGAGGAGGCGCCCTGACCGACAGGAGGAGAAACAGGCCGGGTGTGCGACCTGCCT 2100
DB 2041 CTGCGAGGAGGCGCCCTGACCGACAGGAGGAGAAACAGGCCGGGTGTGCGACCTGCCT 2100
QY 2101 GAGCATCTGTGAATGGCTGGAGTCCGATGAGGAGAAAGGAGGGGCTTGGATGATGA 2160
DB 2101 GAGCATCTGTGAATGGCTGGAGTCCGATGAGGAGAAAGGAGGGGCTTGGATGATGA 2160
QY 2161 GAGAGGCGGAGTCTGCTCCCTCGAGGTCTCATGCAACAGGCCATCCACACCATCGAG 2220
DB 2161 GAGAGGCGGAGTCTGCTCCCTCGAGGTCTCATGCAACAGGCCATCCACACCATCGAG 2220
QY 2221 TTTCTGCTGGGCTGCTCTCAACACCGCTTCTTCTGCGCTGTGGGCCCTGAGGCTG 2280
DB 2221 TTTCTGCTGGGCTGCTCTCAACACCGCTTCTTCTGCGCTGTGGGCCCTGAGGCTG 2280
QY 2281 GCCACGCGGAGTCTGCGAGGTCTTCTGCGGCCATGATGCGCATAGSCCTTGGGCTG 2340
DB 2281 GCCACGCGGAGTCTGCGAGGTCTTCTGCGGCCATGATGCGCATAGSCCTTGGGCTG 2340
QY 2341 GCGCGGAGGTGGGCTGGGCTGGTGTGGTCTCCCATCTTTTGGCGCTTTGGCGTG 2400
DB 2341 GCGCGGAGGTGGGCTGGGCTGGTGTGGTCTCCCATCTTTTGGCGCTTTGGCGTG 2400
QY 2401 ATGACCGGTGGCTATCTGCTGTGTGATGGAGGAGTCTTACGCTTCTTCTGACGCGCTTGGCGG 2460

Dd 2401 ATGACCGTGGCTATCTGCTGGTGATGGAGGACTCTCAGCCTTCTCTGACGCCCTGCGG 2460
Qy 2461 CTGCACTGGGTGGATTTCAGACACAGTTCCTACTCAGGCAACGGCTACAGCTGAGTCCC 2520
Dd 2461 CTGCACTGGGTGGATTTCAGACACAGTTCCTACTCAGGCAACGGCTACAGCTGAGTCCC 2520
Qy 2521 TTACACCTTCGCTGCCACAGATGACTAGGCGCCCACTGACGGTCTCTGCAGACCTCTCTTCT 2580
Dd 2521 TTACACCTTCGCTGCCACAGATGACTAGGCGCCCACTGACGGTCTCTGCAGACCTCTCTTCT 2580
Qy 2581 GACCTCTGAGGAGGAGAGAGAAATAAGACGGTCCGCGCCCTGGCAAAAAA 2640
Dd 2581 GACCTCTGAGGAGGAGAGAGAAATAAGACGGTCCGCGCCCTGGCAAAAAA 2640

RESULT 13

AD128819
ID AD128819 standard; cDNA; 2700 BP.

AC AD128819;

XX 22-APR-2004 (first entry)

XX Human modifier of p53 (MP53) gene TCIRG-1.

XX Human; MP53; modifier of p53; p53; cytostatic; gene therapy;

KW T-cell immune regulator 1; TCIRG-1; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 109..2601
FT CDS
FT /tag= a
FT /product= "MP53 TCIRG-1"

XX WP004004766-A1.
XX 15-JAN-2004.

XX 09-JUL-2003; 2003WO-US021378.
XX 10-JUL-2002; 2002US-0394992P.
XX 07-AUG-2002; 2002US-0401604P.
XX 16-SEP-2002; 2002US-0410988P.
XX 25-NOV-2002; 2002US-0428837P.

XX (EXEL-) EXELIXIS INC.
XX Costa MA, Maxwell ME, Lackner MR, Hung T, O'Brien CL, Jin Y;
XX Nicoll M, Hai B, Zhang H, Lickteig K, Amundsen CD;
XX WPI: 2004-142922/14.
XX P-PSDB; AD128834.
XX REFSEQ; NM_006019.2.

XX Identifying a candidate p53 pathway modulating agent for treating e.g.,
XX cancer, comprises contacting an assay system comprising a MP53
XX polypeptide or nucleic acid with a test agent and detecting a test agent-
XX biased activity.
XX Example 2; SEQ ID NO 10; 139pp; English.

XX In the present invention, genetic screens were designed to identify
XX modifiers of the p53 pathway in caenorhabditis elegans, where a
XX homozygous p53 deletion mutant was used. Various specific genes were
XX silenced by RNA inhibition. Genes causing altered phenotypes in the worms
XX were identified as modifiers of the p53 pathway. Human orthologs, denoted
XX modifiers of p52 (MP53), of these modifiers were identified. These
XX include the present sequence, characterised as encoding T-cell immune
XX regulator 1, ATPase, H+ transporting, or lysosomal V0 protein a isoform
XX 3. MP53 nucleic acids and polypeptides are attractive drug targets for
XX the treatment of pathologies associated with a defective p53 signalling
XX pathway, such as cancer. Methods for modulating MP53 function and/or the

CC p53 pathway in a mammalian cell involve contacting the cell with an agent
CC that specifically binds a MP53 polypeptide or nucleic acid. The agent may
CC be a small molecular modulator, a nucleic acid modulator or an antibody.
XX
SQ Sequence 2700 BP; 451 A; 905 C; 850 G; 494 T; 0 U; 0 Other;
Query Match 98.2%; Score 2592.2; DB 12; Length 2700;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2599; Conservative 0; Mismatches 9; Indels 3; Gaps 1;
Qy 33 GCGCGCGCAGCACACCCGCGGACCATGGGCTCCATGTTCCGGAGCAGAGGTGSCCCT 92
Dd 84 GCGCGCGCAGCACACCCGCGGACCATGGGCTCCATGTTCCGGAGCAGAGGTGSCCCT 143
Qy 93 GGTCCAGCTCTTTCTGCCCCACAGCGGCTGCTACACCTGCGTGAGTGGCTGGCGAGCT 152
Dd 144 GGTCCAGCTCTTTCTGCCCCACAGCGGCTGCTACACCTGCGTGAGTGGCTGGCGAGCT 203
Qy 153 GGGCCTCGTGGAGTTTCAGAGACCTCAACGCTCGGTGAGCGCTTCCAGAGACGCTTTCT 212
Dd 204 GGGCCTCGTGGAGTTTCAGAGACCTCAACGCTCGGTGAGCGCTTCCAGAGACGCTTTCT 263
Qy 213 GGTTCATGTTTGGCGCTGTGAGGAGCTGGAGAAGACCTTCACTTCTCTGACAGAGAGT 272
Dd 264 GGTTCATGTTTGGCGCTGTGAGGAGCTGGAGAAGACCTTCACTTCTCTGACAGAGAGT 323
Qy 273 GCGCGCGGCTGGGCTGTGCTGCCCGCCAAAAGGGAGGCTGCGGCAACCCCAACCCCG 332
Dd 324 GCGCGCGGCTGGGCTGTGCTGCCCGCCAAAAGGGAGGCTGCGGCAACCCCAACCCCG 383
Qy 333 GGAACCTGCTCGCATCCAGAGGAGAGCGCGCTGCGCCAGGAGCTGCGGAGTGGG 392
Dd 384 GGAACCTGCTCGCATCCAGAGGAGAGCGCGCTGCGCCAGGAGCTGCGGAGTGGG 443
Qy 393 GGGCAACAGCAGAGGCGCTGCGGCGCCAGCTGCACAGCTGCAGCTCCACGCGCGTGTCT 452
Dd 444 GGGCAACAGCAGAGGCGCTGCGGCGCCAGCTGCACAGCTGCAGCTCCACGCGCGTGTCT 503
Qy 453 AGCCAGAGGCGCATGAACCTCAGCTGGCAGCGCGCCACACAGATGGGGCTTCAGAGAGGAC 512
Dd 504 AGCCAGAGGCGCATGAACCTCAGCTGGCAGCGCGCCACACAGATGGGGCTTCAGAGAGGAC 563
Qy 513 GCGCCTGTCTCAGAGCGCGCGGGGGCCGACACAGAGACCTGAGGGTCACTTTGTGCGAG 572
Dd 564 GCGCCTGTCTCAGAGCGCGCGGGGGCCGACACAGAGACCTGAGGGTCACTTTGTGCGAG 623
Qy 573 TGCGGTGAGGCGCCACAAAGGCGCTGCGCTAGAGCGCTGTCTCGAGGGCTGCGCGCG 632
Dd 624 TGCGGTGAGGCGCCACAAAGGCGCTGCGCTAGAGCGCTGTCTCGAGGGCTGCGCGCG 683
Qy 633 CTTCCTCATTTGCCAGCTTCAGGAGCTGGAGCAGCGCTGGAGCAACCCCGTACCGGCGA 692
Dd 684 CTTCCTCATTTGCCAGCTTCAGGAGCTGGAGCAGCGCTGGAGCAACCCCGTACCGGCGA 743
Qy 693 GCGACACAGCGGTTCCTCAGCAGCGTGTAGGCGCGGTGTCTGACAGCTGCTCCCGCAG 752
Dd 744 GCGACACAGCGGTTCCTCAGCAGCGTGTAGGCGCGGTGTCTGACAGCTGCTCCCGCAG 803
Qy 753 CGCAAGATCAAGGATCGCTCTTCCACTGCGCAGCTGTTCCTGTTCTGCAAGAGGAGGC 812
Dd 804 CGCAAGATCAAGGATCGCTCTTCCACTGCGCAGCTGTTCCTGTTCTGCAAGAGGAGGC 863
Qy 813 CGGCTCTCGGCGCTTCAGAGCTGCAACAGCAGCGCAGGAGCTGCGAGGAGTCTCTCGG 872
Dd 864 CGGCTCTCGGCGCTTCAGAGCTGCAACAGCAGCGCAGGAGCTGCGAGGAGTCTCTCGG 923
Qy 873 GGAGACAGAGCGGTTCCTCAGCAGCGTGTAGGCGCGGTGTCTGACAGCTGCTCCCGCAG 932
Dd 924 GGAGACAGAGCGGTTCCTCAGCAGCGTGTAGGCGCGGTGTCTGACAGCTGCTCCCGCAG 983
Qy 933 GCAAGTGCAGGTTCACAAAGATGAAGCGCGTGTACCTGCGCCTGAAACCAAGTGCAGGTGAG 992
Dd 984 GCAAGTGCAGGTTCACAAAGATGAAGCGCGTGTACCTGCGCCTGAAACCAAGTGCAGGTGAG 1043

QY 993 CACCACGACAAAGTGCCTCATTTCCGAGGCGCTGCTCTGTGCGAGACCTGCCCGCCT 1052
DB 1044 CACCACGACAAAGTGCCTCATTTCCGAGGCGCTGCTCTGTGCGAGACCTGCCCGCCT 1103
QY 1053 GCAGGAGGCGCTGCGGACAGCTCGATGGAGGAGGAGTGTAGTCCGCTGCGCTCACCGCAT 1112
DB 1104 GCAGGAGGCGCTGCGGACAGCTCGATGGAGGAGGAGTGTAGTCCGCTGCGCTCACCGCAT 1163
QY 1113 CCCCTGCGGACATGCCCCCAACATCATCCGACCAACCGCTTTCACGCGCAGCTTCCA 1172
DB 1164 CCCCTGCGGACATGCCCCCAACATCATCCGACCAACCGCTTTCACGCGCAGCTTCCA 1223
QY 1173 GGGCATCGTGGATCGCTACCGGCGTGGCGGCTACACGAGGTCAACCCCGCTCCCTACAC 1232
DB 1224 GGGCATCGTGGATCGCTACCGGCGTGGCGGCTACACGAGGTCAACCCCGCTCCCTACAC 1283
QY 1233 CATCATCACTTCCCTTCCCTTCTGTTTGTGTGATGTTCCGGGATGTGGGCCACCGGCTGCT 1292
DB 1284 CATCATCACTTCCCTTCCCTTCTGTTTGTGTGATGTTCCGGGATGTGGGCCACCGGCTGCT 1343
QY 1293 CATGTTCTCTTCCGCTTCCGCTATGTCCTTGTGCGGAGAACCGACCGGCTGTGAAGCGCG 1352
DB 1344 CATGTTCTCTTCCGCTTCCGCTATGTCCTTGTGCGGAGAACCGACCGGCTGTGAAGCGCG 1403
QY 1353 GCAGACGAGATCTGGCAGACTTCTTTCAGGGGCGCTACTGCTCTGCTTATGGGCT 1412
DB 1404 GCAGACGAGATCTGGCAGACTTCTTTCAGGGGCGCTACTGCTCTGCTTATGGGCT 1463
QY 1413 GTTCTCCATCTACACCGGCTTCTATCAACGAGTGTCTCATGCGGCCACCGACATCTT 1472
DB 1464 GTTCTCCATCTACACCGGCTTCTATCAACGAGTGTCTCATGCGGCCACCGACATCTT 1523
QY 1473 CCCCTGGGCTGAGTGTGCGCCATGCGCAACAGTCTGGCTGGAGTGTATGATTCCT 1532
DB 1524 CCCCTGGGCTGAGTGTGCGCCATGCGCAACAGTCTGGCTGGAGTGTATGATTCCT 1583
QY 1533 GGGCCAGCACAGATGCTTACCTTGGATCCCAAGTCAACGCTGTCTGGAGCCCTA 1592
DB 1584 GGGCCAGCACAGATGCTTACCTTGGATCCCAAGTCAACGCTGTCTGGAGCCCTA 1643
QY 1593 CCCCTTGGCATCGATCTTATTTGGAGCTTGGTCCCAACAGTGTAGCTTCTCAACTC 1652
DB 1644 CCCCTTGGCATCGATCTTATTTGGAGCTTGGTCCCAACAGTGTAGCTTCTCAACTC 1703
QY 1653 CTTCAAGATGAAGATGTCGTCTATCTCTGCGCGTGTGSCACATGCGCTTTGGGCTGCT 1712
DB 1704 CTTCAAGATGAAGATGTCGTCTATCTCTGCGCGTGTGSCACATGCGCTTTGGGCTGCT 1763
QY 1713 CGAGTCTTCAACACGTCACATTTGGCCAGAGGACCGGCTGTGTGAGAGCGTGC 1772
DB 1764 CGAGTCTTCAACACGTCACATTTGGCCAGAGGACCGGCTGTGTGAGAGCGTGC 1823
QY 1773 GAGACTCACCTTCTCTGCTGGAGCTCTTCCGTTACCTGCTGTCTAGTCACTACAGTG 1832
DB 1824 GAGACTCACCTTCTCTGCTGGAGCTCTTCCGTTACCTGCTGTCTAGTCACTACAGTG 1883
QY 1833 GCTGTGTGTGCTGGGCTGCCAGGCGCGCTCG --- CCCAGATCTCTATCCACTTCATCAA 1889
DB 1884 GCTGTGTGTGCTGGGCTGCCAGGCGCGCTCGGCCCGGAGCATCTCATCCACTTCATCAA 1943
QY 1890 CATGTTCTCTTCTCCAGAGCCCGAGCAACAGGCTGCTTACCCCGGAGAGGTGGT 1949
DB 1944 CATGTTCTCTTCTCCAGAGCCCGAGCAACAGGCTGCTTACCCCGGAGAGGTGGT 2003
QY 1950 CCAGGCGACGCTGCTGTGCTGTGCGCTTGGCCATGTTGCCCATCTGCTGTGTCGACACC 2009
DB 2004 CCAGGCGACGCTGCTGTGCTGTGCGCTTGGCCATGTTGCCCATCTGCTGTGTCGACACC 2063
QY 2010 CTTGCACTGTGCTGACCGCCACCGCCGCTGCGGAGGAGGCGCTGACCGACAGGA 2069
DB 2064 CTTGCACTGTGCTGACCGCCACCGCCGCTGCGGAGGAGGCGCTGACCGACAGGA 2123

QY 2070 GGAACAACAGCGCGGTTGCTGGACCTGCTGAGCGATCTGTGAATGGCTGGAGCTCGGA 2129
DB 2124 GGAACAACAGCGCGGTTGCTGGACCTGCTGAGCGATCTGTGAATGGCTGGAGCTCGGA 2183
QY 2130 TGAGGAAAAGCAGAGGCGCTTGGATGATGAAGAGGAGCCGAGCTCTGCTCCCTCCGAGGT 2189
DB 2184 TGAGGAAAAGCAGAGGCGCTTGGATGATGAAGAGGAGCCGAGCTCTGCTCCCTCCGAGGT 2243
QY 2190 GCTCATGCAACAGGCCATCCACACCATCGAGTTCTGCTGGGCTGCTTCCCAACACCGC 2249
DB 2244 GCTCATGCAACAGGCCATCCACACCATCGAGTTCTGCTGGGCTGCTTCCCAACACCGC 2303
QY 2250 CTCTACCTGGGCTGTGGGCGCTTGGACCTGAGCCCTGAGCCAGCCGAGCTGTCCGAGGTTCTGTG 2309
DB 2304 CTCTACCTGGGCTGTGGGCGCTTGGACCTGAGCCCTGAGCCAGCCGAGCTGTCCGAGGTTCTGTG 2363
QY 2310 GGGCATGCTGATGCGCATAGGCTTGGGCGCTTGGGCGGAGGTGGGCGCTGTGGT 2369
DB 2364 GGGCATGCTGATGCGCATAGGCTTGGGCGCTTGGGCGGAGGTGGGCGCTGTGGT 2423
QY 2370 GCTGGTCCCATCTTGGCCGCTTGGCGTGTGATGACCGTGGCTATCTGCTGGTGTGGA 2429
DB 2424 GCTGGTCCCATCTTGGCCGCTTGGCGTGTGATGACCGTGGCTATCTGCTGGTGTGGA 2483
QY 2430 GGGACTCTAGCCTTCTGCAACGCTTGGGCTGAGTCCCTTCCCTGCGCCACAGATGACTAGGG 2489
DB 2484 GGGACTCTAGCCTTCTGCAACGCTTGGGCTGAGTCCCTTCCCTGCGCCACAGATGACTAGGG 2543
QY 2490 CTACTCAGGCAACGGGCTTACAGCTGAGTCCCTTCCCTGCGCCACAGATGACTAGGG 2549
DB 2544 CTACTCAGGCAACGGGCTTACAGCTGAGTCCCTTCCCTGCGCCACAGATGACTAGGG 2603
QY 2550 CCCACTGCAAGTCTTCCGACAGCTTCTGCTGACCTTCTGAGGCAAGGAGGAAATAAGAC 2609
DB 2604 CCCACTGCAAGTCTTCCGACAGCTTCTGCTGACCTTCTGAGGCAAGGAGGAAATAAGAC 2663
QY 2610 GGTCCGCGCTGGCAAAAAAAAAAAAAAAAAAAAA 2640
DB 2664 GGTCCGCGCTGGCAGTGAATAAAAAAAAAAAAAA 2694

RESULT 14

ADP10401
ID ADP10401 standard; DNA; 2700 BP.

XX AC ADP10401;

XX XX 12-AUG-2004 (first entry)

XX Reference mRNA sequences for marker probe #78.

XX transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.

XX Homo sapiens.

XX WO2004042346-A2.

XX 21-MAY-2004.

XX 24-APR-2003; 2003WO-US012946.

XX 24-APR-2002; 2002US-00131831.

XX 20-DEC-2002; 2002US-00325899.

XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;

XX Rosenberg S;

XX WPI; 2004-400724/37.

XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver.

PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX

PS Claim 80; SEQ ID NO 410; 1762pp; English.

XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis
CC and monitoring of allograft rejection and other disorders.
XX

8Q Sequence 2700 BP; 451 A; 905 G; 850 G; 494 T; 0 U; 0 Other;

Query Match 98.2%; Score 2592.2; DB 12; Length 2700;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2599; Conservative 0; Mismatches 9; Indels 3; Gaps 1;

QY	33	GGCGCGCGCAGACACACCGCGGACCCATGGGCTCCATGTTCCGAGGAGGAGGTGCCCT	92
DB	84	GGCGCGCGCAGACACACCGCGGACCCATGGGCTCCATGTTCCGAGGAGGAGGTGCCCT	143
QY	93	GGTCAGGCTTTTTCGCCACAGCGGCTGCCTACACCTCGGAGGTCGGCTCGGCGAGCT	152
DB	144	GGTCAGGCTTTTTCGCCACAGCGGCTGCCTACACCTCGGAGGTCGGCTCGGCGAGCT	203
QY	153	GGGCTCGTGGAGTTCCAGAGACCTCAACGCTCGGTGAGCGCTTCCAGAGACGCTTTGT	212
DB	204	GGGCTCGTGGAGTTCCAGAGACCTCAACGCTCGGTGAGCGCTTCCAGAGACGCTTTGT	263
QY	213	GTTTATGTTTGGCGCTGTGAGAGCTGGAGAAGACCTTCACCTCTCTCGCAGGAGAGT	272
DB	264	GTTTATGTTTGGCGCTGTGAGAGCTGGAGAAGACCTTCACCTCTCTCGCAGGAGAGT	323
QY	273	GGCGCGGCTGGGCTGCTCCGCCCGCCAAAGGAGGAGGCTGCGGACACCCACCCCG	332
DB	324	GGCGCGGCTGGGCTGCTCCGCCCGCCAAAGGAGGAGGCTGCGGACACCCACCCCG	383
QY	333	GGACTGTGCGCATCCAGGAGGAGACGGAGCGCTTGGCCACAGGAGCTGCGGATGTGG	392
DB	384	GGACTGTGCGCATCCAGGAGGAGACGGAGCGCTTGGCCACAGGAGCTGCGGATGTGG	443
QY	393	GGGCAACAGCAGGCGCTCGGGCCAGCTGCACAGCTGACGCTCCAGCGCGCGTGT	452
DB	444	GGGCAACAGCAGGCGCTCGGGCCAGCTGCACAGCTGACGCTCCAGCGCGCGTGT	503
QY	453	ACGCCAGGCGCCATGAACCTCAGCTGGCAGCGCCACACAGATGGGCTCAGAGAGGAC	512
DB	504	ACGCCAGGCGCCATGAACCTCAGCTGGCAGCGCCACACAGATGGGCTCAGAGAGGAC	563
QY	513	GCCCTGTCTCAGGCGCCCGGGGCGCGCACAGACCTGAGGGTCAACTTTGTGGCAGG	572
DB	564	GCCCTGTCTCAGGCGCCCGGGGCGCGCACAGACCTGAGGGTCAACTTTGTGGCAGG	623
QY	573	TGCCGTGAGCGCCACAGGCGCCCTCCTAGAGCGCTGCTCTGGAGGGCTTCGCGGG	632
DB	624	TGCCGTGAGCGCCACAGGCGCCCTCCTAGAGCGCTGCTCTGGAGGGCTTCGCGGG	683
QY	633	CTTCTCATTTGCGAGCTTCAGGAGCTGGAGCAGCGCTGGAGCACCCCGTGACGGCGA	692
DB	684	CTTCTCATTTGCGAGCTTCAGGAGCTGGAGCAGCGCTGGAGCACCCCGTGACGGCGA	743
QY	693	GCCAGCAGGTGAGTACCTTCTCATCTCTAGCTGGGGTGGAGAGTCGGACAGAAAT	752
DB			

DB	744	GCCAGCCAGCTGGATGACCTTCTCATCTCTCTACTGGGGTGGACAGATCGGACAGAGAT	803
QY	753	CCGCAAGATCACGGACTGCTTCCACTGCCACGCTCTTCCCGTTTCTGACAGAGAGGCG	812
DB	804	CCGCAAGATCACGGACTGCTTCCACTGCCACGCTCTTCCCGTTTCTGACAGAGAGGCG	863
QY	813	CCGCTCGGGGCGCTGACAGCTGCAACAGCAGAGACCGAGAGCTGACAGAGTCTCTCG	872
DB	864	CCGCTCGGGGCGCTGACAGCTGCAACAGCAGAGACCGAGAGCTGACAGAGTCTCTCG	923
QY	873	GGAGACAGACGGTTCCTGAGCCAGTGTAGCCGGTGTCTGACGCTGCTGCGCCAGG	932
DB	924	GGAGACAGACGGTTCCTGAGCCAGTGTAGCCGGTGTCTGACGCTGCTGCGCCAGG	983
QY	933	GCAGTGCAGGTCCACAAAGATGAAGCCGTGTACTTGGCCCTGAAACCAAGTGCAGGCTG	992
DB	984	GCAGTGCAGGTCCACAAAGATGAAGCCGTGTACTTGGCCCTGAAACCAAGTGCAGGCTG	1043
QY	993	CACCAAGCAGAGTGCCTCATTTGCCAGGCGCTGTGTGCGAGACCTGCGGCCCT	1052
DB	1044	CACCAAGCAGAGTGCCTCATTTGCCAGGCGCTGTGTGCGAGACCTGCGGCCCT	1103
QY	1053	GCAGAGGCGCTTGGCGGACAGCTCGATGGAGGAGGAGTGAAGTGCCTCACCGCAT	1112
DB	1104	GCAGAGGCGCTTGGCGGACAGCTCGATGGAGGAGGAGTGAAGTGCCTCACCGCAT	1163
QY	1113	CCCCCTGCGGAGACATGCCCGCCACACTCATTCGCAACCAACCGCTTCAACGCGCTTCCA	1172
DB	1164	CCCCCTGCGGAGACATGCCCGCCACACTCATTCGCAACCAACCGCTTCAACGCGCTTCCA	1223
QY	1173	GGGCAATCGTGGATCGCTACGGCGTGGCGGCTTACAGGAGGTCAACCGCTTCTTACAC	1232
DB	1224	GGGCAATCGTGGATCGCTACGGCGTGGCGGCTTACAGGAGGTCAACCGCTTCTTACAC	1283
QY	1233	CATCATACCTTCCCTTCTCTGCTGTGATGTTCCGGGATGTGGGCGACGGGCTGT	1292
DB	1284	CATCATACCTTCCCTTCTCTGCTGTGATGTTCCGGGATGTGGGCGACGGGCTGT	1343
QY	1293	CATGTTCTTCTTGGCGCTGGCGCATGGTCTTTCGCGAGAACCGACCGGCTGTGAAAGCCGC	1352
DB	1344	CATGTTCTTCTTGGCGCTGGCGCATGGTCTTTCGCGAGAACCGACCGGCTGTGAAAGCCGC	1403
QY	1353	GCAGAACAGAGATCTGGCAGACTTCTTCAGGGGCGCTACCTGCTCTTATGGGCT	1412
DB	1404	GCAGAACAGAGATCTGGCAGACTTCTTCAGGGGCGCTACCTGCTCTTATGGGCT	1463
QY	1413	GTTCTCCATCTACACCGGCTTCTCATCAACGAGTGTCTTTCAGTTCGCGCACACGATCTT	1472
DB	1464	GTTCTCCATCTACACCGGCTTCTCATCAACGAGTGTCTTTCAGTTCGCGCACACGATCTT	1523
QY	1473	CCCTTCGGGCTGGAGTGTGGCGCCATGGCCAAACAGTCTGGCTGGAGTGAATTCCT	1532
DB	1524	CCCTTCGGGCTGGAGTGTGGCGCCATGGCCAAACAGTCTGGCTGGAGTGAATTCCT	1583
QY	1533	GGCCAGCAGACAGTGTCTTACCTCGATCCCAACGCTCACCGGTCTTCTTGGGACCTTA	1592
DB	1584	GGCCAGCAGACAGTGTCTTACCTCGATCCCAACGCTCACCGGTCTTCTTGGGACCTTA	1643
QY	1593	CCCTTTTGGCATTCGATCTTATTTGGAGCTTGCTGCGCAACCACTTTCCTCAACTC	1652
DB	1644	CCCTTTTGGCATTCGATCTTATTTGGAGCTTGCTGCGCAACCACTTTCCTCAACTC	1703
QY	1653	CTTCAAGATGAGTGTCTTCTGCGGCTGTGCAATGGGCTTGGGGTGGTCT	1712
DB	1704	CTTCAAGATGAGTGTCTTCTGCGGCTGTGCAATGGGCTTGGGGTGGTCT	1763
QY	1713	CGGAGTCTTCAACCAAGTGCATTTTGGCAGAGGACCGGCTGTCTGGAGACGCTGCC	1772
DB	1764	CGGAGTCTTCAACCAAGTGCATTTTGGCAGAGGACCGGCTGTCTGGAGACGCTGCC	1823
QY	1773	GGAGCTCACCTTCTGCTGGAGCTTTCGGTTTACTCTGTGTTCTTCTAGTCACTCAAGTG	1832
DB	1824	GGAGCTCACCTTCTGCTGGAGCTTTCGGTTTACTCTGTGTTCTTCTAGTCACTCAAGTG	1883

QY 1833 GCTGTGTCTGGCTGCCAGGGCGGCTCG---CCAGAGATCTCTATCCATCTTCATCAA 1889
DB 1884 GCTGTGTGTCTGGCTGCCAGGGCGGCTCGGCCCCAGAGATCTCTATCCATCTTCATCAA 1943
QY 1890 CATGTTCTCTCTTCCACAGCCCGCCAGAGGCTGCTTACCCCGGAGGAGGAGT 1949
DB 1944 CATGTTCTCTTCCACAGCCCGCCAGAGGCTGCTTACCCCGGAGGAGGAGT 2003
QY 1950 CCAGGCGACGCTGTGTCTCTGGCTTGGCCATGTTGCCATCTCTGTCTGTGGCACACC 2009
DB 2004 CCAGGCGACGCTGTGTCTCTGGCTTGGCCATGTTGCCATCTCTGTCTGTGGCACACC 2063
QY 2010 CTTGCACTCTGTGACCGCCAGCCCGCCGCTGCGAGAGAGGCGCCGCTGACCGACAGGA 2069
DB 2064 CTTGCACTCTGTGACCGCCAGCCCGCCGCTGCGAGAGAGGCGCCGCTGACCGACAGGA 2123
QY 2070 GGAAGAACAGCGCGGCTGTGACCTGCTGACCGCATCTGTGAATGCTGGAGCTCCGA 2129
DB 2124 GGAAGAACAGCGCGGCTGTGACCTGCTGACCGCATCTGTGAATGCTGGAGCTCCGA 2183
QY 2130 TGAGGAAAGCGAGGCGCTGTGATGATGAGAGGAGCGGAGCTCTCCCTCCGAGGT 2189
DB 2184 TGAGGAAAGCGAGGCGCTGTGATGATGAGAGGAGCGGAGCTCTCCCTCCGAGGT 2243
QY 2190 GCTCATGACAGGCGCATCCACCATCGAGTTCTGCTGGCTGTGCTTCCACACCGC 2249
DB 2244 GCTCATGACAGGCGCATCCACCATCGAGTTCTGCTGGCTGTGCTTCCACACCGC 2303
QY 2250 CTCTACCTGCGCTGTGGCGCTGAGCTGGCCAGCCAGCTGTCGAGGCTCTGTG 2309
DB 2304 CTCTACCTGCGCTGTGGCGCTGAGCTGGCCAGCCAGCTGTCGAGGCTCTGTG 2363
QY 2310 GGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2369
DB 2364 GGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2423
QY 2370 GCTGTGCTCCATCTTTCGCGCTTTCGCGTGTGATGATGATGATGATGATGATGATGATGAT 2429
DB 2424 GCTGTGCTCCATCTTTCGCGCTTTCGCGTGTGATGATGATGATGATGATGATGATGATGAT 2483
QY 2430 GGCACTCTAGCTTCTGACCGCCCTGCGGCTGCACTGGGCTGATTCAGAACAGTT 2489
DB 2484 GGCACTCTAGCTTCTGACCGCCCTGCGGCTGCACTGGGCTGATTCAGAACAGTT 2543
QY 2490 CTACTCAGGCAAGGCTTACAGCTGAGTCCCTTCCCTTCCCTGCGCCACAGATGATGAGG 2549
DB 2544 CTACTCAGGCAAGGCTTACAGCTGAGTCCCTTCCCTTCCCTGCGCCACAGATGATGAGG 2603
QY 2550 CCACCTGCAAGTCTCTGACAGCTCTCTTCTGACCTTCTGAGGAGGAGGAGGATTAAGAC 2609
DB 2604 CCACCTGCAAGTCTCTGACAGCTCTCTTCTGACCTTCTGAGGAGGAGGAGGATTAAGAC 2663
QY 2610 GGTCCGCTCTGGCAAAAAAAAAAAAAAAAAAAAA 2640
DB 2664 GGTCCGCTCTGGCAGTGAATAAAAAAAAAAAAAA 2694

RESULT 15

ACN39267

ID ACN39267 standard; cDNA; 2700 BP.

XX ACN39267;

XX ACN39267;

DT 18-NOV-2004 (first entry)

DE Tumour-associated antigenic target (TAT) cDNA DNAS25509, SEQ ID NO:3304.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW Tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic; gene; ss.

XX Homo sapiens.

XX WO2004030615-A2.

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Claim 1; SEQ ID NO 3304; 7273pp; English.

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acid of the invention.

Sequence 2700 BP; 451 A; 905 C; 850 G; 494 T; 0 U; 0 Other;

Query Match 98.2%; Score 2592.2; DB 13; Length 2700;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2599; Conservative 0; Mismatches 9; Indels 3; Gaps 1;

QY 33 GCGCGCGCAGCAGCACCCGCGGACCATGGCTCCATGTTCCGAGGAGGAGTGGCCCT 92
DB 84 GCGCGCGCAGCAGCACCCGCGGACCATGGCTCCATGTTCCGAGGAGGAGTGGCCCT 143
QY 93 GGTCCAGCTCTTCTGCCCCACAGCGGCTGCTTACCTGAGTGGCTGGCGGAGCT 152
DB 144 GGTCCAGCTCTTCTGCCCCACAGCGGCTGCTTACCTGAGTGGCTGGCGGAGCT 203
QY 153 GGGCTCTGTTGGAGTTTCAGAGACCTCAACGCTCGGTGAGCGCTTCCAGAGAGCTTTGT 212
DB 204 GGGCTCTGTTGGAGTTTCAGAGACCTCAACGCTCGGTGAGCGCTTCCAGAGAGCTTTGT 263
QY 213 GGTGTGATGTTTGGCGCTGTGAGGAGCTGGAGAGACCTTCACTTCTCTGAGGAGGAGT 272
DB 264 GGTGTGATGTTTGGCGCTGTGAGGAGCTGGAGAGACCTTCACTTCTCTGAGGAGGAGT 323
QY 273 GCGCGCGCTGGGCTGGTCTGCCCCCGCCAAAGGGGAGGCTCCCGGACCCACCCCG 332
DB 324 GCGCGCGCTGGGCTGGTCTGCCCCCGCCAAAGGGGAGGCTCCCGGACCCACCCCG 383

333 GGACCTGTGCGCATCCAGGAGGAGCGAGCGCTGGCCCGCAGGAGCTCGGGGATGTGG 392
Db GGACCTGTGCGCATCCAGGAGGAGCGAGCGCTGGCCCGCAGGAGCTCGGGATGTGG 443
393 GGGCAACAGCAGCGCCCTCGGGCCAGCTGCACCAAGCTGCAAGCTCCAGCCGCGTGT 452
Db GGGCAACAGCAGCGCCCTCGGGCCAGCTGCACCAAGCTGCAAGCTCCAGCCGCGTGT 503
453 AGCCAGGGCCATGAACCTCAGCTGGCAGCGCCGCCACACAGATGGGGCTCAGAGAGGAC 512
Db AGCCAGGGCCATGAACCTCAGCTGGCAGCGCCGCCACACAGATGGGGCTCAGAGAGGAC 563
513 GCCCCTGTCTCAGGCCCCCGGGGGCGCGCACAGGACCTGAGGCTCAACTTTGTGCGAG 572
Db GCCCCTGTCTCAGGCCCCCGGGGGCGCGCACAGGACCTGAGGCTCAACTTTGTGCGAG 623
573 TGCCGTGAGAGCCCAAGAGCCCCCTGCCCTAGAGCGCTGTCTGAGGGCCCTGCGCGGG 632
Db TGCCGTGAGAGCCCAAGAGCCCCCTGCCCTAGAGCGCTGTCTGAGGGCCCTGCGCGGG 683
633 CTTCTCATTTGCGAGCTTCAGGAGCTGAGCAGCGCGCTGGAGCACCCCGTGCAGGGCGA 692
Db CTTCTCATTTGCGAGCTTCAGGAGCTGAGCAGCGCGCTGGAGCACCCCGTGCAGGGCGA 743
693 GCCAGCCAGTGGATGACCTTCTCATCTCTACTAGGGGTGAGCAGATCGGACAGAAGAT 752
Db GCCAGCCAGTGGATGACCTTCTCATCTCTACTAGGGGTGAGCAGATCGGACAGAAGAT 803
753 CGCGAAGATCAAGGACTGTTCACATGCACTCTTCCGTTTCTGCGAGCAGGAGAGGC 812
Db CGCGAAGATCAAGGACTGTTCACATGCACTCTTCCGTTTCTGCGAGCAGGAGAGGC 863
813 CCGCCTCGGGGCCCTGCAGACCTGCAACAGCAGAGCCAGGAGCTGCAGGAGGTCTCGG 872
Db CCGCCTCGGGGCCCTGCAGACCTGCAACAGCAGAGCCAGGAGCTGCAGGAGGTCTCGG 923
873 GAGACAGAGCCGTTCTGAGCAGGCTGCTAGCGCGGGTGTGCACTGCTGCGCGCAGG 932
Db GAGACAGAGCCGTTCTGAGCAGGCTGCTAGCGCGGGTGTGCACTGCTGCGCGCAGG 983
933 GAGGTGAGGTGCAAGATGAAGGCGGTGTACTTGGCCCTGAAACCAAGTGCAGCGTGA 992
Db GAGGTGAGGTGCAAGATGAAGGCGGTGTACTTGGCCCTGAAACCAAGTGCAGCGTGA 1043
993 CACCAAGCAAGTGCCTCATTTGCCGAGGCGCTGCTGTGCGAGACCTGCGCGCCCT 1052
Db CACCAAGCAAGTGCCTCATTTGCCGAGGCGCTGCTGTGCGAGACCTGCGCGCCCT 1103
1053 CGAGGAGGCCCTGCGGAGCAGCTCGATGAGGAGGAGTGAAGTGCCTGCGCTCAGCGCAT 1112
Db CGAGGAGGCCCTGCGGAGCAGCTCGATGAGGAGGAGTGAAGTGCCTGCGCTCAGCGCAT 1163
1113 CCCCTGCGGAGCATGCCCCCCCACTCATTCGCGACCAACCGCTTCAAGGCGAGTTCCA 1172
Db CCCCTGCGGAGCATGCCCCCCCACTCATTCGCGACCAACCGCTTCAAGGCGAGTTCCA 1223
1173 GGGCATCGTGATCGCTACGGCGTGGCGCTACAGGAGGTCAACCCGCTCCCTACAC 1232
Db GGGCATCGTGATCGCTACGGCGTGGCGCTACAGGAGGTCAACCCGCTCCCTACAC 1283
1233 CATCATCACTTCCCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1292
Db CATCATCACTTCCCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1343
1293 CATGTTCTTTCGCGCTGGCCATGCTTTCGCGAGAACCAACCGCTGTGAAGCGCGC 1352
Db CATGTTCTTTCGCGCTGGCCATGCTTTCGCGAGAACCAACCGCTGTGAAGCGCGC 1403
1353 GCGAAGCAGGATCTGGCAGCTTCTTCAGGGGGCGCTACCTGCTCCTGCTTATGGGCT 1412
Db GCGAAGCAGGATCTGGCAGCTTCTTCAGGGGGCGCTACCTGCTCCTGCTTATGGGCT 1463

1413 GTTCTCCATCTACACCGCTTCATCTACAA CGAGTGTCTTCACTCGGCCACACGATCTT 1472
Db GTTCTCCATCTACACCGCTTCATCTACAA CGAGTGTCTTCACTCGGCCACACGATCTT 1523
1473 CCCCTCGGCTGGAGTGTGGCGCATGGCCAAACAGTCTGGCTGGAGTGATGCAATCTCT 1532
Db CCCCTCGGCTGGAGTGTGGCGCATGGCCAAACAGTCTGGCTGGAGTGATGCAATCTCT 1583
1533 GGCACGACACAGATGCTTACCTCGATCCCAACGTCAACCGTGTCTTCTGGGACCCCTA 1592
Db GGCACGACACAGATGCTTACCTCGATCCCAACGTCAACCGTGTCTTCTGGGACCCCTA 1643
1593 CCCCTTTGGCATCGCATCTTATTGAGAGCTGTGCTGCAACCACTTGAGCTTCTCAACTC 1652
Db CCCCTTTGGCATCGCATCTTATTGAGAGCTGTGCTGCAACCACTTGAGCTTCTCAACTC 1703
1653 TTCTAAGATGAAGATGTCCGTCACTCTGGGCGTCTGTGCAATGGCTTTTGGGTGGTCT 1712
Db TTCTAAGATGAAGATGTCCGTCACTCTGGGCGTCTGTGCAATGGCTTTTGGGTGGTCT 1763
1713 CGGAGTCTTCAACCACTGTGCACTTTGGCCAGAGGCAACCGGCTGTCTGGAGACGCTGCC 1772
Db CGGAGTCTTCAACCACTGTGCACTTTGGCCAGAGGCAACCGGCTGTCTGGAGACGCTGCC 1823
1773 GGAGCTCACCTTCTGCTGGGACTCTTGGGTTACCTCGTGTCTTAGTCTCATCTACAAGTG 1832
Db GGAGCTCACCTTCTGCTGGGACTCTTGGGTTACCTCGTGTCTTAGTCTCATCTACAAGTG 1883
1833 GCTGTGTCTGGGTGCGCAGGGCCGCTCG --- CCCAGCATCTCTCACTTCACTCAA 1889
Db GCTGTGTCTGGGTGCGCAGGGCCGCTCG --- CCCAGCATCTCTCACTTCACTCAA 1943
1889 CATGTTCTCTTCTTCCACAGCCCCCAGCAACAGGTGTCTTACCCCGGCGAGAGGTGT 1949
Db CATGTTCTCTTCTTCCACAGCCCCCAGCAACAGGTGTCTTACCCCGGCGAGAGGTGT 2003
1949 CCAGGCCACGCTGTGTCTTGGCTTGGCCATGTGTGCCATCTCTGCTGTGGCACACC 2009
Db CCAGGCCACGCTGTGTCTTGGCTTGGCCATGTGTGCCATCTCTGCTGTGGCACACC 2063
2010 CTTGCACTGTGTGCAACCGCCACCGCGCGCTGCGGAGGAGCCGCTGTGACCGACAGA 2069
Db CTTGCACTGTGTGCAACCGCCACCGCGCGCTGCGGAGGAGCCGCTGTGACCGACAGA 2123
2070 GGAAACAAAGCGCGGTTGTGCACTGCTGTGACGCACTGTGTAATGCTGTGAGTCTCGA 2129
Db GGAAACAAAGCGCGGTTGTGCACTGCTGTGACGCACTGTGTAATGCTGTGAGTCTCGA 2183
2130 TGAGGAAAGGCGAGGGGCTTGGATGATGAAGAGGAGGCGCGAGCTCTGCTCCCTCGAGGT 2189
Db TGAGGAAAGGCGAGGGGCTTGGATGATGAAGAGGAGGCGCGAGCTCTGCTCCCTCGAGGT 2243
2190 GCTCATGCAACAGGCGCATCCACCATCGAGTTTCTGCTGGGCTGCTGTCTCAACACCGC 2249
Db GCTCATGCAACAGGCGCATCCACCATCGAGTTTCTGCTGGGCTGCTGTCTCAACACCGC 2303
2250 CTTCTACCTGCGCTGTGGGCCCTTGGCCACCGCCACCGCAGCTGTCCGAGTTCTGTG 2309
Db CTTCTACCTGCGCTGTGGGCCCTTGGCCACCGCCACCGCAGCTGTCCGAGTTCTGTG 2363
2310 GGGCATGTGTATGCGCATAGGCTTGGGCTTGGGCGGAGGTGGGCTGTGGCTGTGTGT 2369
Db GGGCATGTGTATGCGCATAGGCTTGGGCTTGGGCGGAGGTGGGCTGTGGCTGTGTGT 2423
2370 GCTGTGCCCATCTTTTGTGCGCTTTTGGCGTATGACCGTGTGCTATCTCTGCTGGTATGA 2429
Db GCTGTGCCCATCTTTTGTGCGCTTTTGGCGTATGACCGTGTGCTATCTCTGCTGGTATGA 2483
2430 GGGAGCTCTCAGCTTCTGCAACCGCTGCGCTGCACTGGGTGGAAATCCAGAAACAGTT 2489
Db GGGAGCTCTCAGCTTCTGCAACCGCTGCGCTGCACTGGGTGGAAATCCAGAAACAGTT 2543
2490 CTACTCAGGCGAGGGCTACAAGCTGAGTCCCTTCACTTCTGCTGCCACAGATGCTAGGG 2549

Db	2544	CTACTCAGGCACGGGCTACAAAGCTGAGTCCCTTCACCTTCGCTGCCACAGATGACTAGGG	2603
Qy	2550	CCCACTGCAGGTCCTGCCAGACCTCCTTCTGTACCTCTGAGGCAGGAGGGAATAAAGAC	2609
Db	2604	CCCACTGCAGGTCCTGCCAGACCTCCTTCTGTACCTCTGAGGCAGGAGGGAATAAAGAC	2663
Qy	2610	GGTCCGCCCTGGCAAAAAAAAAAAAAAAAAA	2640
Db	2664	GGTCCGCCCTGGCAGTCAAAAAAAAAAAAAAAAAA	2694

Search completed: June 30, 2006, 04:27:43
Job time : 1513 secs

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Query Match 90.0%; Score 2376.6; DB 14; Length 2493; Best Local Similarity 95.9%; Pred. No. 0; Matches 2392; Conservative 0; Mismatches 98; Indels 3; Gaps 1;									
QY	58	ATGGGCTCCATGTTCCGGAGCGAGGAGTGCGCCCTGGTCCAGCTCTTTCTGCCCCACAGCG	117	DB	1	ATGGGCTCCATGTTCCGGAGCGAGGAGTGCGCCCTGGTCCAGCTCTTTCTGCCCCACAGCG	60		
QY	118	GCTGCTTACACCTGCGTGGCTGGCTGGCGAGCTGGGCTCGTGGAGTTTCAGAGCCCTC	177	DB	61	GCTGCTTACACCTGCGTGGCTGGCTGGCGAGCTGGGCTCGTGGAGTTTCAGAGCCCTC	120		
QY	178	AACGCTCCGCTGAGCGCTTCAGAGACGCTTTGTGTTGATGTTTGGCGCTGTGAGGAG	237	DB	121	AACGCTCCGCTGAGCGCTTCAGAGACGCTTTGTGTTGATGTTTGGCGCTGTGAGGAG	180		
QY	238	CTGGAGAAAGCTTCACTTCTGCAAGAGAGGTGCGCGCTGGGTGCTCTGCGCC	297	DB	181	CTGGAGAAAGCTTCACTTCTGCAAGAGAGGTGCGCGCTGGGTGCTCTGCGCC	240		
QY	298	CGGCCAAAGGGAGGCTGCGGCAACCCCAACCCCGGCACTGCTGGCATCCAGAGGAG	357	DB	241	CGGCCAAAGGGAGGCTGCGGCAACCCCAACCCCGGCACTGCTGGCATCCAGAGGAG	300		
QY	358	ACGGAGCGCTTGGCCAGAGCTGCGGATGTGCGGGCAACAGCAGGCGCTTGGCGGC	417	DB	301	ACGGAGCGCTTGGCCAGAGCTGCGGATGTGCGGGCAACAGCAGGCGCTTGGCGGC	360		
QY	418	CAGCTGCAACAGCTGAGCTCAACGCGCGCTGTACGCCAGGGCCATGAACCTCAGCTG	477	DB	361	CAGCTGCAACAGCTGAGCTCAACGCGCGCTGTACGCCAGGGCCATGAACCTCAGCTG	420		
QY	478	GCAGCGGCCCAACAGATGGGCGCTCAGAGAGAGCGCCCTGCTCAGGCGCCCGGGGG	537	DB	421	GCAGCGGCCCAACAGATGGGCGCTCAGAGAGAGCGCCCTGCTCAGGCGCCCGGGGG	480		
QY	538	CGGCACAGGACCTGAGGGTCAACTTTGTGGCAGGTGCGGTGGAGCCCAAGGCGCCCT	597	DB	481	CGGCACAGGACCTGAGGGTCAACTTTGTGGCAGGTGCGGTGGAGCCCAAGGCGCCCT	540		
QY	598	GCCCTAGAGCGCTGCTGAGAGGGCTGCGCGGCTTCTCATTTGCCAGCTTTCAGGGAG	657	DB	541	GCCCTAGAGCGCTGCTGAGAGGGCTGCGCGGCTTCTCATTTGCCAGCTTTCAGGGAG	600		
QY	658	CTGGAGCAGCGCTGAGACACCCGTGACGGCGGAGCCAGCCAGCTGGATGACCTTCCTC	717	DB	601	CTGGAGCAGCGCTGAGACACCCGTGACGGCGGAGCCAGCCAGCTGGATGACCTTCCTC	660		
QY	718	ATCTCTACTGGGGTGAGCAGATCGGACAGAAAGATCCGCAAGATCACGGACTGCTTCCAC	777	DB	661	ATCTCTACTGGGGTGAGCAGATCGGACAGAAAGATCCGCAAGATCACGGACTGCTTCCAC	720		
QY	778	TGCCAGCTTCCCGTTTCTGCAGCAGGAGGAGGCGCGCTCGGGGCCCTGACGAGCTG	837	DB	721	NN	780		
QY	838	CAACAGCAGAGCGAGGCTGACGAGGTCTCTCGGGAGACAGCGGTTCTTGAGCCAG	897	DB	781	NN	840		
QY	898	GTGCTAGGCGCGGTTGCTGAGCTGCTGCGCCAGGCGAGGTGCAGTCCACAAGATGAAG	957	DB	841	GTGCTAGGCGCGGTTGCTGAGCTGCTGCGCCAGGCGAGGTGCAGTCCACAAGATGAAG	900		
QY	958	GCCGTGTACTGCGCCCTGAACCAAGTGCAGCTGAGCAACCAAGTGCCTCATTTGCC	1017	DB	901	GCCGTGTACTGCGCCCTGAACCAAGTGCAGCTGAGCAACCAAGTGCCTCATTTGCC	960		
QY	1018	GAGGCTGTGCTGTGCGACCTGCGCGCTGCGAGGCGCTTGGGAGAGCTCG	1077	DB	961	GAGGCTGTGCTGTGCGACCTGCGCGCTGCGAGGCGCTTGGGAGAGCTCG	1020		
QY	1078	ATGGAGGAGGAGTGAAGTCCGCTGCTACCGCATCCCTCGCGGAGCATGCCCCCACA	1137	DB					
QY	1021	ATGGAGGAGGAGTGAAGTCCGCTGCTACCGCATCCCTCGCGGAGCATGCCCCCACA	1080	DB					
QY	1138	CTCATCCGACCAACCGCTTTCACGCGGAGCTTCCAGGGCATCGTGGATCGCTACGCGCTG	1197	DB					
QY	1081	CTCATCCGACCAACCGCTTTCACGCGGAGCTTCCAGGGCATCGTGGATCGCTACGCGCTG	1140	DB					
QY	1198	GCGCTTACCAAGGAGGTCAACCCGCTCCCTACACATCATCACCTTCCCTTCCCTTCTT	1257	DB					
QY	1141	GCGCTTACCAAGGAGGTCAACCCGCTCCCTACACATCATCACCTTCCCTTCCCTTCTT	1200	DB					
QY	1258	GCTGTGATGTTTCGGGATGTGGGCCACCGGCTGCTCATGTTCTCTTCCCTTCCCTTCCCT	1317	DB					
QY	1201	GCTGTGATGTTTCGGGATGTGGGCCACCGGCTGCTCATGTTCTCTTCCCTTCCCTTCCCT	1260	DB					
QY	1318	GTCTTTCGGAGAACCGACCGGCTGTGAAAGCGCGCAGAAACGAGATCTGGCAGACTTTC	1377	DB					
QY	1261	GTCTTTCGGAGAACCGACCGGCTGTGAAAGCGCGCAGAAACGAGATCTGGCAGACTTTC	1320	DB					
QY	1378	TTTCAGGGGCGGCTACCTGCTCTGCTTATGGGCTGTTTCTCATCTACACCGGCTTTCATC	1437	DB					
QY	1321	TTTCAGGGGCGGCTACCTGCTCTGCTTATGGGCTGTTTCTCATCTACACCGGCTTTCATC	1380	DB					
QY	1438	TACAAACGAGTGTTCAGTCCGCCACACGACATCTTCCCTCGGCTGGAGTGTGGCGGC	1497	DB					
QY	1381	TACAAACGAGTGTTCAGTCCGCCACACGACATCTTCCCTCGGCTGGAGTGTGGCGGC	1440	DB					
QY	1498	ATGGCCAAACAGTCTGGCTGGAGTGAATGCAATTCCTGGGCCACACACGATGCTTACCTG	1557	DB					
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CR594613 1864 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DD004Y118 of Neuroblastoma Cot
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CR594613
HTC; CNSLT cDNA.
http://50475420
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Li W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
JOURNAL
REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 1864)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
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QY 828 GCAGCAGCTGCCAACAGCAGAGCGCAGGAGTGTGACGAGGTCTCTCGGGGAGACAGAGCGGTT 887

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RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
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TITLE
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AUTHORS
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleschmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, P., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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Nature 420 (6915), 563-573 (2002)
12466851
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Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R.,
- Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Aurali, R.N., Bailey, J.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crome, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., Fletcher, C.D., Down, T., Engstrom, P., Fagioli, M., Faulkner, G., Feilcher, C.F., Fukushima, T., Furuno, M., Putaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Humnietz, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Larsen, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Noi, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavese, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugliura, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yang, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hilde, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori, K., Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watahiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
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Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.
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Science 309 (5740), 1564-1566 (2005)
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- 8 (bases 1 to 3031)
Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome

Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>

FEATURES

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DB 1468 CAGGCGCTGCAGAGCGCTCAAGTGAAGAGGAGTGAAGTGTGTGCTCACCGCATCCCC 1527
QY 1117 TGGCGGAGCATGCCCGCCACACTCATCCGCAACAAACCGCTTTCAGGCGCAGCTTCCAGGGC 1176
DB 1528 TGCAGGAGCATGCTCCAAACCTCATCAGAGCAACCGCTTTCAGCTCCAGCTTCCAGGGC 1587
QY 1177 ATGCTGATCGCTACGCGTGGGCGCTACAGAGGAGTCAACCGCTGCTTACACCATC 1236
DB 1588 ATTGTGATGCTTATGTTGGGCGCTACAGGAGTTAACTGCTTCTTACCATC 1647
QY 1237 ATCACTTCCCTTCTTCTGTTGTGTATGTTTCGGGAGTATGGGCCACGCGCTGCTCATG 1296
DB 1648 ATCACTTCCCTTCTTCTGCTGTGTATGTTTGGCGATGTGGGCGACGACTGCTCATG 1707
QY 1297 TTTCTTCTTGGCGCATGCTTTCAGGGCGCTACCTGCTGCTGCTTATGGGCTGCTTC 1356
DB 1708 TTTCTTCTTGGCGCATGCTTTCAGGGCGCTTTCAGGGCGCTTTCAGGGCGCTGCAAA 1767
QY 1357 AACGAGATCGGAGACTTTTTCAGGGCGCTACCTGCTGCTGCTTATGGGCTGCTTC 1416
DB 1768 AACGAGATCGGAGACTTTCAGGGCGCTGATACCTACTCTGCTCATGGGCTGCTTC 1827
QY 1417 TCCATCTACACCGCTTTCATCTAACAGTGTCTCAGTGCAGCGCACAGCATCTTCCCC 1476
DB 1828 TCCGCTCTACACTGCTTTCATCTAACATGAGTGTCTCAGCGCGAGCCACCACTATTTTCCC 1887
QY 1477 TCGGGCTGAGTGTGGCGCGCATGGCCAAACAGTCTGGCTGGAGTGAATGCTTCTGGCC 1536
DB 1888 TCAGGTTGAGTGTGGCTGCATGGCCAAACAGTTCAGGCTGGAGTGAAGTATCTGTCC 1947
QY 1537 CAGCAGAGTGTACCTGGATCCCAAGTCAACCGGTGCTTCTTCTGGGAGCCCTA-CCC 1595
DB 1948 CAGCATCTCATGCTCACCTTGAACCTTAACATCACTGTGTGTCTTCTTGGACCATATCCC 2007
QY 1596 CTTTGGCATGCTTATTTGGAGCTTGGCTGCCAACCACTTGAAGTTCCTCAACTCCTT 1655
DB 2008 TTTTGGCATTGAACCGATCTGGAGCTTGGCCACGAAACCACTGAGCTTCTCAACTCCTT 2067
QY 1656 CAAGATGAAGTGTGCTGAT-CTGGGCGTGTGACATGAGCTTGGGGTGTGCTCTCG 1714
DB 2068 CAAGATGAAGTGTGCTGATCTTGGGCTACGACATGGGCTTGGGGTGTGCTCTCA 2127
QY 1715 GAGTCTTCAACAGCTGCACTTTGGCCAGAGGAGCAGGCTGCTGCTGGAGCGCTGCGG 1774
DB 2128 GCATCTTCAACACAGCTGCACTTTGGCCAGGCCACCGGCTACTGCTGGAGACCTTGGCTG 2187
QY 1775 AGCTCACTTCTGCTGGGACTTCTGCTTACCTGCTGTGTGTCTTCTAGTCACTTACAAGTGGC 1834
DB 2188 AGCTCATCTCTGCTGGGCTCTTGGGCTACCTTGTGTCTTCTCATGTCTCAAGTGGG 2247
QY 1835 TGTGTGTGCTGGGCTGCGAGGGCGCGCTCG---CCAGCATTCCTCATCCTCATCAACA 1891

Db	2248	TGAATGCTCAGCTGCTAGGCGCTCTCTCGGCCCCAGTATCCTCATTTCACTTATCAATA	2307
Qy	1892	TGTTCTCTTTCTCCACAGCCCCAGCAACAGGCTGCTTACCCCGGACGAGAGTGGTCC	1951
Db	2308	TGTTCTCTTCTCTCAAAAACCCACCAATCATCTGCTCTTCCATGGGACGAGAGTGGTAC	2367
Qy	1952	AGGCCACGCTGGTGGTCTCTGGCTTGGCCATGFGGCCATCTGCTGCTTGGCACACCCC	2011
Db	2368	AGTACGTGCTGGTGGTCTCTGGCTTGGCTACCGTTCTATCCTGTTCTGGGCACACCT	2427
Qy	2012	TGCACCTGCTGCACCGCCACGCGCGCG-----CCTGCGGAGGAGCCCGCTGACCGAC	2065
Db	2428	TGTACCTGCTGCGCCAGCACCGCCACAGAAAGAAACACTCAGAGAGGCCACGAGGCCGACG	2487
Qy	2066	AGGAGGAAAAACAAGCCCGGGTTGCTGCACCTTGCCTGACGCATC-----TGTGAATGGCT	2119
Db	2488	AGGATGAGGACACGGACAAGCTTCTGGCTCCCTCGATGCATCCACTTGGAGAACAGCT	2547
Qy	2120	GGAGCTCCGATGAGGAAAGCGACGGGGCTGGATGATGAGAGGAGGCCGAGCTGTGTCC	2179
Db	2548	GGAGCCCTGATGAGGAGAGGGCTGGGAGCCACGGGGATGAA---GAAACTGAGTTTGTTC	2604
Qy	2180	CCTCCGAGGTGCTCATGCACACAGGCCATCCACACCATCGAGTTCTGCTGGGCTGGGTCT	2239
Db	2605	CTTCTGAGATCTTCATGCAACAGCAATCACACCATTGAGTTCTGCTGGGCTGCATCT	2664
Qy	2240	CGAACCCGCTCTTACTCTGGGCTGTGGGCCCTGAGCCTGGGCCACCGCCAGCTGTFCG	2299
Db	2665	CCAAACAGCGCTCTACTTTCGCTCTCTGGGCCCTTAGCCCTGGGCCCATGCCCCAGCTGTCTG	2724
Qy	2300	AGGTTCTGGGGCCATGGTGATGGCATAGGCTTAGCCCTGGGCGCGGAGGTGGGCGTGG	2359
Db	2725	AGGTCTGTGGGGCCATGGTATGGCATAGGCCCTGGGCATGGGCCGAGAGATCGGGGTGG	2784
Qy	2360	CGGCTGTGTGCTGCTCCCATCTTTTGCCGCCCTTTGGCGTGATGACCGTGGCTATCCTGC	2419
Db	2785	CAGCTGTGGTGTGTTCCCTGTTGCTGCTTGTGTTGCTGTTGACTGTGGCCATCCTGT	2844
Qy	2420	TGTTGATGGAGGAGCTCTCAGCTTCTCTGACGCGCTTGCGGCTGCATCTGGGTGGAATTC	2479
Db	2845	TAGTGATGGAGGGCTCTCAGCCTTCTGTGATGCTGCGGTTGCACTGGGTGGAGTTC	2904
Qy	2480	AGAACAGTTCTACTCAGGCACGGGCTACAGGCTGAGTCCCTTCACCTTCGCTGCCACAG	2539
Db	2905	AGAACAGTTCTATTAGGCAACGGCTACAGCTCAGCCCCCTTCACTTCACTGTGGACA	2964
Qy	2540	ATGACTAGGCCCC	2552
Db	2965	GTGACTAGCTACC	2977

RESULT 5	
AY407801	
LOCUS	2514 bp DNA linear GSS 15-DEC-2003
DEFINITION	Mus musculus TCIRG1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION	AY407801
VERSION	AY407801.1 GI:39763772
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chordontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Murinae; Mus. 1 (bases 1 to 2514)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tansbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Slninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Infering nonneutral evolution from human-chimp-mouse orthologous gene trices
JOURNAL	Science 302 (5652), 1960-1963 (2003)

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QY 775 CACTGCCACGCTTCTCCCGTTCTGCACAGGAGGCGCCCGCTCGGGGCGCTGCAGCAG 834
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QY 835 CTGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 894
Db 781 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 840
QY 895 CAGGTGCTAGGCGGGGTGCTGAGCTGCTGCGCGCAGGCGAGGTGCGAGGTCCCAAGATG 954
Db 841 CAGGTGTTGGGCGGGGTGCGAGCAGCTGCTGCGCCCATGCGAGGTGCGAGATCCCAAGATG 900
QY 955 AAGSCGCTGTACCTGGCCCTGAAACAGTGCAGGTGAGCCAGCAGCAAGTGCCTATT 1014
Db 901 AAGCAGTGTACCTGACCTCAACAGTGCAGGTGAAACACACACAAGTGCCTCATC 960
QY 1015 GCGAGGCTGTGCTCTGTGCGAGACCTGCGCGCCCTGCAGGAGGCGCTGCGGAGCAGC 1074
Db 961 GCGAGGTCTGTGTGCGCGAGGAGCCTTGCCCACTGTGCAGCAGGCGCTGCAGAGCGGC 1020
QY 1075 TCGATGAGGAGGAGTGAAGTGCCTGCGGTCAACGCAATCCCTGCGGGGAGATGCCCGCC 1134
Db 1021 TCAAGTGAGGAGGAGTGAAGTGTGCTCAACGCAATCCCTGCCAGGACATGCCCTCCA 1080
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QY 1195 GTGGGCGCTACAGGAGGTCAACCCCGCTCCCTACACCATCATCACTTCCCTTCTCTG 1254
Db 1141 GTGGGCGCTACAGGAGGTCAACCCCTGCTCCCTACACCATCATCACTTCCCTTCTCTC 1200
QY 1255 TTTGCTGTGATTTGCGGGATGTGGGCACCGGCTGCTCAATGTTCTTCTTCCGCTTGCC 1314
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QY 1315 ATGCTCTTGGGAGACCAACCGCTGTGAAGCGCGCAGACAGATCTGGCAGACT 1374
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QY 1435 ATCTACAAAGAGTGTTCAGTTCGCGCACAGCATCTTCCCTCTGGGCTGGAGTGGCC 1494
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QY 1795 CTCTCGGTACCTCGTGTTCCTAGTCACTACAAGTGGCTGTGTGCTGGGCTGCGCAGG 1854
Db 1741 CTCTTTGGCTACCTTGTGTTCTCATTTCTACAAGTGGGTGAATGCTCAGCTGCTAGC 1800
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Db 1801 GCCTCTCGGCCCCAGTATCTCACTTCAATAATGTTCCTTCTCTCAAAC 1860
QY 1912 CCCAGCAACAGGCTGTCTTACCCCGCAGGAGGTGGTCCAGGCACGCTGGTGGTCTCTG 1971
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QY 1972 GCCTGGCCATGTGTGCCATCTGCTGTCTGGGCAACCCCTGCACTGCTGTGCAACGCGCAC 2031
Db 1921 GCTTTGGCTACCGTTCCTATCTGTTGCTGGGCAACCCCTGTGTAACCTGCTGCGCAGCAC 1980
QY 2032 CGCGGCG-----CCTGGGAGGAGCGCGCTGACCGACAGGAGNAACAGGCGCGG 2085
Db 1981 CGCCACAGAAGAACTCAGAGAGCCAGCAGGCGCAGGATGAGGACAGGACAAG 2040
QY 2086 TTGCTTGACCTGCTGACGCAATC-----TGTGAATGGCTGGAGCTCCGATGAGGAAAAG 2139
Db 2041 CTCTGSGCTCCCTGATGATCATCCACTTGGAGAACAGCTGGAGCCCTGATGAGGAGAAG 2100
QY 2140 GAGGGGCGCTGATGATGAA-----GAGGAGGCGAGCTGCTGCCCTCCGAGGTGCTC 2193
Db 2101 GCTGGGAGGCCAGGGGATGAAGAACTGAGGTGGGAGATTTGTCTCTGAGATCTTC 2160
QY 2194 ATGCACAGGCGCATCCACCATCGAGTCTGCTGGGCTGCTCTCCAAACCGCTCC 2253
Db 2161 ATGCACAAAGCAATCCACCATTTGAGTCTGCTGGGCTGCACTCTCCAAACAGCGCTCC 2220
QY 2254 TACTCGGCTGTGGGCGCTGAGCTGGGCCAGCGCCAGCTGTCCGAGGTCTCTGTGGGCC 2313
Db 2221 TACTTGGCTCTTGGGCGCTGAGCTGGGCCATGCCCATGCCAGCTGTCTGAGGTCTCTGTGGGCC 2280
QY 2314 ATGGTGAATGCGCATAGCGCTGGGCGCTGGGCGGAGGTGGGCGGTGCTGTGGTGTG 2373
Db 2281 ATGGTGAATGCGCATAGCGCTGGGCGATGGGCGAGAGATCGGCGTGGCAGCTGTGGTGTG 2340
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Db 2341 GTCCCTGTGTGCTGCTGCTTGTGTGCTGTGGCCATCTCTGTAGTGGAGGGG 2400
QY 2434 CTCTCAGCTTCTCTGCACGCGCTTGGCGTGCATGGGTGGAAATTCAGAAACAAGTTCTAC 2493
Db 2401 CTCTCAGCTTCTCTGCATGCCCTGGGTTGCATGGGTGGAGTTCAGAAACAAGTTCTAT 2460
QY 2494 TCAGGACAGGGCTACAGGTGCTGCTTCACTTCCGCTGCCACAGATGACTAG 2547
Db 2461 TCAGGACAGGGCTACAGGTGCTGCTTCACTTCACTTGGACAGTGTACTAG 2514
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RESULT 6

CR602058

LOCUS

DEFINITION

full-length cDNA clone CS0DI059VF06 of Placenta Cot 25-normalized

of Homo sapiens (human).

CR602058

CR602058.1 GI:50482865

HTC; CNSLT_CDNA.

Full-length cDNA libraries and normalization

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1655)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Paradise Avenue

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:

BP 191 91060 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dr) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

source

Location/Qualifiers
1..1655
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1059YF06"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 55.6%; Score 1468.6; DB 6; Length 1655;
Best Local Similarity 94.9%; Pred. No. 3.1e-274;
Matches 1571; Conservative 0; Mismatches 4; Indels 80; Gaps 2;

QY 1022 CTTGCTGCTCTGTGGAGACCTGCCCGCTCGAGAGCCCTCGAGGAGCTCGATGG 1081
DB 1 CTTGCTGCTCTGTGGAGACCTGCCCGCTCGAGAGCCCTCGAGGAGCTCGATGG 60

QY 1082 AGGAGGAGTGTAGTCGCTGCTACCGCATCCCTGCGGAGCATGCCCCACACTCA 1141
DB 61 AGGAGGAGTGTAGTCGCTGCTACCGCATCCCTGCGGAGCATGCCCCACACTCA 120

QY 1142 TCGGACCAACCGCTTCAGGCGAGCTTCAGGGCATCTGTGATCGCTACGGCGTGGCC 1201
DB 121 TCGGACCAACCGCTTCAGGCGAGCTTCAGGGCATCTGTGATCGCTACGGCGTGGCC 180

QY 1202 GCTACAGGAGTCAACCCGCTCCCTACACCATCATACCTTCCCTTCCTGTTGCTG 1261
DB 181 GCTACAGGAGTCAACCCGCTCCCTACACCATCATACCTTCCCTTCCTGTTGCTG 240

QY 1262 TGATGTTCCGGGATGTGGCCACGGCTGCTCATGTTCTTTCGCCCTGGCCATGGTCC 1321
DB 241 TGATGTTCCGGGATGTGGCCACGGCTGCTCATGTTCTTTCGCCCTGGCCATGGTCC 300

QY 1322 TTGCGGAGAACCGAGCTGTGAAGCCGCGCAGAACGAGATCTGGGAGCTTCTTCA 1381
DB 301 TTGCGGAGAACCGAGCTGTGAAGCCGCGCAGAACGAGATCTGGGAGCTTCTTCA 360

QY 1382 GGGGCGCTTACCTGCTCTGCTTATGGGCTGTGTTCCATCTACACCGGCTTCACTCA 1441
DB 361 GGGGCGCTTACCTGCTCTGCTTATGGGCTGTGTTCCATCTACACCGGCTTCACTCA 420

QY 1442 ACGAGTCTTACGTGCGGCCACAGCATCTTCCCTCGGCTGTGAGTGTGGCCCATGG 1501
DB 421 ACGAGTCTTACGTGCGGCCACAGCATCTTCCCTCGGCTGTGAGTGTGGCCCATGG 480

QY 1502 CCAACGAGTCTGGCTGG----- 1518
DB 481 CCAACGAGTCTGGCTGGAGGTGAGGCCCGGGCCCCAGCCCGCTGGGGCCCCCGCAGCAC 540

QY 1519 -----AGTGATGATCAATTCCTGGCCGAGTGTGATCTCTGGCCAGCACAC 1544
DB 541 CGCAGCCCTGACCGCCCTCCCTGGGTTGCCGAGTGTGATCTCTGGCCAGCACAC 600

QY 1545 GATGTTACCTGGATCCCAACGTCACCGGTGTCTTCTGGGACCTTACCTCTTGGCAT 1604
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QY 1605 CGATCCTATTTGGAGCCCTGGCCCAACACCTTGAGCTTCTCACTCTCAAGATGAA 1664
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DB 721 GATGTCCTGATCTCTGGGCGTGTGTCACATGGCCCTTTGGGTTGGTCTCTCAA 780

QY 1725 CCACGTGCATTTGGCCAGAGGACCGGGCTGTGCTGGAGACGCTGCGGAGCTCACCTT 1784

DB 781 CCACGTGCACCTTTGGCCAGAGGACCGGCTGTGCTGTGGAGACGCTGCGGAGCTCACCTT 840
QY 1785 CTTGCTGGAGCTCTTGGGTTACCTGTTCTTAGTCACTCTACAGTGGCTGTGTCTG 1844
DB 841 CTTGCTGGAGCTCTTGGGTTACCTGTTCTTAGTCACTCTACAGTGGCTGTGTCTG 900

QY 1845 GGTGCTGCTGGCCTTGGCCATGGTCCCATCTCTGCTGTGGCACACCCCTGCACCTGCT 1901
DB 901 GGTGCTGCTGGCCTTGGCCATGGTCCCATCTCTGCTGTGGCACACCCCTGCACCTGCT 960

QY 1902 TTCCACAGCCCCACAAACAGGCTGCTCTACCCCCGCGAGGAGTGTTCAGGCCACGCT 1961
DB 961 TTCCACAGCCCCACAAACAGGCTGCTCTACCCCCGCGAGGAGTGTTCAGGCCACGCT 1020

QY 1962 GGTGCTGCTGGCCTTGGCCATGGTCCCATCTCTGCTGTGGCACACCCCTGCACCTGCT 2021
DB 1021 GGTGCTGCTGGCCTTGGCCATGGTCCCATCTCTGCTGTGGCACACCCCTGCACCTGCT 1080

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DB 1081 GCACCGCCACCGCCCGCTCGAGAGGAGGCGGCTGACCGACAGGAGGAAAAAAGGC 1140

QY 2082 CGGTTGTGACCTGCTGACGCACTCTGTGAATGGCTGGAGCTCCGATGAGGAAAAAGGC 2141
DB 1141 CGGTTGTGACCTGCTGACGCACTCTGTGAATGGCTGGAGCTCCGATGAGGAAAAAGGC 1200

QY 2142 AGGGGGCTGTGATGATGAGAGGAGGCGGCTGCTCCCTCGAGGAGTCTCATGACCA 2201
DB 1201 AGGGGGCTGTGATGATGAGAGGAGGCGGCTGCTCCCTCGAGGAGTCTCATGACCA 1260

QY 2202 GGCATCACACACATCGAGTTCTGCTGGGCTGCTCTCAACACGCGCTCTACTGG 2261
DB 1261 GGCATCACACACATCGAGTTCTGCTGGGCTGCTCTCAACACGCGCTCTACTGG 1320

QY 2262 CTTGCGGCTTGGCTGCGCCACGCTGCTCGAGCTGTCCGAGTCTTGTGGGCTATGGTAT 2321
DB 1321 CTTGCGGCTTGGCTGCGCCACGCTGCTCGAGTCTTGTGGGCTATGGTAT 1380

QY 2322 CGCATAGGCTGCGGCTGCGGCGGAGTGGGCTGCGGCTGCTGCTGCTGCTGCTGCT 2381
DB 1381 CGCATAGGCTGCGGCTGCGGCGGAGTGGGCTGCGGCTGCTGCTGCTGCTGCTGCT 1440

QY 2382 CTTTCCGCTTGGCTGATGACCGTGGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 2441
DB 1441 CTTTCCGCTTGGCTGATGACCGTGGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1500

QY 2442 CTTCTGCAACGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2501
DB 1501 CTTCTGCAACGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560

QY 2502 GGGCTACAGCTGAGTCCCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2561
DB 1561 GGGCTACAGCTGAGTCCCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620

QY 2562 CTTGCGACACCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2596
DB 1621 CTTGCGACACCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1655

RESULT 7

AK004094

LOCUS

DEFINITION

Mus musculus 18-day embryo whole body cDNA, RIKEN full-length
enriched library, clone:1110034K16 product:ATPASE, H+ TRANSPORTING,
LYSOSOMAL I (FRAGMENT), full insert sequence.

ACCESSION

AK004094.1

VERSION

AK004094.1

KEYWORDS

HTC; Cap trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

AK004094

Mus musculus

enriched library

18-day embryo

whole body

cDNA

RIKEN full-length

ATPASE, H+

TRANSPORTING,

LYSOSOMAL I

(FRAGMENT), full

insert sequence.

GI:12835141

HTC; Cap trapper.

Mus musculus

(house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;


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QY 1565 AGTCAACCGGTGTCTCTGGAGACCTACCCCTTTGGCATCGATCTATTGGAGCCTGG 1624
Db 481 ATATCACTGCTGTCTCTCTGGAGCATATCCCTTTGGCATTGACCGATCTGGAGCCTGG 540
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Db 541 CCACGAACCACTGTAGCTCTCACTCTTCAAGATGAAGATGTCGTCATCTCTGGGG 600
QY 1685 TGTGTCACATGCTCTTGGGGTGTCTCTGGAGTCTTCAACACGTCGATCTTGGCCAGA 1744
Db 601 TCAGCAGATGCTCTTGGGGTGTCTCTCAGCATCTTCAACACGTCGATCTTGGCCAGG 660
QY 1745 GGCACCGCTGTCTGTGGAGAGCTGCGCGAGCTCACCTTCTCTGCTGGAGCTCTTCGGTT 1804
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Db 721 ACTTGTGTCTCTCATTTGTCTCAAGTGGGTGAATGTCTCAGCTGTCTAGGCTCTCTCG 780
QY 1864 --CCAGCATCTCTCATCTTCAACATGTTCTCTTCTCTCCACAGCCCGCAGCAACA 1921
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QY 1922 GCTGCTCTTACCCCGCGCAGAGGTGTCTCAGCCACGCTGTGTCTCTGGCTTTGGCCA 1981
Db 841 ATCTGCTCTTCCATGGCGAGGAAGTGTACAGTGTGTGTCTGTCTGTGGCTTTGGCTA 900
QY 1982 TGGTGGCCATCTCTGTCTTGGCAGACCCCTGCACTGTGTGCAACGCGCAACCGCGCG- 2039
Db 901 CGGTTCTTATCTGTGTGTGGGACACCCCTTGTACCTGTGTGGCCAGCAGCCAGAA 960
QY 2040 ---CCTGGAGGAGGCGGCTGTACCGACAGAGGAAACAGCGCGGTTGCTGGACC 2095
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QY 2096 TGCCTGACGCATC-----TGTGAATGGCTGGAGCTCCGATGAGGAAAGGAGGCGGC 2149
Db 1021 CCCTGTATGATCCACCTTTGGAGAACAGCTGGAGCCCTGATGAGGAGGCTGGAGCC 1080
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Db 1138 ACACCATGAGTTCTGCTGGGCTGTCTTCAACACAGCCCTTCTACTTGGTCTCTGG 1197
QY 2270 CCCTGAGCTGCCCCACGCTGTCCGAGGTTCTGTGGGCCATGTTGATGCGCATAG 2329
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QY 2330 GCTTGGGCTTGGGCGGAGGTGGGGTGTGGGCTGTGTGTCTGTGTCTTCCCATCTTGGCG 2389
Db 1258 GCTTGGGCTATGGGCGGAGAGATCGGGGTGGCAGCTGTGGTGTGGTCTTGTGTCTG 1317
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Db 1318 CTTTGGCTGTGTGATGTGTGGCATCTCTGTAGTGAAGAGGGGCTCTCAGCTTCTCTGC 1377
QY 2450 AGCCCTCGGCTGCACTGGGTGGAATTCAGAAACAAGTTCTACTCAGCAGCGGCTACA 2509
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Db 1438 AGCTCAGGCCCTTCACTTCACTGTGGACAGTGAAGTACTACC 1480
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RESULT 8
BX332189
LOCUS BX332189 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION
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CDNA clone CS0DC008YL06 5-PRIME, mRNA sequence.
ACCESSION BX332189
VERSION BX332189.2 GI:46274586
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1070)
AUTHORS Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:30341122.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6186.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DC008DF03QPl&c=6186.f.
Location/Qualifiers
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/clone="CS0DC008YL06"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized."
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 36.8%; Score 970.2; DB 4; Length 1070;
Best Local Similarity 95.5%; Pred. No. 1.5e-177;
Matches 1021; Conservative 8; Mismatches 36; Indels 4; Gaps 3;
QY 838 CAACAGCAGAGCCAGAGCTGCAGAGCTGCTGCCGCGCAGGCTGAGTCCACAAGATGAAG 957
Db 1 CAACAGCAGAGCCAGAGCTGCAGAGCTGCTGCCGCGCAGGCTGAGTCCACAAGATGAAG 60
QY 898 GTGCTAGGCCCGGGTCTGCAGCTGCTGCCGCGCAGGCTGAGTCCACAAGATGAAG 957
Db 61 GTGCTAGGCCCGGGTCTGCAGCTGCTGCCGCGCAGGCTGAGTCCACAAGATGAAG 120
QY 958 GCCGTGTACCTGGCCCTGAAACAGTGCAGCGTGTGAGCACCACCAAGTGCCTCATTTGCC 1017
Db 121 GCCGTGTACCTGGCCCTGAAACAGTGCAGCGTGTGAGCACCACCAAGTGCCTCATTTGCC 180
QY 1018 GAGGCTGTGTCTGTGCGAGACCTGCCCGCTGAGGAGGCGCTGCGGGACAGCTCG 1077
Db 181 GAGGCTGTGTCTGTGCGAGACCTGCCCGCTGAGGAGGCGCTGCGGGACAGCTCG 240
QY 1078 ATGAGGAGGAGTGTGAGTCCGTGTGCTCACCGCATCCCTTGCCTGGGAGATGCCCCCA 1137
Db 241 ATGAGGAGGAGTGTGAGTCCGTGTGCTCACCGCATCCCTTGCCTGGGAGATGCCCCCA 300
QY 1138 CTATCCGCAACCAACCGCTTTCAGCGCAGCTTTCAGGGGATCGTGTGATCGCTACGCGTGG 1197
Db 301 CTATCCGCAACCAACCGCTTTCAGCGCAGCTTTCAGGGGATCGTGTGATCGCTACGCGTGG 360
QY 1198 GCGCGCTACCAAGAGGTCAACCCGCTCCCTTACACCATCATCACCTTCCCTTCTCTGTTT 1257
Db 361 GCGCGCTACCAAGAGGTCAACCCGCTCCCTTACACCATCATCACCTTCCCTTCTCTGTTT 420
QY 1258 GCTGTGATGTTTGGGGATGTGTGGGCCAGCGGCTGTCTCATGTTCTCTTCCCTTGGCCATG 1317
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Db 421 GCTGTGATGTTGGGGATGTTGGCCAGCGGTGCTCATGTTCTCTTGGCCCTGGCCATG 480
Qy 1318 GTCTTTCGGAGAACCGACCGGTGTGAAAGCCCGCAGAGACTGTGGCAGACTTTC 1377
Db 481 GTCTTTCGGAGAACCGACCGGTGTGAGGCGCGCAGAGACTGTGGCAGACTTTC 540
Qy 1378 TTACAGGGCGCTACCTGCTCTGCTTATGAGGCGCTGTTCCTCATCTACACGGCTTCATC 1437
Db 541 TTACAGGGCGCTACCTGCTCTGCTTATGAGGCGCTGTTCCTCATCTACACGGCTTCATC 600
Qy 1438 TACAACAGGTCTTCACTCGCGCCACACAGCATCTTCCCTCGGCTGAGTGTGGCGCC 1497
Db 601 TACAACAGGTCTTCACTCGCGCCACACAGCATCTTCCCTCGGCTGAGTGTGGCGCC 660
Qy 1498 ATGGCCAAACAGTCTGGCTGGAGTGATGCTTCTTGGCCCGCAGCACAGATGCTTACCCCTG 1557
Db 661 ATGGCCAAACAGTCTGGCTGGAGTGATGCTTCTTGGCCCGCAGCACAGATGCTTACCCCTG 720
Qy 1558 GATCCCAACAGTCAACCGGTGTCTTCTGGGACCTTACCCCTTGGCATCGATCTTATTTGG 1617
Db 721 GATCCCAACAGTCAACCGGTGTCTTCTGGGACCTTACCCCTTGGCATCGATCTTATTTGG 780
Qy 1618 AGCTGGCTGCACCACTTGAAGTCTTCAACTCTTCAAGATGAAAGATGTCGGTCATC 1677
Db 781 AGCTGGCTGCACCACTTGAAGTCTTCAACTCTTCAAGATGAAAGATGTCGGTCATC 840
Qy 1678 CT-GGGGCTGTCACATGAGCTTTT-GGGGTGCTCTCGGAGTCTTCAACCAAGTGCAC 1735
Db 841 CTGGGGCTGTCACATGAGCTTTTGGGGTGGTCTCGGAGTCTTCAACCAAGTGCAC 900
Qy 1736 TTGG--CCAGAGGACCGGTGTCTGTCGAGAGCGTCCGGAGTCACTTCTGCTGGG 1793
Db 901 TTGGGGCAGAGSACCGGTGTCTGTCGAGAGCGTCCGGAGTCACTTCTGCTGGG 960
Qy 1794 ACTCTTGGTTACTCTGTTCTTAGTCATCTCAAGTGGCTGCTGCTGGGCTGCAG 1853
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Qy 1854 GGCGGCTCGCCAGCATCTCTATCCACTTCACTCAACATGCTTCTCTTC 1902
Db 1021 GGCGCTCGGCCCAACATCTCTCATOMTTTCAATAAGTTCYTYTTTC 1069
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RESULT 9
BX358008 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
LOCUS BX358008 909 bp mRNA linear EST 08-APR-2004
DEFINITION clone CS0DI032YN10 5-PRIME, mRNA sequence.
ACCESSION BX358008
VERSION BX358008.2 GI:46285730
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 909)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 5, 2003 this sequence version replaced gi:30366180.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6186.f
For more information about this cluster, see
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http://www.genoscope.cns.fr/cdna?s=CS0DI032D050QP1&c=6186.f.
FEATURES
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/clone="CS0DI032YN10"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 33.5%; Score 885.4; DB 4; Length 909;
Best Local Similarity 99.3%; Pred. No. 4.2e-161;
Matches 889; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 599 CCTAGAGCGCTGCTCTGGAGGGCTGCGCGGCTTCTCATTTGCGAGCTTCAGGAGC 658
Db 1 CCGGGATCGCTGCTCTGGAGGGCTGCGCGGCTTCTCATTTGCGAGCTTCAGGAGC 60
Qy 659 TGGAGCAGCGCTGGAGCACCCCGTACGCGGCGAGCCAGCCAGGTGAGTGCCTTCTCA 718
Db 61 TGGAGCAGCGCTGGAGCACCCCGTACGCGGCGAGCCAGCCAGGTGAGTGCCTTCTCA 120
Qy 719 TCTCTACTTGGGTGAGCAGATCGGACAGAGATCCGCAAGATCACGGACTGCTTCCACT 778
Db 121 TCTCTACTTGGGTGAGCAGATCGGACAGAGATCCGCAAGATCACGGACTGCTTCCACT 180
Qy 779 GCCACGCTTCTCCGTTCTGACAGAGAGAGCCCGCTCTCGGGGCGCTTCAGCAGCTGC 838
Db 181 GCCACGCTTCTCCGTTCTGACAGAGAGAGCCCGCTCTCGGGGCGCTTCAGCAGCTGC 240
Qy 839 AACAGCAGACCGAGGAGTCTGAGAGGTCTCTCGGGAGACAGACGGTCTCTGAGCCAG 898
Db 241 AACAGCAGACCGAGGAGTCTGAGAGGTCTCTCGGGAGACAGACGGTCTCTGAGCCAG 300
Qy 899 TGCTAGCGCGGTGCTGTCAGCTCTGCGCGCAGGCGAGGTGTCAGGTCCACAAGATGAAG 958
Db 301 TGCTAGCGCGGTGCTGTCAGCTCTGCGCGCAGGCGAGGTGTCAGGTCCACAAGATGAAG 360
Qy 959 CGGTGTACTTGGCCCTTGAACAGTGCAGCTGAGCACCGACAGCAAGTGCCTCATTTGCCG 1018
Db 361 CGGTGTACTTGGCCCTTGAACAGTGCAGCTGAGCACCGACAGCAAGTGCCTCATTTGCCG 420
Qy 1019 AGGCTGTGCTCTGTCGAGAGCTGCGCGCTCTGAGAGGCGCTTCGCGGAGCAGCTCGA 1078
Db 421 AGGCTGTGCTCTGTCGAGAGCTGCGCGCTCTGAGAGGCGCTTCGCGGAGCAGCTCGA 480
Qy 1079 TGGAGGAGGAGTGTAGTGCCTGCTCACCGCATCCCTTGCCTGGGACATGCCCGCCACAC 1138
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Qy 1139 TCATCCGCACCAACCGCTTTCAGGCCAGCTTCAGGGCATTCGTTGATCGCTACGGCGTGG 1198
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Qy 1199 GCGCTTACAGAGGTCACCGGCTTCCCTACACCATCATCCTTCCCTCTCTGTTTGG 1258
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Qy 1259 CTGTGATGTTTCGGGGATGTGGCCAGCGGTGCTCATGTTCTTCTTTCGCTTCGCTTCGCTTCG 1318
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Qy 1319 TCCTTCGGAGAACCGACCGGTGTGAAGACCGCGCAGAACAGAGATCTGCGACATTTCT 1378
Db 721 TCCTTCGGAGAACCGACCGGTGTGAAGACCGCGCAGAACAGAGATCTGCGACATTTCT 780
Qy 1379 TCAGGGGCGCTTACCTGCTCTGCTTATGGGCTGTTCTTCCATCTACCGGCTTCATCT 1438
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Db	781	TCAGGGGCGGTACTGCTCTGCTGTTTATGGGCGCTGTTCTCATTCAACCGGCTTCACT	840
Qy	1439	ACAACGAGTGTCTCAGTCGGGCCACACAGCATCTTCCCTCGGCTGGGCTGAGTGTGCG	1493
Db	841	ACAACGAGTGTCTCAGTCGGGCCACACAGCATCTTCCCTCGGCTGGGCTGAGTGTGCG	895
RESULT 10			
BX385317/c			
LOCUS			
DEFINITION	BX385317 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED		
ACCESSION	BX385317		
VERSION	BX385317.2 GI:46575483		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	On May 8, 2003 this sequence version replaced gi:30451332. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6186.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?S=CSODL009CH05NP1&c=6186.f. Location/Qualifiers 1. 1067 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODL009YP09" /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED" /cell_line="RAMOS CELL LINE" /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
FEATURES			
source			
ORIGIN			
Query Match			
Best Local Similarity	33.2%; Score 877.4; DB 4; Length 1067;		
Matches	942; Conservative 17; Mismatches 10; Indels 8; Gaps 6;		
Qy	1580	TCCTGGGACCTACCTTGGCATCGATCTATTGGAGCCTGGCTGCCAACCACTTGA	1639
Db	1009	TTCTGGACCTACCTTGGCATCGATCTATTGGAGCCTGGCTGCCAACCACTTGA	950
Qy	1640	GCTTCTTCAACTCTT-CAAGATGAAGATGTCGTCATCC-TGGGGCTGTCGACATGGC	1697
Db	949	GCTCCCTCACTCTTCCAAGATGAAGATGTCGTCATCTTGGGCTGTCGACATGGC	890
Qy	1698	CTTTGGGGTGGTCTCGAGTCTTCAACCACTGCACTTTGGCCAGAGGACCGGCTGCT	1757
Db	889	CTTTGGGGTGGTCTCGAGTCTTCAACCACTGCACTTTGGCCAGAGGACCGGCTGCT	830
Qy	1758	GCTGGAGACGCTGCGGAGCTCACCCTCCGCTGGGACTTTGCTTACCTCTGTTCTCT	1817
Db	829	GCTGGAGACGCTGCGGAGCTCACCCTCTGCTGGGACTCTTCGGTTACCTCTGTTCTCT	770


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Db 972 GCTGCTCCMACCACTTGRSTTCTCTCAMCCCTTCAAGATRAAR-TGTCCGTCACTCTGGG 914
Qy 1683 CTTCTGTCACATGGCTTTGGGGTGTCTCTCGAGTCTTCAACCAAGTCACTTTTGCCCA 1742
Db 913 -STCGTGCAATGAGCTTTGGGGTGTCTCTCGAGTCTTCAACCAAGTCACTTTTGCCCA 855
Qy 1743 GAGGACACCGCTGCTGCTGAGACGCTGCGGAGCTCACTTCTCTGCTGGAGCTCTTCGG 1802
Db 854 GAGGACACCGCTGCTGCTGAGACGCTGCGGAGCTCACTTCTCTGCTGGAGCTCTTCGG 795
Qy 1803 TTACTCTGCTTCTAGTCACTTACAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1862
Db 794 TTMCCCTGCTTCTAGTCACTTACAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 735
Qy 1863 G---CCAGCATCTCATCTTCAATCAATGATGTTCTTCTTCTCCACAGCCCAAGCAA 1919
Db 734 GGGCCCCAGCATCTCATCTTCAATCAATGATGTTCTTCTTCTCCACAGCCCAAGCAA 675
Qy 1920 CAGGCTGCTTACCCCGGACGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1979
Db 674 CAGGCTGCTTACCCCGGACGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 615
Qy 1980 CATGTGTCCTTCTGCTTGTGACACCTTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGT 2039
Db 614 CATGTGTCCTTCTGCTTGTGACACCTTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGT 555
Qy 2040 CTTGGGAGGAGGCGCTGACGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2099
Db 554 -CTGGGAGGAGGCGCTGACGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 496
Qy 2100 TGACGATCTGTGAATGCTGTGAGTCCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2159
Db 495 TGACGATCTGTGAATGCTGTGAGTCCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 436
Qy 2160 AGAGAGGCGAGTGTCTTCCCTTCCGAGTGTCTATGACACAGGAGGAGGAGGAGGAGG 2219
Db 435 AGAGAGGCGAGTGTCTTCCCTTCCGAGTGTCTATGACACAGGAGGAGGAGGAGGAGG 376
Qy 2220 GTTCTGCTGGCTGGCTGTCTCAACACCGCTTCTTACCTGCGCTGTGTGGGCTGTAGCT 2279
Db 375 GTTCTGCTGGCTGGCTGTCTCAACACCGCTTCTTACCTGCGCTGTGTGGGCTGTAGCT 316
Qy 2280 GGGCCACGCGGAGTGTCTGAGGTTCTGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2339
Db 315 GGGCCACGCGGAGTGTCTGAGGTTCTGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 256
Qy 2340 GGGCCGAGGAGTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2399
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Qy 2400 GATGACGCTGCTATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2459
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Qy 2460 GCTGCACTGGTGGAAATTCAGAACAAAGTTCTACTCAGGACGAGGCTTCAAGCTGAGTCC 2519
Db 135 GCTGCACTGGTGGAAATTCAGAACAAAGTTCTACTCAGGACGAGGCTTCAAGCTGAGTCC 76
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Qy 2580 TG 2581
Db 15 TG 14
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RESULT 13
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DBFINITION Homo sapiens cdna clone CS0DL009YP09 5-PRIME, mRNA sequence.
ACCESSION BX385318
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VERSION BX385318.2 GI:46620145
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1074)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30453326.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6186.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DL009CH05QP1&c=6186.f.
Location/Qualifiers
1..1074
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 32.7%; Score 863.4; DB 4; Length 1074;
Best Local Similarity 97.3%; Pred. No. 7,8e-157;
Matches 923; Conservative 6; Mismatches 14; Indels 6; Gaps 5;
Qy 3 GGTGCGGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 61
Db 48 GTGCGGAGGNGNGCAGCCAGCAGCGGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 107
Qy 62 GCTCCATGTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 121
Db 108 GCTCCATGTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 167
Qy 122 CTTACACCTGCGTGTGAGTGTGCGGAGCTGTGGGCTCTGTGGAGTTTCAAGAGACCTCAACG 181
Db 168 CTTACACCTGCGTGTGAGTGTGCGGAGCTGTGGGCTCTGTGGAGTTTCAAGAGACCTCAACG 227
Qy 182 CTTCCGTGAGCGCTTCCAGAGACGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 241
Db 228 CTTCCGTGAGCGCTTCCAGAGACGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 287
Qy 242 AGAAGACCTTACCTTCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 301
Db 288 AGAAGACCTTACCTTCTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 347
Qy 302 CAAAGGGAGGCTGCGGACACCCCGGAGCTGTGCGCATCCAGAGGAGGAGGAGGAGGAGGAGG 361
Db 348 CAAAGGGAGGCTGCGGACACCCCGGAGCTGTGCGCATCCAGAGGAGGAGGAGGAGGAGGAGG 407
Qy 362 AGCGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 421
Db 408 AGCGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 466
Qy 422 TGCACGAGTGTGAGCTTCCACGCGCGGCTGTACGCGAGGGGCGATGAACCTCAGCTGGCAG 481
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527	Db	 CCGCCCAACACAGATGGGGCCTCAGAGAGAGCCGCCCTGTCTCAGGCCCCCGGGGGGGCCGC	586
542	Qy	 ACCAAGGACCTGAGGGTCAACTTTGTGGAGAGTGCCTGTGGAGGCCCCACAAAGGCCCTCGGCC	601
587	Db	 ACCAAGGACCTGAGGGTCAACTTTGTGGAGAGTGCCTGTGGAGGCCCCACAAAGGCCCTCGGCC	646
602	Qy	 TAGAGCGCTCTCTGGAGGGCCCTGCCCGGCTTCTCATTTGCCAGGTTTCAGGGAGCTGG	661
647	Db	 TAGAGCGCTCTCTGGAGGGCCCTGCCCGGCTTCTCATTTGCCAGGTTTCAGGGAGCTGG	706
662	Qy	 AGCAGCCGCTGGAGCACCCCGTGAGCGGGCGAGCCACGCCACGTGGATGACCTTCTCTCATCT	721
707	Db	 AGCAGCCGCTGGAGCACCCCGTGAGCGGGCGAGCCACGCCACGTGGATGACCTTCTCTCATCT	766
722	Qy	 CCTACTGGGTGAGCAGATCCGACAGAAAGATCCGCAAGATCACCGACTGCTTCTCACTGCC	781
767	Db	 CCTACTGGGTGAGCAGATCCGACAGAAAGATCCGCAAGATCACCGACTGCTTCTCACTGCC	826
782	Qy	 ACGTCCTCCGTTTCTCAGACAGAGAGAGGCCCGCCTCGGGGCCCTGCAGCAGCTGCACAC	841
827	Db	 ACGTCCTCCGTTTCTCAGACAGAGAGAGGCCCGCCTCGGGGCCCTGCAGCAGCTGCACAC	885
842	Qy	 AGCAGAGCCAGGAGCTGCAGGAGGTCTCTCGGGGAGACAGAGCGGTTCTCTGAGCCAGGTGC	901
886	Db	 AGCAGAGCCAGGAGCTGCAGGAGGTCTCTCGGGGAGACAGAGCGGTTCTCTGAGCCAGGTGC	945
902	Qy	 TAGGCCGGGTGCTGCAGGTCTGCCGCCAGGGGAGGTCGAGGTCCACAA	950
946	Db	 TAGGCCGGGTGCTG-ARCTGTGC--GCMAGGAGGTGCAGTCAAAA	991

RESULT	14
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DEFINITION	AL528871 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens CDNA clone CSDD004Y118 5-PRIME, mRNA sequence.
ACCESSION	AL528871
VERSION	AL528871.3 GI:45703928
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Hemimidae; Homo.
REFERENCE	1 (bases 1 to 897)
AUTHORS	Li,W.B., Gruber,C.; Jesse,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On Feb 13, 2001 this sequence version replaced gi:31066721.

FEATURES
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/tissue type="NEUROBLASTOMA COT 50-NORMALIZED"
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match      32.3%; Score 853; DB 1; Length 897;
Best Local Similarity 98.6%; Pred. No. 8e-155;
Matches 853; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY      CTGCTTCCACTGCCAGCTCTTCCGTTCTGTCAGCAGGAGGAGGCCGCTCGGGGCCCT 827
DB      |||||
QY      23  CAGCTTCCACTGCCAGCTCTTCCCGTTCTGTCAGCAGGAGGAGGCCGCTCGGGGCCCT 82
DB      |||||
QY      828  GCAGCAGCTGCAACAGCAGAGCCAGGAGCTGTCAGGAGGTCTCTCGGGGAGACAGAGCGGTT 887
DB      |||||
QY      888  CCTGAGCAGCGTGTAGGCCGGGTGCTGCAGCTGCTGTCGCCGACAGGGAGGTGCAGGTCCA 947
DB      |||||
QY      143  CCTGAGCCAGGTGTAGGCCGGGTGCTGTCAGCTGCTGTCGCCGACAGGGCAGGTGCAGGTCCA 202
DB      |||||
QY      948  CAAAGTAAAGCCGCTGTACTGCGCCCTGAAACAGTGCAGCTGACGACACGACACAGATG 1007
DB      |||||
QY      203  CAAAGTAAAGCCGCTGTACTGCGCCCTGAAACAGTGCAGCTGACGACACGACACAAATG 262
DB      |||||
QY      1008  CCTCATTTGCCGAGGCCCTGGTGTCTGTGCGAGACCTGTCGCCGCCCTCGAGAGGCCCTGCG 1067
DB      |||||
QY      263  CCTCATTTGCCGAGGCCCTGGTGTCTGTGCGAGACCTGTCGCCGCCCTCGAGAGGCCCTGCG 322
DB      |||||
QY      1068  GGCAGCTCGATGGAGAGGAGGTGATGTCGCGTGGGTCTACCGCATCCCTTCGCCGGACAT 1127
DB      |||||
QY      323  GGCAGCTCGATGGAGAGGAGGTAAAGTTCCGTGGCTCACCGCATCCCTTCGCCGGACAT 382
DB      |||||
QY      1128  GCCCCACACTCATCGGCACCAACCGCTTCACGGCCAGCTTCACGGGATCGTGATCG 1187
DB      |||||
QY      383  GCCCCACACTCATCGGCACCAACCGCTTCACGGCCAGCTTCACGGGATCGTGATCG 442
DB      |||||
QY      1188  CTACGGCGTGGGCGCTACACGAGGTTCACACCCCGCTCCCTACACCATCATCACTTCCC 1247
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QY      443  CTACGGCGTGGGCGCTACACGAGGTTCACACCCCGCTCCCTACACCATCATCACTTCCC 502
DB      |||||
QY      1248  CTTCTCTGTTGCTGTGATGTTTGGGAGTGGGCCACGGGTGCTCATGTTCTCTTCGC 1307
DB      |||||
QY      503  CTTCTCTGTTGCTGTGATGTTTGGGAGTGGGCCACGGGTGCTCATGTTCTCTTCGC 562
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QY      1308  CTTGGCCATGGTCTTTCGGAGAACCGACGGCTGTGAAGCCGCGACGACGAGATCTG 1367
DB      |||||
QY      563  CTTGGCCATGGTCTTTCGGAGAACCGACGGCTGTGAAGCCGCGACGACGAGATCTG 622
DB      |||||
QY      1368  GCAGACTTTCTTCAGGGGCGCTACCTGCTCTCTGCTTATGGGCTGTTCTCCATCTACAC 1427
DB      |||||
QY      623  GCAGACTTTCTTCAGGGGCGCTACCTGCTCTCTGCTTATGGGCTGTTCTCCATCTACAC 682
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QY      1428  CGGCTTCACTCAACAGAGTCTTACGTGCGGCCACAGCATTTCCCTCGGGCTGGAG 1487
DB      |||||
QY      683  CGGCTTCACTCAACAGAGTCTTACGTGCGGCCACAGCATTTCCCTCGGGCTGGAG 742
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QY      1488  TGTGGCGGCATGGCCAAACAGTCTGGCTGGATGATGATTCCTGGGCCACGACACGAT 1547
DB      |||||
QY      743  TGTGGCGGCATGGCCAAACAGTCTGGCTGGAGTGAATGATTCCTGGGCCACGACACGAT 802
DB      |||||
QY      1548  GCTTACCTGGATCCCAACGTCAACCGGTGCTTCTCTGGGACCTTACCCCTTTGGCATCGA 1607
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QY      803  GCTTACCTGGATCCCAACGTCAACCGGTGCTTCTCTGGGACCTTACCCCTTTGGCATCGA 862
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QY      1608  TCCTATTTGGAGCCTGGCTGCCAAC 1632
DB      |||||
QY      863  TCCTATTTGGAGCCTGGCTGCMAC 887
DB      |||||

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RESULT 15

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 05:18:12 ; Search time 343 Seconds
(without alignments)
9101.427 Million cell updates/sec

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Perfect score: 2640
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:
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2: /EMC Celerra SID33/ptodata/2/pubpna/US06 NEW PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2592.2	98.2	2700	6	US-10-511-937-410
2	1474.2	55.8	1696	7	US-11-266-748A-76629
3	1474.2	55.8	1696	7	US-11-266-748A-109489
4	1474.2	55.8	1696	7	US-11-266-748A-129440
5	1093.2	41.4	1839	7	US-11-266-748A-361154
6	1093.2	41.4	1839	7	US-11-266-748A-444533
7	973.2	36.9	1000	7	US-11-266-748A-221798
8	973.2	36.9	1000	7	US-11-266-748A-287153
9	973.2	36.9	1000	7	US-11-266-748A-338582
10	973.2	36.9	1000	7	US-11-266-748A-397768
11	973.2	36.9	1000	7	US-11-266-748A-468814
12	707.2	26.8	738	7	US-11-266-748A-76628
13	707.2	26.8	738	7	US-11-266-748A-109488
14	707.2	26.8	738	7	US-11-266-748A-129439
15	674.4	25.5	1042	7	US-11-266-748A-76627
16	674.4	25.5	1042	7	US-11-266-748A-109487
17	674.4	25.5	1042	7	US-11-266-748A-129438
18	668.6	25.3	671	7	US-11-266-748A-54130
19	639	24.2	4681	7	US-11-266-748A-29886
20	617.2	23.4	3137	7	US-11-266-748A-30495
21	551.2	20.9	561	7	US-11-266-748A-362824
22	551.2	20.9	561	7	US-11-266-748A-446203
23	549.4	20.8	831	7	US-11-266-748A-8067
24	532.8	20.2	705	7	US-11-266-748A-367398
25	532.8	20.2	705	7	US-11-266-748A-450777

26	531.6	20.1	884	7	US-11-266-748A-76631	Sequence 76631, A
27	531.6	20.1	884	7	US-11-266-748A-109491	Sequence 109491, A
c 28	531.6	20.1	884	7	US-11-266-748A-129442	Sequence 129442, A
29	461.6	17.5	1469	7	US-11-266-748A-98830	Sequence 98830, A
c 30	461.6	17.5	1469	7	US-11-266-748A-151641	Sequence 151641, A
c 31	345	13.1	1151	7	US-11-266-748A-185488	Sequence 185488, A
32	345	13.1	1151	7	US-11-266-748A-240948	Sequence 240948, A
33	340.8	12.9	1127	7	US-11-266-748A-76630	Sequence 76630, A
34	340.8	12.9	1127	7	US-11-266-748A-109490	Sequence 109490, A
c 35	340.8	12.9	1127	7	US-11-266-748A-129441	Sequence 129441, A
36	308.8	11.7	444	6	US-10-488-619-1101	Sequence 1101, Ap
c 37	301	11.4	446	6	US-10-488-619-1101	Sequence 1101, Ap
38	262.4	9.9	3310	6	US-10-449-902-13157	Sequence 13157, A
39	225	8.5	1147	7	US-11-266-748A-260923	Sequence 260923, A
c 40	225	8.5	1147	7	US-11-266-748A-321440	Sequence 321440, A
c 41	220	8.3	1548	7	US-11-266-748A-99200	Sequence 99200, A
42	220	8.3	1548	7	US-11-266-748A-152011	Sequence 152011, A
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44	179.4	6.8	598	6	US-10-488-619-2079	Sequence 2079, Ap
45	166.2	6.3	605	7	US-11-266-748A-51893	Sequence 51893, A

ALIGNMENTS

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US-10-511-937-410
; Sequence 410, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 410
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-410

Query Match 98.2%; Score 2592.2; DB 6; Length 2700;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 2599; Conservative 0; Mismatches 9; Indels 3; Gaps 1;
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Db 84 GCGCGCGGAGCAGCACCCCGGGGACCATGGGCTCCATGTTCCGAGCGAGGTGGCCCT 143
QY 93 GGTTCAGCTCTTCTTCTCCACACAGCGGCTGCTACCTCGTGGTGGCTGGCGGCT 152
Db 144 GGTTCAGCTCTTCTTCTCCACACAGCGGCTGCTACCTCGTGGTGGCTGGCGGCT 203
QY 153 GGGCTCTGGGAGTTCAGAGACCTCAACGCTCGGTGAGCGCTTCCAGAGAGCGCTTTGT 212
Db 204 GGGCTCTGGGAGTTCAGAGACCTCAACGCTCGGTGAGCGCTTCCAGAGAGCGCTTTGT 263

213 GGTGATGTTTGGCGCTGTGAGAGCTGGAAGACCTTCACTTCTCTGAGGAGGT 272
264 GGTGATGTTTGGCGCTGTGAGAGCTGGAAGACCTTCACTTCTCTGAGGAGGT 323
273 GGGCGGGCTGGGCTGGTCTCTGCCCCGCAAGGGAGGCTGCGGCAACCCCG 332
324 GGGCGGGCTGGGCTGGTCTCTGCCCCGCAAGGGAGGCTGCGGCAACCCCG 383
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393 GGGCAACCAAGAGGCGCTGGGGCCCAAGCTGCAACAGCTGCAAGCTCACGCGCGTGTCT 452
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453 AGCCAGGGCCATGAACCTCAGCTGGCAGCGCCCAACAGATGGGGCTTCAGAGAGGAC 512
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513 GCGCCCTGCTCAGAGCGCCCGGGGGCGCACAGGAGCTGAGGGTCACTTTGTGGCAGG 572
564 GCGCCCTGCTCAGAGCGCCCGGGGGCGCACAGGAGCTGAGGGTCACTTTGTGGCAGG 623
573 TGCCGTGGAGGCCCAAGAGCGCCCTGCGCTAGAGCGCTGCTCTGGAGGGCTGCGCGCG 632
624 TGCCGTGGAGGCCCAAGAGCGCCCTGCGCTAGAGCGCTGCTCTGGAGGGCTGCGCGCG 683
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804 CGCAGAGTCAAGGAGCTGCTTCCACTGCCACGCTTTCCTCCGTTTCTGACAGAGAGGC 863
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1284 CATCATACCTTCCCTTCTGTTGCTGTGTGTGTGTGTTGCGGGATGTGGGCAAGCGGCTGTCT 1343
1293 CATGTTCTCTTTCGCGCTTGGCCATGGTCTCTTGGAGAACCGACCGGCTGTGAAAGCGCG 1352

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1593 CCGCTTGGCATCGATCTTATTTGGAGCTTGGCTGCGCAACCACTTGGAGCTTCTCAACTC 1652
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1713 CGGAGTCTTCAACCAAGTGCATTTTGGCGAGAGCACCGGCTGTCTGTGAGACGCTGCC 1772
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1824 GGAGCTCACTTCTGCTGGGACTCTTGGTTACTCTGTGTCTTAGTCTATCTACAGTG 1883
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1890 CATGTTCTCTTCTCCCAAGCCCCAGCAACAGGTGTCTTACCCCGGAGAGGTGT 1949
1944 CATGTTCTCTTCTCCCAAGCCCCAGCAACAGGTGTCTTACCCCGGAGAGGTGT 2003
1950 CCAGGCGCAGCTGTGTCTTGGGCTTGGCCATGTGTGCCATCTCTGCTGTTGGCACAC 2009
2004 CCAGGCGCAGCTGTGTGTCTTGGGCTTGGCCATGTGTGCCATCTCTGCTGTTGGCACAC 2063
2010 CCGTCACTGCTGCAACCGCGCGCTGCGAGAGGGCGGCTGACCGCAGGA 2069
2064 CCGTCACTGCTGCAACCGCGCGCTGCGAGAGGGCGGCTGACCGCAGGA 2123
2070 GGAAGAACGCGCGGCTTGTGGAACCTGCTGACGATCTGTGAATGGCTGAGTCTCGA 2129
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Qy	2430	GGGACTCTCAGCCTTCCTGCA CGCCCTGCGGCTGCACCTGGGTGGAATTCAGAA CAAGTT	2489
Db	2484	GGGACTCTCAGCCTTCCTGCA CGCCCTGCGGCTGCACCTGGGTGGAATTCAGAA CAAGTT	2543
Qy	2490	CTACTCAGGCACGGGCTACAGCTGATGTCCTTCACCTTCGCTGCCACAGATGACTAGGG	2549
Db	2544	CTACTCAGGCACGGGCTACAGCTGATGTCCTTCACCTTCGCTGCCACAGATGACTAGGG	2603
Qy	2550	CCCACTGCAGGTCTCTGCCAGACCTCTTCTCTGACCTCTGAGGCAGGAGAGGAAATAAGAC	2609
Db	2604	CCCACTGCAGGTCTCTGCCAGACCTCTTCTCTGACCTCTGAGGCAGGAGAGGAAATAAGAC	2663
Qy	2610	GGTCCGCCCTGGCAAAAAAAAAAAAAAAAAAAAA	2640
Db	2664	GGTCCGCCCTGGCAGTGAIAAAAAAAAAAAAAA	2694

RESULT 2

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US-11-266-748A-76629
; Sequence 76629, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Patrick
; APPLICANT: Johnston, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76629
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-266-748A-76629

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Query Match 55.8%; Score 1474.2; DB 7; Length 1696;

Best Local Similarity 99.1%; Pred. No. 1.3e-255;

Matches 1504; Conservative 0; Mismatches 8;

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Qy	841	CAGCAGGCCAGGAGCTGCA	GAGGAGTCTCTCGGGGAGACAGAGCGGTTCTCTGAGCCAGGTG	900	
Db	88	CAGCAGAGCCAGGAGCTGCA	GAGGAGTCTCTCGGGGAGACAGAGCGGTTCTCTGAGCCAGGTG	147	
Qy	901	CTAGGCGGGGTGCTGAGCTG	TCCGCCACAGGCGAGGTGCA	CAGATGAAAGGCC	960
Db	148	CTAGGCGGGGTGCTGAGCTG	TCCGCCACAGGCGAGGTGCA	CAGATGAAAGGCC	207
Qy	961	GTGTACTGTCGCCCTGAAC	CCAGTGCAGCGGTGAGCA	CCACGCAAGAGTGCCTCATTTGCCGAG	1020

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Qy 2096 TGCTGACGATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGGAGGCGGCTGGATG 2155
Db 1348 TGCTGACGATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGGAGGCGGCTGGATG 1407
Qy 2156 ATGAGAGGAGGCGGAGCTGCTCCCTCCGAGGTGCTCATGCCAGGCGCATCCACACCA 2215
Db 1408 ATGAGAGGAGGCGGAGCTGCTCCCTCCGAGGTGCTCATGCCAGGCGCATCCACACCA 1467
Qy 2216 TCGAGTTCTGCTGGGCTGGCTTCCAAACCCGCTCTCTACCTGCGGCTGTGGGCCCTGA 2275
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Qy 2276 GCTGCGCCACGCGCCAG 2292
Db 1528 GCTGCGCCACGCGCCG 1544

RESULT 4

US-11-266-748A-129440/c
; Sequence 129440, Application US/11266748A
; Publication No. US20060134663A1

GENERAL INFORMATION:

; APPLICANT: Harkin, Paul
; APPLICANT: Mulligan, Patrick
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A

; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482.6

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105483.4

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485.9

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105484.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: US 60/662,276

; PRIOR FILING DATE: 2005-03-14

; PRIOR APPLICATION NUMBER: US 60/700,293

; PRIOR FILING DATE: 2005-07-18

; NUMBER OF SEQ ID NOS: 483996

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 129440

; LENGTH: 1696

; TYPE: DNA

; ORGANISM: Homo Sapiens

US-11-266-748A-129440

Query Match 55.8%; Score 1474.2; DB 7; Length 1696;

Best Local Similarity 99.1%; Pred. No. 1.3e-255;

Matches 1504; Conservative 0; Mismatches 8; Indels 5; Gaps 2;

Qy 781 CAGCTTCCCGTTCTGACGAGGAGGAGGCGCGCTCGGGGCGCTGACGAGCTGCAC 840
Db 1669 CAGCTTCCCGTTCTGACGAGGAGGAGGCGCGCTCGGGGCGCTGACGAGCTGCAC 1610
Qy 841 CAGCAGGCGGAGCTGACGAGGAGGCTCCGCGGAGACAGAGCGGTCTTCGACGAGGTG 900
Db 1609 CAGCAGGCGGAGGCTGACGAGGAGGCTCCGCGGAGACAGAGCGGTCTTCGACGAGGTG 1550
Qy 901 CTAGGCGGCGGTGCTGAGCTGTGCTCCGCGGAGGAGGCTGACGAGTGAAGGCC 960
Db 1549 CTAGGCGGCGGTGCTGAGCTGTGCTCCGCGGAGGAGGCTGACGAGTGAAGGCC 1490
Qy 961 GTGTACTGCGCCCTGAACCGAGTGCAGGTGAGCACCACGCAAGTGCTCATTTGCCGAG 1020

Db 1489 GTGTACTGCGCCCTGAACCAAGTGCAGCTGAGCACCAAGTGCCTCATTTGCCGAG 1430
Qy 1021 GCCTGGTGTCTGTGCGAGACCTGCCCGCTGCGAGAGGCGCTGCGGAGCAGCTCGATG 1080
Db 1429 GCCTGGTGTCTGTGCGAGACCTGCCCGCTGCGAGAGGCGCTGCGGAGCAGCTCGATG 1370
Qy 1081 GAGGAGGAGTGTAGTGTCCGCTGCTACCCGATCCCTGCGGGGACATGCCCCCACAATC 1140
Db 1369 GAGGAGGAGTGTAGTGTCCGCTGCTACCCGATCCCTGCGGGGACATGCCCCCACAATC 1310
Qy 1141 ATCGGACCAACCGCTTCAAGGCGGCTTCCAGGCGATCGTGTGATCGTGTGCTGCTG 1200
Db 1309 ATCGGACCAACCGCTTCAAGGCGGCTTCCAGGCGATCGTGTGATCGTGTGCTGCTG 1250
Qy 1201 CGCTACCGAGAGGTCAACCCCGCTCCCTACACCATCATCACCTTCCCTTCTGCTGCT 1260
Db 1249 CGCTACCGAGAGGTCAACCCCGCTCCCTACACCATCATCACCTTCCCTTCTGCTGCT 1190
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Db 1189 GTGATGTTGCGGAGTGTGGGCCACGCGCTGCTCATGTTCTTCTGCGCCCTGGCCATGCT 1130
Qy 1321 CTTGCGGAGAACCGACCGGCTGTGAAGGCGCGCAGAACGAGATCTGGCAGACTTCTTC 1380
Db 1129 CTTGCGGAGAACCGACCGGCTGTGAAGGCGCGCAGAACGAGATCTGGCAGACTTCTTC 1070
Qy 1381 AGGGGCGCTTACCTGCTTCTGCTTATGGGCTGTCTTCTCATCTACACCGGCTTCTCATC 1440
Db 1069 AGGGGCGCTTACCTGCTTCTGCTTATGGGCTGTCTTCTCATCTACACCGGCTTCTCATC 1010
Qy 1441 AACGAGTGTTCAGTGTGCGGCCACAGCATCTTCCCTCGGGCTGGAGTGTGGCGCCATG 1500
Db 1009 AACGAGTGTTCAGTGTGCGGCCACAGCATCTTCCCTCGGGCTGGAGTGTGGCGCCATG 950
Qy 1501 GCCAACGAGTCTGCGTGGAGTGTGATTCCTGGGCCAGCACAGATGCTTACCTGAT 1560
Db 949 GCCAACGAGTCTGCGTGGAGTGTGATTCCTGGGCCAGCACAGATGCTTACCTGAT 890
Qy 1561 CCCAAGCTCACCGGTGTCTTCTGCGGACCTACCCCTTTGGCATCGATCTTATTTGAGC 1620
Db 889 CCCAAGCTCACCGGTGTCTTCTGCGGACCTACCCCTTTGGCATCGATCTTATTTGAGC 830
Qy 1621 CTGGCTGCCAACCACTTGAGCTTCTCAACTCTTCAAGATGAAGATGCTCGTCACTG 1680
Db 829 CTGGCTGCCAACCACTTGAGCTTCTCAACTCTTCAAGATGAAGATGCTCGTCACTG 770
Qy 1681 GCGGTGTCGACATGCGCTTTTGGGGTGGGTCTCGAGTCTTCAACCAAGTGCACCTTG 1738
Db 769 GCGGTGTCGACATGCGCTTTTGGGGTGGGTCTCGAGTCTTCAACCAAGTGCACCTTG 710
Qy 1739 GCCAGAGGACCGGCTGCTGCGAGACGCTGCGGAGCTCACCTTCTGCTGGGACTCT 1798
Db 709 GCCAGAGGACCGGCTGCTGCGAGACGCTGCGGAGCTCACCTTCTGCTGGGACTCT 650
Qy 1799 TCGGTTACCTGCTGCTTCTAGTCACTTCAAGTGGTGTGTGTGCTGGGCTGCGAGGCG 1858
Db 649 TCGGTTACCTGCTGCTTCTAGTCACTTCAAGTGGTGTGTGTGCTGGGCTGCGAGGCG 590
Qy 1859 CTTGCG---CCCAGCATCTTCACTTCAACATGTTCTTCTTCTCCACAGCCCCA 1915
Db 589 CTTGCGCCCCCAGCATCTTCACTTCAACATGTTCTTCTTCTCCACAGCCCCA 530
Qy 1916 GCAACAGGTGTCTTACCCCGGAGGAGTGTGTCAGGCGAGCTGCTGCTGCTGCTGCTG 1975
Db 529 GCAACAGGTGTCTTACCCCGGAGGAGTGTGTCAGGCGAGCTGCTGCTGCTGCTGCTG 470
Qy 1976 TGGCCATGTGCGCATCTTCTGCTGTCGCAACCCCTGCACTGCTGCTGCAACCGCC 2035
Db 469 TGGCCATGTGCGCATCTTCTGCTGTCGTCAGCAGCCCCCTGCACTGATGCAACCGCC 410
Qy 2036 GCGGCTGCGGAGGAGGCGGCTGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2095

Db 409 GCCGCTCGGAGGAGGCCGCTGACCGACAGAGGAAAAAAGGCGGGTGTGCGACC 350
QY 2096 TGCCTGACGCATCTGTAATGGCTGGAGCTCCGATGAGGAAAGGAGGGGCGCTGGATG 2155
Db 349 TGCCTGACGCATCTGTAATGGCTGGAGCTCCGATGAGGAAAGGAGGGGCGCTGGATG 290
QY 2156 ATGAAGAGGAGGCGGAGCTCGTCCCTCCGAGGTGCTCATGACACAGGCCATCCACACCA 2215
Db 289 ATGAAGAGGAGGCGGAGCTCGTCCCTCCGAGGTGCTCATGACACAGGCCATCCACACCA 230
QY 2216 TCGAGTTCCTGGGCTGGCTCTCCAAACACCGCTCTTACCTGCGCCCTGTGGGCCCTGA 2275
Db 229 TCGAGTTCCTGGGCTGGCTCTCCAAACACCGCTCTTACCTGCGCCCTGTGGGCCCTGA 170
QY 2276 GCCTGGCCCAAGCCGAG 2292
Db 169 GCCTGGCCCAAGCCGAG 153

RESULT 5

US-11-266-748A-361154
; Sequence 361154, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 361154
; LENGTH: 1839
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1709)..(1709)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1799)..(1799)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1803)..(1803)
; OTHER INFORMATION: n is a, c, g, or t

US-11-266-748A-361154

Query Match 41.4%; Score 1093.2; DB 7; Length 1839;
Best Local Similarity 98.6%; Pred. No. 2.9e-187;
Matches 1157; Conservative 8; Mismatches 9; Gaps 5;
QY 781 CACGTCTTCCCGTTTCTGACGAGGAGGCGCCGCTCGGGGCGCTGACAGCAGCTGCAA 840

Db 28 CACGTCTTCCCGTTTCTGACGAGGAGGCGCCGCTCGGGGCGCTGACAGCAGCTGCAA 87
QY 841 CACGAGAGCCAGAGAGCTGACAGAGTCTCTCGGGGAGACAGAGCGTCTCTGAGCCAGGTG 900
Db 88 CACGAGAGCCAGAGAGCTGACAGAGTCTCTCGGGGAGACAGAGCGTCTCTGAGCCAGGTG 147
QY 901 CTAGGCGGGTCTGCTGAGTCTGCTGCGGAGGAGGAGGTCAGGTCCACAAGATGAAGGCC 960
Db 148 CTAGGCGGGTCTGCTGAGTCTGCTGCGGAGGAGGAGGTCAGGTCCACAAGATGAAGGCC 207
QY 961 GTGTACTTGGCCCTGAACCAAGTGCAGGTGAGCACCAAGTGCCTCTCAATTGCGGAG 1020
Db 208 GTGTACTTGGCCCTGAACCAAGTGCAGGTGAGCACCAAGTGCCTCTCAATTGCGGAG 267
QY 1021 GCCTGGTCTCTGTGCGAGACCTGCGCCCTCTGAGGAGGCGCTCGGGAGCAGTCCGATG 1080
Db 268 GCCTGGTCTCTGTGCGAGACCTGCGCCCTCTGAGGAGGCGCTCGGGAGCAGTCCGATG 327
QY 1081 GAGGAGGAGTGAAGTCCGCTGAGTCAACCGCATCCCTGCGGGAGCATGCCCCCACACTC 1140
Db 328 GAGGAGGAGTGAAGTCCGCTGAGTCAACCGCATCCCTGCGGGAGCATGCCCCCACACTC 387
QY 1141 ATCCGACCAACCGCTTCAAGGCGAGCTTCCAGGCGCATCGTGGATCGCTACGCGGTGGC 1200
Db 388 ATCCGACCAACCGCTTCAAGGCGAGCTTCCAGGCGCATCGTGGATCGCTACGCGGTGGC 447
QY 1201 CGCTACGAGGAGTCAACCGCTCTCTACACCATCATCATCTCCCTTCTCTGTTGCT 1260
Db 448 CGCTACGAGGAGTCAACCGCTCTCTACACCATCATCATCTCCCTTCTCTGTTGCT 507
QY 1261 GTGATGTTTC-GGGGATGTGGGCGACGCGCTGCTCATGTCTCTTTCGCGCTGGCCATGCT 1319
Db 508 GTGATGTTTCGGGGGATGTGGGCGACGCGCTGCTCATGTCTCTTTCGCGCTGGCCATGCT 567
QY 1320 CCTTCGGAGAAACCGAGCGGCTGTGAAGCGCGGAGAACGAGATCTGGCAGACTTCTT 1379
Db 568 CCTTCGGAGAAACCGAGCGGCTGTGAAGCGCGGAGAACGAGATCTGGCAGACTTCTT 627
QY 1380 CAGGGGCGCTTACCTGCTCTGCTTATGGGCGCTGTCTTCCATCTACACGGCTTCACTA 1439
Db 628 CAGGGGCGCTTACCTGCTCTGCTTATGGGCGCTGTCTTCCATCTACACGGCTTCACTA 687
QY 1440 CAAAGAGTCTTCAAGTTCGGGCGACAGCATCTTCCCTTCGGGCTGGAGTGTGGCGGCC 1497
Db 688 CAAAGAGTCTTCAAGTTCGGGCGACAGCATCTTCCCTTCGGGCTGGAGTGTGGCGGCC 747
QY 1498 ATGGCCAAACAGTCTGCGTGGAGTGAATGATTCCTTCGGGCGACACAGATGCTTACCCCTG 1557
Db 748 ATGGCCAAACAGTCTGCGTGGAGTGAATGATTCCTTCGGGCGACACAGATGCTTACCCCTG 807
QY 1558 GATCCAAAGTCAACGGTGTCTTCTGGGAGCCCTACCCCTTTGGGATCGATCTATTTGG 1617
Db 808 GATCCAAAGTCAACGGTGTCTTCTGGGAGCCCTACCCCTTTGGGATCGATCTATTTGG 867
QY 1618 AGCTGGGCTGCCAACCACTTGAAGTCTCTCAACTCTTCAAGATGAAGATGTCGCTCATC 1677
Db 868 AGCTGGGCTGCCAACCACTTGAAGTCTCTCAACTCTTCAAGATGAAGATGTCGCTCATC 927
QY 1678 CTGGGCGTGTGACATGCGCTTT--GGGTGGTCTCTGGAGTCTTCAACCAAGTGCATC 1735
Db 928 CTGGGCGTGTGACATGCGCTTTTGGGGTGGGTCTCTGGAGTCTTCAACCAAGTGCATC 987
QY 1736 TTGGCCAGAGGACCGGCTGTCTGGAGAGCGCTCGGAGGCTACCTTCTCTGCTGGGAC 1795
Db 988 TTGGCCAGAGGACCGGCTGTCTGGAGAGCGCTCGGAGGCTACCTTCTCTGCTGGGAC 1047
QY 1796 TC-TTCGGTTACCTCGTGTCTTCTAGTCACTACAAAGTGGCTGTGTGTCTGGGCTGCCAG 1854
Db 1048 TCTTTTCGGTTACCTCGTGTCTTCTAGTCACTACAAAGTGGCTGTGTGTCTGGGCTGCCAG 1107
QY 1855 GCGCGCTCG---CCAGCATCTCATCCACTTTCATCAACATGTTCTCTTCTTCCACAGC 1911

Db 1108 GCGCCCTCGGCCCCAGCATCTCATCCACTTCATCAACATGTTCTCTCTCCACAGC 1167

Qy 1912 CCCAGCAACAGGCTGCTCTACCCCGCGGAGG 1945
|||||

Db 1168 CCCAGCAACAGGCTGCTCTACCCCGCGAGTGG 1201

RESULT 6

US-11-266-748A-444533/c
; Sequence 444533, Application US/11266748A
; Publication No. US20060134663A1

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: GENERAL INFORMATION: Paul
: APPLICANT: Harkin, Paul
: APPLICANT: Johnston, Patrick
: APPLICANT: Mulligan, Karl
: TITLE OF INVENTION: Transcendence Microarray Technology and
: TITLE OF INVENTION: Methods of Using the Same
: FILE REFERENCES: 55815-0102 (319189)
: CURRENT APPLICATION NUMBER: US/11/2666,749A
:

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Query Match	41.4%;	Score 1093.2;	DB 7;	Length 1839;
Best Local Similarity	98.6%;	Pred. No. 2.9e-187;		
Matches 1157;	Conservative	0;	Mismatches 8;	Indels 9;
				Gaps 5;

QY	841	1752	900
Db	CAGCAGAGCCAGGAGCTGCAGGAGGTCTCGGGGAGACAGCGGTTCTGAGCCAGGTG	CAGCAGAGCCAGGAGCTGCAGGAGGTCTCGGGGAGACAGCGGTTCTGAGCCAGGTG	CAGCAGAGCCAGGAGCTGCAGGAGGTCTCGGGGAGACAGCGGTTCTGAGCCAGGTG

Qy	901	1692	Db	1633
	CTAGGCGGGTCTGCAGCTGCTGCCGCGCAGGCAGGTGCAGGTCCAAGATGAGGCC	CTAGGCGGGTCTGCAGCTGCTGCCGCGCAGGCAGGTGCAGGTCCAAGATGAGGCC	CTAGGCGGGTCTGCAGCTGCTGCCGCGCAGGCAGGTGCAGGTCCAAGATGAGGCC	CTAGGCGGGTCTGCAGCTGCTGCCGCGCAGGCAGGTGCAGGTCCAAGATGAGGCC

QY 961 GTGTACCTGGCCCTGAACCACTGCAGCGTGAGCACCAAGTGCCCTCATTTGCCGAG 1020

RESULT 7

US-11-266-748A-221798
; Sequence 221798, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:

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; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 221798
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-221798
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Query Match 36.9%; Score 973.2; DB 7; Length 1000;
Best Local Similarity 99.4%; Pred. No. 8.5e-166;
Matches 988; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
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QY 1650 CTCCTTCAAGATGAAGATGTCGTATCTCTGGCGTGTGACATGGCCCTTTGGGGTGT 1709
DB 1 CTCCTTCAAGATGAAGATGTCGTATCTCTGGCGTGTGACATGGCCCTTTGGGGTGT 60
QY 1710 CTCGGAGTCTTCAACACAGTGCATCTTGGCCAGAGGACCCGGCTGCTCGAGACGT 1769
DB 61 CTCGGAGTCTTCAACACAGTGCATCTTGGCCAGAGGACCCGGCTGCTCGAGACGT 120
QY 1770 GCCGAGCTCACTTCTGCTGGGACTCTTCGGTTACCTCGTTCCTAGTCTATCTACAA 1829
DB 121 GCCGAGCTCACTTCTGCTGGGACTCTTCGGTTACCTCGTTCCTAGTCTATCTACAA 180
QY 1830 GTGGCTGTGTCTGGGCTGCAGGGCCGCTCG---CCGAGCTCTCATCCACTTCAT 1886
DB 181 GTGGCTGTGTCTGGGCTGCAGGGCCGCTCGGGCCGAGCATCTCATCTTCAT 240
QY 1887 CAACATGTCTCTTCTCCACAGCCCCAGCAAGGCTGCTTACCCCCGCGAGAGGT 1946
DB 241 CAACATGTCTCTTCTCCACAGCCCCAGCAAGGCTGCTTACCCCCGCGAGAGGT 300
QY 1947 GGTCCAGGCGAGCTGTGGTCTTGGCTTGGCCATGGTCCCATCTCTGCTTGGC 2006
DB 301 GGTCCAGGCGAGCTGTGGTCTTGGCTTGGCCATGGTCCCATCTCTGCTTGGC 360
QY 2007 ACCCTGCACTGCTGCACCGCACCGCCGCGCTTGGGAGGCGCGCTGACCGACA 2066
DB 361 ACCCTGCACTGCTGCACCGCACCGCCGCGCTTGGGAGGCGCGCTGACCGACA 420
QY 2067 GGAGGAAACAAAGCGCGGTGCTGGAACCTGCTGACGCATCTGTGAATGGCTGAGCTC 2126
DB 421 GGAGGAAACAAAGCGCGGTGCTGGAACCTGCTGACGCATCTGTGAATGGCTGAGCTC 480
QY 2127 CGATGAGGAAAGGCGGGGCTGGATGATGAGGAGGCGGAGCTGCTCCCTCCGA 2186
DB 481 CGATGAGGAAAGGCGGGGCTGGATGATGAGGAGGCGGAGCTGCTCCCTCCGA 540
QY 2187 GGTGCTCATGCAACGAGGCGATCCACACCATCGAGTTCTTCCCTGGGCTGCTCACAACAC 2246
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RESULT 8
US-11-266-748A-287153
; Sequence 287153, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 287153
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-287153
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Query Match 36.9%; Score 973.2; DB 7; Length 1000;
Best Local Similarity 99.4%; Pred. No. 8.5e-166;
Matches 988; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
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QY 1650 CTCCTTCAAGATGAAGATGTCCTCATCTGGGCGTGTGCAATGGCTTTGGGGTGGT 1709
Db 1 CTCCTTCAAGATGAAGATGTCCTCATCTGGGCGTGTGCAATGGCTTTGGGGTGGT 60
QY 1710 CCTCGAGTCTTCAACACGTGCACTTTGGCCAGAGGACCGGCTGTCTGGAGAGCGT 1769
Db 61 CCTCGAGTCTTCAACACGTGCACTTTGGCCAGAGGACCGGCTGTCTGGAGAGCGT 120
QY 1770 GCGGAGCTCACTCTCTGCTGGGACTTCTGGGTACTCTGTTCTAGTCACTACAA 1829
Db 121 GCGGAGCTCACTCTCTGCTGGGACTTCTGGGTACTCTGTTCTAGTCACTACAA 180
QY 1830 GTGGCTGTGTCTGGGCTGCCAGGCGGCTCG---CCAGCATCTCATCACTTCAT 1886
Db 181 GTGGCTGTGTCTGGGCTGCCAGGCGGCTCGGGCCCCCAGCATCTCATCACTTCAT 240
QY 1887 CAACATGTTCTCTTCTCCACAGCCCCAGCAACAGGCTGTCTACCCCCCGGAGGAGT 1946
Db 241 CAACATGTTCTCTTCTCCACAGCCCCAGCAACAGGCTGTCTACCCCCCGGAGGAGT 300
QY 1947 GTTCCAGGCAACGCTGTGTCTTGGCTTGGCCATGTTGCCATCTCTGTCTTGGCAC 2006
Db 301 GTTCCAGGCAACGCTGTGTCTTGGCTTGGCCATGTTGCCATCTCTGTCTTGGCAC 360
QY 2007 ACCCTGCACTGTGCAACGCCACCGCGCGGCTGTGGAGAGGCGGCTGACCAACA 2066
Db 361 ACCCTGCACTGTGCAACGCCACCGCGCGGCTGTGGAGAGGCGGCTGACCAACA 420
QY 2067 GGAGGAAAAAAGGCGGGTGTCTGGACCTGCGCTGAGCATCTGTGAATGGCTGGAGCTC 2126
Db 421 GGAGGAAAAAAGGCGGGTGTCTGGACCTGCGCTGAGCATCTGTGAATGGCTGGAGCTC 480
QY 2127 CGATGAGAAAAAGGCGGGCTTGGATGATGAAGAGAGGCGGAGCTGCTCCCTCCGA 2186
Db 481 CGATGAGAAAAAGGCGGGCTTGGATGATGAAGAGAGGCGGAGCTGCTCCCTCCGA 540
QY 2187 GTGTCTCATGCACACGAGCCATCCACACATCGAGTTCGTCTGGGCTGGCTTCCCAAC 2246
Db 541 GTGTCTCATGCACACGAGCCATCCACACATCGAGTTCGTCTGGGCTGGCTTCCCAAC 600
QY 2247 CGCTCTCTACTGCGGCTGTGGGCGCTGAGCTGGCGCCACCGCCAGCTGCCAGGTTCT 2306
Db 601 CGCTCTCTACTGCGGCTGTGGGCGCTGAGCTGGCGCCACCGCCAGCTGCCAGGTTCT 660
QY 2307 GTGGGCCATCGTATGCGCATAGGCTTGGGCTGGGCGGAGAGTGGGCGGCTGT 2366
Db 661 GTGGGCCATCGTATGCGCATAGGCTTGGGCTGGGCGGAGAGTGGGCGGCTGT 720
QY 2367 GTGTCTGGTCCCATCTTTGCGGCTTTGCGGTGATGACCGTGGCTATCTCTGTGTGAT 2426
Db 721 GTGTCTGGTCCCATCTTTGCGGCTTTGCGGTGATGACCGTGGCTATCTCTGTGTGAT 780
QY 2427 GGAGGAGTCTTACGCTTCTGACAGCCCTGCGGCTGSCATGGGTGGAATTCAGAACAA 2486
Db 781 GGAGGAGTCTTACGCTTCTGACAGCCCTGCGGCTGSCATGGGTGGAATTCAGAACAA 840
QY 2487 GTTCTACTCAGGCAACGCGCTTACAGCTGAGTCCCTTCACTTGGCTGCCACAGATGACTA 2546
Db 841 GTTCTACTCAGGCAACGCGCTTACAGCTGAGTCCCTTCACTTGGCTGCCACAGATGACTA 900
QY 2547 GGGCCCACTGAGGCTCTGCAACCTCTTCTGAGCTTGTAGGCGAGGAGAGGATATAA 2606
Db 901 GGGCCCACTGAGGCTCTGCAACCTCTTCTGAGCTTGTAGGCGAGGAGAGGATATAA 960
QY 2607 GACGGTCCGCTGGCAAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
Db 961 GACGGTCCGCTGGCAAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 994

RESULT 9

US-11-266-748A-338582/c

; Sequence 338582, Application US/11266748A

; Publication No. US2006013463A1

GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 338582
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-338582

Query Match 36.9%; Score 973.2; DB 7; Length 1000;

Best Local Similarity 99.4%; Pred. No. 8 Se-166;

Matches 988; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 1650 CTCCTTCAAGATGAAGATGTCCTCATCTGGGCGTGTGCAATGGCTTTGGGGTGGT 1709
Db 1000 CTCCTTCAAGATGAAGATGTCCTCATCTGGGCGTGTGCAATGGCTTTGGGGTGGT 941
QY 1710 CCTCGAGTCTTCAACACGTGCACTTTGGCCAGAGGACCGGCTGTCTGGAGAGCGT 1769
Db 940 CCTCGAGTCTTCAACACGTGCACTTTGGCCAGAGGACCGGCTGTCTGGAGAGCGT 881
QY 1770 GCGGAGCTCACCTTCTGCTGGGACTCTTTCGGTTACCTCGTGTCTAGTCACTACAA 1829
Db 880 GCGGAGCTCACCTTCTGCTGGGACTCTTTCGGTTACCTCGTGTCTAGTCACTACAA 821
QY 1830 GTGGCTGTGTCTGGGCTGCCAGGCGGCTCG---CCAGCATCTCATCACTTCAT 1886
Db 820 GTGGCTGTGTCTGGGCTGCCAGGCGGCTCGGGCCCCCAGCATCTCATCACTTCAT 761
QY 1887 CAACATGTTCTCTTCTCCACAGCCCCAGCAACAGGCTGTCTACCCCCCGGAGGAGT 1946
Db 760 CAACATGTTCTCTTCTCCACAGCCCCAGCAACAGGCTGTCTACCCCCCGGAGGAGT 701
QY 1947 GTTCCAGGCAACGCTGTGTCTTGGCCATGTTGCCATCTCTGTCTTGGCAC 2006
Db 700 GTTCCAGGCAACGCTGTGTCTTGGCCATGTTGCCATCTCTGTCTTGGCAC 641
QY 2007 ACCCTGCACTGTGCAACCGCCAGCGGCTGCGGAGGAGGCGGCTGACCGACA 2066
Db 640 ACCCTGCACTGTGCAACCGCCAGCGGCTGCGGAGGAGGCGGCTGACCGACA 581
QY 2067 GGAGGAAAAAAGGCGGGTGTGTCGACTGTGAGCATCTGTGAATGGCTGGAGCTC 2126
Db 580 GGAGGAAAAAAGGCGGGTGTGTCGACTGTGAGCATCTGTGAATGGCTGGAGCTC 521
QY 2127 CGATGAGAAAAAGGCGGGGCTTGGATGATGAAGAGGAGGCGGAGCTGCTCCCTCCGA 2186
Db 520 CGATGAGAAAAAGGCGGGGCTTGGATGATGAAGAGGAGGCGGAGCTGCTCCCTCCGA 461


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; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnstone, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 468814
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-468814

Query Match      36.9%; Score 973.2; DB 7; Length 1000;
Best Local Similarity 99.4%; Pred. No. 8.5e-166;
Matches 988; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy 1650 CTCCTTCAAGATGAAGATGTCCTGTCATCTGCGGCGTCGTCACATGCGCCCTTTGGGGTGGT 1709
Db 1000 CTCCTTCAAGATGAAGATGTCCTGTCATCTGCGGCGTCGTCACATGCGCCCTTTGGGGTGGT 941

Qy 1710 CCTCGGAGTCTTCAACACAGTGCATCTTGGCCAGAGGACGCGCTGCTGGAGAGCT 1769
Db 940 CCTCGGAGTCTTCAACACAGTGCATCTTGGCCAGAGGACGCGCTGCTGGAGAGCT 881

Qy 1770 GCCGGAGCTCACCTTCTGCTGGGACTCTTTCGGTTACTCTGCTGCTTCTAGTCTATCTACAA 1829
Db 880 GCCGGAGCTCACCTTCTGCTGGGACTCTTTCGGTTACTCTGCTGCTTCTAGTCTATCTACAA 821

Qy 1830 GTGGCTGTGTCTGGGCTGCCAGGGCGGCTCG---CCAGCATCTCTCATCCACTTTCAT 1886
Db 820 GTGGCTGTGTCTGGGCTGCCAGGGCGGCTCGGGCCCGCAGCATCTCTCATCCACTTTCAT 761

Qy 1887 CAACATGTTCTCTTCTCCACAGCCCCCAGCATGCTCTACCCCGGAGAGGT 1946
Db 760 CAACATGTTCTCTTCTCCACAGCCCCCAGCATGCTCTACCCCGGAGAGGT 701

Qy 1947 GGTCCAGGCCACGCTGTGTGTCTTGGGCTTGGCCATGCTGCCATCTGCTGCTTGGCAC 2006
Db 700 GGTCCAGGCCACGCTGTGTGTCTTGGGCTTGGCCATGCTGCCATCTGCTGCTTGGCAC 641

Qy 2007 ACCCTCTGCACCTGTGTCACCCGACCGCCGCTGCGGAGGAGGCGCCGCTGACCGACA 2066
Db 640 ACCCTCTGCACCTGTGTCACCCGACCGCCGCTGCGGAGGAGGCGCCGCTGACCGACA 581

Qy 2067 GGAGGAAAAAAGCCCGGGTGTGTGACCTGCTGACGATCTGTGAATGGCTGGAGCTC 2126
Db 580 GGAGGAAAAAAGCCCGGGTGTGTGACCTGCTGACGATCTGTGAATGGCTGGAGCTC 521

Qy 2127 CGATGAGGAAAAAGCCCGGGTGTGTGATGATGATGAGGAGGCGGAGCTGCTCCCTCCGA 2186
Db 520 CGATGAGGAAAAAGCCCGGGTGTGTGATGATGATGAGGAGGCGGAGCTGCTCCCTCCGA 461
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RESULT 12
US-11-266-748A-76628
; Sequence 76628, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnstone, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76628
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45)..(45)
; OTHER INFORMATION: n is a, c, g, or t
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US-11-266-748A-76628

Query Match 26.8%; Score 707; DB 7; Length 738;
Best Local Similarity 99.0%; Pred. No. 4.5e-118;
Matches 721; Conservative 0; Mismatches 6; Indels

Result No.	Query			Description	
	Score	Match	Length	ID	Description
1	2640	100.0	2640	10	US-10-783-519-1
2	2640	100.0	2655	3	US-09-962-436-278
3	2640	100.0	2655	3	US-09-880-107-3363
4	2640	100.0	2655	3	US-09-968-070-2192
5	2640	100.0	2655	7	US-10-305-720-1014
6	2640	100.0	2655	8	US-10-641-643-916
7	2640	100.0	2655	10	US-10-843-641A-2737
8	2640	100.0	2655	10	US-10-843-641A-6682
9	2640	100.0	2655	16	US-11-122-329-72
10	2068	78.3	2488	7	US-10-145-012-1
11	2068	78.3	2488	13	US-11-126-866-1
12	2068	78.3	2488	15	US-11-126-841A-1
13	2066.4	78.3	2488	7	US-10-145-012-12
14	2066.4	78.3	2488	13	US-11-126-866-12
15	2066.4	78.3	2488	15	US-11-126-841A-12
16	1989.4	75.4	3104	7	US-10-264-049-481
17	742.8	28.1	2937	10	US-10-764-420-2037

181 GCCTGGTGAGCGCTTCAGAGAGCGCTTTGTGTGATGTTTGGCGCTGTGAGAGCTG 240
241 GAGAGACCTTCACTTCTCTGAGAGAGAGGTGCGGGCTGGGTGCTTGTCTGCCCCCG 300
241 GAGAGACCTTCACTTCTCTGAGAGAGAGGTGCGGGCTGGGTGCTTGTCTGCCCCCG 300
301 CAAAGGGAGGCTGCGGCAACCCACCCCGGAGCTGTGCGCATCCAGAGGAGAGCG 360
301 CAAAGGGAGGCTGCGGCAACCCACCCCGGAGCTGTGCGCATCCAGAGGAGAGCG 360
361 GAGCGCTTGGCCAGAGCTGCGGATGTGCGGGCAACCCAGAGCGCTTGGCGGCCAG 420
361 GAGCGCTTGGCCAGAGCTGCGGATGTGCGGGCAACCCAGAGCGCTTGGCGGCCAG 420
421 CTGACACAGCTGAGCTCAGCGCGCGCTGCTACGCGAGGCGCATGAACCTCAGCTGGCA 480
421 CTGACACAGCTGAGCTCAGCGCGCGCTGCTACGCGAGGCGCATGAACCTCAGCTGGCA 480
481 GCGGCCACACAGATGGGGCTCAGAGAGAGCGCCCTGTCTCCAGGCCCCCGGGGGCG 540
481 GCGGCCACACAGATGGGGCTCAGAGAGAGCGCCCTGTCTCCAGGCCCCCGGGGGCG 540
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1261 GTGATTTGGGAGTGGGCCACCGGCTGCTCATGTTCTCTTGCCTTGGCCATGGTC 1320
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1321 CTTGGGAGAACCGACCGCTGTGAAGCGCGGCAAGAGATCTGGCAGACTTCTTTC 1380
1381 AGGGGCGGTACCTGCTCTGCTTATGGGCTGTCTCATCTTACACCGGCTTCATCTAC 1440
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1441 AACAGTGTCTCAGTCGCGCCACAGCATTTTCCCCTCGGGCTGGAGTGTGCGGCCATG 1500
1441 AACAGTGTCTCAGTCGCGCCACAGCATTTTCCCCTCGGGCTGGAGTGTGCGGCCATG 1500
1501 GCAACACAGTCTGGCTGGAGTGTGATGATTCCTGGGCCAGCAACAGTGTACCTTGGAT 1560
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1561 CCAACAGTCTGGCTGGAGTGTGATGATTCCTGGGCCAGCAACAGTGTACCTTGGAT 1620
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1621 CTGGCTGCAACCACTTGGAGCTTCTCAACTCTTCAAGATGAAGATGTCGCTCATCTTC 1680
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1861 TCGCCAGGACTCTCATCCACTTCAATGATGTTCTTCTTCCACAGCGCCAGCAAC 1920
1861 TCGCCAGGACTCTCATCCACTTCAATGATGTTCTTCTTCCACAGCGCCAGCAAC 1920
1921 AGGCTGCTTACCCCGGAGAGGTGCTCAGGCGCAGCTGCTGCTGCTTGGCTTGGCC 1980
1921 AGGCTGCTTACCCCGGAGAGGTGCTCAGGCGCAGCTGCTGCTGCTTGGCTTGGCC 1980
1981 ATGGTGGCCATCTGCTGCTTGGCACAACCTTGCACCTGCTGCAACCGCCCGCGC 2040
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2041 CTTGGGAGGAGGCGCGCTGACCGAGAGGAGAAACAGGCGGGTGTGCTGGACCTGCT 2100
2041 CTTGGGAGGAGGCGCGCTGACCGAGAGGAGAAACAGGCGGGTGTGCTGGACCTGCT 2100
2101 GACGATCTGTGAATGGCTGAGCTCCGATGAGGAGAAAGCGAGGCGCTGATGATGA 2160
2101 GACGATCTGTGAATGGCTGAGCTCCGATGAGGAGAAAGCGAGGCGCTGATGATGA 2160
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1981 ATGGTCCCATCTGCTTGTGGACACACCTTGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
1981 ATGGTCCCATCTGCTTGTGGACACACCTTGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
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RESULT 3
US-09-880-107-3363
; Sequence 3363, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3363
; LENGTH: 2655
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U45285
US-09-880-107-3363

Query Match 100.0%; Score 2640; DB 3; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CGCGCTGCGGACGCGGACGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGGAGCGGCGG 60
QY 61 GGCTCCATGTTCCGGAGCGGAGGAGTGGCTTGGTCCAGCTCTTCTTCCAGCGGCT 120
DB 61 GGCTCCATGTTCCGGAGCGGAGGAGTGGCTTGGTCCAGCTCTTCTTCCAGCGGCT 120
QY 121 GCCTACACCTCGCTGAGTGGGCGGAGCTGGGCTCGTGGAGTTCCAGAGACCTCAAC 180
DB 121 GCCTACACCTCGCTGAGTGGGCGGAGCTGGGCTCGTGGAGTTCCAGAGACCTCAAC 180
QY 181 GCCTCGGTGAGCGCTTCCAGAGACGCTTGTGGTGTGATGTTTGGCGCTGTGAGGAGCTG 240
DB 181 GCCTCGGTGAGCGCTTCCAGAGACGCTTGTGGTGTGATGTTTGGCGCTGTGAGGAGCTG 240
QY 241 GAGAGACCTTCACTTCTTCCAGAGGAGTGGCGGCGGCTGGGCTGGCTTCTTCCGCGG 300
DB 241 GAGAGACCTTCACTTCTTCCAGAGGAGTGGCGGCGGCTGGGCTGGCTTCTTCCGCGG 300
QY 301 CCAAGGAGGAGGCTGCGGCGACCCACCCCGGAGCTGCTGCGCATCCAGAGGAGAGCG 360
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QY 361 GAGCGCTGGGCCAGAGCTGCGGATGTGCGGGGCAACCCAGAGGCGCTTGGGGGCCAG 420
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QY 421 CTGCAACGAGCTGAGCTCCAGCGCGCTGTCTACGCCAGGCGCATGAACTCAGCTGGCA 480
DB 421 CTGCAACGAGCTGAGCTCCAGCGCGCTGTCTACGCCAGGCGCATGAACTCAGCTGGCA 480
QY 481 GCGCGCCACACAGATGGGCGCTCAGAGGAGACGCGCTTCTTCCAGGCGCCCGGGGGCGG 540
DB 481 GCGCGCCACACAGATGGGCGCTCAGAGGAGACGCGCTTCTTCCAGGCGCCCGGGGGCGG 540
QY 541 CACAGGAGCTGAGGCTCACTTTGTGGCAGGTGGCGGAGCCCAAGGCGCTTCTTCC 600
DB 541 CACAGGAGCTGAGGCTCACTTTGTGGCAGGTGGCGGAGCCCAAGGCGCTTCTTCC 600

Qy	601	CTAGAGCGCCTGCTCTGAGAGCGCCTGCGCGGCTTCTCTCATTTGCCAGCTTCAGGAGCTG	660
Db	601		660
Qy	661	GAGCAGCGCTGAGGACACCCCGTGAACGGCGGAGCCAGCCACAGTGGATGACCTTCCTCATC	720
Db	661		720
Qy	721	TCCTACTGGGGTGAAGCAGATCGGACAGAAAGATCCGCAAGATCAACGGAATGCTTCCACTGC	780
Db	721		780
Qy	781	CACGCTTCCCGTTCTGACAGAGAGAGAGCGCGCTCGGGGCCCTGACAGCTGCAA	840
Db	781		840
Qy	841	CAGCAGAGCCAGGAGCTCGAGAGGTCTCGGGGAGACAGAGCGGTTCTGAGCCAGGTG	900
Db	841		900
Qy	901	CTAGGCGGGTGTGAGCTGCTGCGCCAGGGCAGGGTCCAAAGATGAAGGCC	960
Db	901		960
Qy	961	GTGTACTGGCCCTGAACCAAGTCAGGTGAGCACCGGCAAGTGGCTCATTTGCCGAG	1020
Db	961		1020
Qy	1021	GCTGTGTGCTCTGTGCGAGACCTGCGCCCTGACAGGAGCGCTCGGGGAGACAGTCCGATG	1080
Db	1021		1080
Qy	1081	GAGGAGGAGTGAAGTGGCTGCAACGATCCCTGCGGGGACATGCCCCCAGCATC	1140
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Qy	1141	ATCCGACCAACCGCTTCAAGGCGAGCTTCAGGGGATCGTGGATCGTACGGGTGGGC	1200
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Qy	1201	CGCTACAGGAGGTCAACCCCGCTCCCTACACCATCATCATCTTCCCTCTCTCTTTGCT	1260
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Qy	1261	GTGATGTTGGGGATGTGGGCCACCGGCTGCTCATGTTCTCTTCTTCTTGGCCATGCTC	1320
Db	1261		1320
Qy	1321	CTTGGGAGAACCGACCGGCTGTGAAGCCGCGCAGAACGAGATCTGGCAGACTTTCTTC	1380
Db	1321		1380
Qy	1381	AGGGGCGCTACCTGCTCTGCTTATGGGCTGTCTTCCATCTACACCGGCTTCATCTAC	1440
Db	1381		1440
Qy	1441	AACGAGTGTTCAGTTCGCGCCACAGCATCTTCCCTCGGGCTGAGTGTGGCCGCCATG	1500
Db	1441		1500
Qy	1501	GCCNACAGTCTGGCTGGATGATGATTCCTTGGCCGAGCAGCATGCTTACCTGGAT	1560
Db	1501		1560
Qy	1561	CCCAAGCTCACCGGTGTCTTCTGGGACCTTACCCCTTTGGCATCGATCTTATTTGGAGC	1620
Db	1561		1620
Qy	1621	CTGGCTGCCAACCACTTGAGCTTCTCAACTCTTCAAGATGAAGATGTCGCTCATCTG	1680
Db	1621		1680

Qy	1681	GGCGTCTGTGCATATGGCCCTTTGGGGTGTCTCTCGAGTCTTCAACCAAGTGCATTTGGC	1740
Db	1681		1740
Qy	1741	CAGAGGACCCGGCTGCTGTGAGACGCTGCGGAGCTCACCTTCTCTGCTGGGACTCTTC	1800
Db	1741		1800
Qy	1801	GGTTACCTCTGTCTTCTAGTCACTACAAAGTGGCTGTGTCTGGGCTCCAGGCGCCGC	1860
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Qy	1861	TCGCGCAGCATCTCATCCACTTCAACATGTCTCTTCTCCCAAGCCCCAGCAAC	1920
Db	1861		1920
Qy	1921	AGGCTGTCTTACCCCGGACGAGGTGTCCAGGCAACGCTGTGTCTCTGCTGGCTTGGCC	1980
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Qy	1981	ATGTGTGCCATCTCTGCTGTGGCACACCTCTGCACTGTCTGCAACGCGCCGCGC	2040
Db	1981		2040
Qy	2041	CTGCGGAGAGCGCCGCTGACCCAGCAGGAGGAAAACAAAGGCGGGTCTGTGACCTGCT	2100
Db	2041		2100
Qy	2101	GACGCATCTGTGAATGCTGGAGCTCCGATGAGGAAAAGGAGGGGCTCGATGATGAA	2160
Db	2101		2160
Qy	2161	GAGGAGCCGAGTCTGCTCCCTCCGAGGTGTCTATGCAACAGGCGCATCACACCATCGAG	2220
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Qy	2221	TTCTGCTGGGCTGCTCTCCAAACACCGCTCTTACTGCGGCTGTGGGCGCTGAGGCTG	2280
Db	2221		2280
Qy	2281	GCCCAACCCAGCTGTCGAGGTCTGTGGGCGCATGTGTGCGCATAGGCTGGGCGCTG	2340
Db	2281		2340
Qy	2341	GGCGGAGGTGGCGGT	2400
Db	2341		2400
Qy	2401	ATGACCGTGGCTATCTCTGCTGGTGTGATGGAGGACTCTCAGGCTTCTGCAAGGCTGCGG	2460
Db	2401		2460
Qy	2461	CTGCATGGGTGGAATTCAGAACAAAGTCTTACTCAGGCGGCTACAAAGTCAAGCTGAGTCCC	2520
Db	2461		2520
Qy	2521	TTCACTTCTGCTGCACAGATGACTAGGCGCCCACTGAGGTCCTTCCAGGCTCTCTTCT	2580
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Qy	2581	GACCTCTGAGGCGAGGAGGAAATAAGACGGTCCGCTCGCAAAAAAATAAAAAA	2640
Db	2581		2640

RESULT 4

US-09-968-007A-212
; Sequence 212, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
; TITLE OF INVENTION: Gene Sets

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/ FILE REFERENCE: 689290-71
/ CURRENT APPLICATION NUMBER: US/09/968,007A
/ CURRENT FILING DATE: 2001-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,172
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,173
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,278
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,294
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,295
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,316
/ PRIOR FILING DATE: 2000-10-02
/ NUMBER OF SEQ ID NOS: 1001
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 212
/ LENGTH: 2655
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-968-007A-212

Query Match      100.0%; Score 2640; DB 3; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CGCGCTGCGGAGCGGCGAGCCAGCAGCGGAGCGCGGCGGAGCACAACCCGGGGACCATG 60

QY 61 GCCTCACTGTCGGAGCGAGGAGTGCCCTGGTCCAGCTCTTTCTGCCCACAGGGCT 120
DB 61 GGTCTCATGTTCCGAGCGAGGAGTGCCCTGGTCCAGCTCTTTCTGCCCACAGGGCT 120

QY 121 GCCTACACCTGCTGAGTGGGCTGGCGAGCTGGGCTCTGTGAGTTCAGAGACCTCAAC 180
DB 121 GCCTACACCTGCTGAGTGGGCTGGCGAGCTGGGCTCTGTGAGTTCAGAGACCTCAAC 180

QY 181 GCCTGGTGAAGCCCTTCAGAGACGCTTTGTGTTGATGTTTGGCGCTGTGAGAGCTG 240
DB 181 GCCTGGTGAAGCCCTTCAGAGACGCTTTGTGTTGATGTTTGGCGCTGTGAGAGCTG 240

QY 241 GAGAGACCTTCACTTCTTCAGAGGAGGAGTGCGCGGCTGGGCTGGGCTGGTCTGCCCCG 300
DB 241 GAGAGACCTTCACTTCTTCAGAGGAGGAGTGCGCGGCTGGGCTGGGCTGGTCTGCCCCG 300

QY 301 CCAAGGGGAGGCTGCCGCAACCCCAACCCCGGACCTGCTGCGCATCCAGGAGAGAGCG 360
DB 301 CCAAGGGGAGGCTGCCGCAACCCCAACCCCGGACCTGCTGCGCATCCAGGAGAGAGCG 360

QY 361 GAGCGCTGGCCAGAGCTGGGATGTGCGGGGCAACAGAGGCGCTTGGCGGCCAG 420
DB 361 GAGCGCTGGCCAGAGCTGGGATGTGCGGGGCAACAGAGGCGCTTGGCGGCCAG 420

QY 421 CTGCAACAGCTGAGCTTCAACGCGCGCTGCTACGCGGCGGATGATGATGATGATGATG 480
DB 421 CTGCAACAGCTGAGCTTCAACGCGCGCTGCTACGCGGCGGATGATGATGATGATGATG 480

QY 481 GCGGCCACACAGATGGGCTTCAGAGAGAGCGCCCTGCTCCAGGCGCCCGGGGGCGG 540
DB 481 GCGGCCACACAGATGGGCTTCAGAGAGAGCGCCCTGCTCCAGGCGCCCGGGGGCGG 540

QY 541 CACAGGACCTGAGGCTCAACTTTGTGAGAGGCGCTGCGGAGGCGGAGGCGGCGGCGG 600
DB 541 CACAGGACCTGAGGCTCAACTTTGTGAGAGGCGCTGCGGAGGCGGAGGCGGCGGCGG 600

QY 601 CTAGAGCGCTGCTCTGAGAGGCGCTGCGGCGGCTCTCATTTGCGAGGCTTCAGGAGCTG 660
DB 601 CTAGAGCGCTGCTCTGAGAGGCGCTGCGGCGGCTCTCATTTGCGAGGCTTCAGGAGCTG 660

QY 661 GAGCAGCCGCTGAGGACCCCGGTGACGGGCGAGCCAGCCAGCTGGATGACCTTCTCTCATC 720
DB 661 GAGCAGCCGCTGAGGACCCCGGTGACGGGCGAGCCAGCCAGCTGGATGACCTTCTCTCATC 720
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Db 901 CTAGGCGGGTGTCTGAGCTGCTGCGCCAGGAGGTGAGTCCACAGATGAGGCC 960
QY 961 GTGTACTGCGCCCTGAACAGTGCAGGTGAGCAACAAGTGCCTCATTTGCGGAG 1020
Db 961 GTGTACTGCGCCCTGAACAGTGCAGGTGAGCAACAAGTGCCTCATTTGCGGAG 1020
QY 1021 GCTGTGTCTGTGCGAGACCTGCGCCCTGCGAGAGGCGCTGCGGAGACGCTCGATG 1080
Db 1021 GCTGTGTCTGTGCGAGACCTGCGCCCTGCGAGAGGCGCTGCGGAGACGCTCGATG 1080
QY 1081 GAGGAGGAGTGAAGTGCCTGAGTGCAGGATGCTGCGGAGACGCTCGATG 1140
Db 1081 GAGGAGGAGTGAAGTGCCTGAGTGCAGGATGCTGCGGAGACGCTCGATG 1140
QY 1141 ATCCGACCAACCGCTTCAAGGAGTGCAGGATGCTGCGGAGACGCTCGATG 1200
Db 1141 ATCCGACCAACCGCTTCAAGGAGTGCAGGATGCTGCGGAGACGCTCGATG 1200
QY 1201 CGCTACGAGAGTGAAGTGCCTGAGTGCAGGATGCTGCGGAGACGCTCGATG 1260
Db 1201 CGCTACGAGAGTGAAGTGCCTGAGTGCAGGATGCTGCGGAGACGCTCGATG 1260
QY 1261 GTGATGTTGGGATGTTGGGATGTTGGGATGTTGGGATGTTGGGATGTTGGG 1320
Db 1261 GTGATGTTGGGATGTTGGGATGTTGGGATGTTGGGATGTTGGGATGTTGGG 1320
QY 1321 CTTGGGAGAAACCGAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGT 1380
Db 1321 CTTGGGAGAAACCGAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGT 1380
QY 1381 AGGGGCGGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Db 1381 AGGGGCGGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 AACGAGTGTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1500
Db 1441 AACGAGTGTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1500
QY 1501 GCGAACGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1560
Db 1501 GCGAACGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1560
QY 1561 CCGAACGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1620
Db 1561 CCGAACGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1620
QY 1621 CTGGCTGCGCAACCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1680
Db 1621 CTGGCTGCGCAACCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1680
QY 1681 GGGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1740
Db 1681 GGGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1740
QY 1741 CAGAGGACCGGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1800
Db 1741 CAGAGGACCGGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1800
QY 1801 GGTACCTGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1860
Db 1801 GGTACCTGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1860
QY 1861 TGCGCCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Db 1861 TGCGCCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
QY 1921 AGGCTGCTTACCCCGGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1980
Db 1921 AGGCTGCTTACCCCGGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1980
QY 1981 ATGGTCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040

RESULT 6

US-10-641-643-916

; Sequence 916, Application US/10641643

; Publication No. US2004007003A1

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; Jeffrey J. Seilhamer

; Susan G. Stuart

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL

; GENE EXPRESSION

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESS: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/641,643

; FILING DATE: 14-Aug-2003

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: <Unknown>

; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 916:
SEQUENCE CHARACTERISTICS:
LENGTH: 2655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 91245045
SEQUENCE DESCRIPTION: SEQ ID NO: 916 :
US-10-641-643-916

Query Match 100.0%; Score 2640; DB 8; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCTGCGCGGACGCGGACGACGAGCGCGCGGCGGACGACACACCGGGGACCATG 60
DB 1 CGCGCTGCGCGGACGCGGACGACGAGCGCGGCGGCGGACGACACACCGGGGACCATG 60
QY 61 GGCTCCATGTTCCGAGCGAGGAGGTGGCCCTGGTCCAGTCTTTTGGCCACAGCGGCT 120
DB 61 GGCTCCATGTTCCGAGCGAGGAGGTGGCCCTGGTCCAGTCTTTTGGCCACAGCGGCT 120
QY 121 GCCTACACCTGCTGAGTGGCTGGGCGAGCTGGGCTCTGGAGTTACAGACCTCAAC 180
DB 121 GCCTACACCTGCTGAGTGGCTGGGCGAGCTGGGCTCTGGAGTTACAGACCTCAAC 180
QY 181 GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGTGTTGATGTTTGGCGCTGTGAGGAGCTG 240
DB 181 GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGTGTTGATGTTTGGCGCTGTGAGGAGCTG 240
QY 241 GAGAAGACCTTACCTTCTGAGAGGAGGAGGTGGCGGCGGTGGCTGTGCTGCCCGCG 300
DB 241 GAGAAGACCTTACCTTCTGAGAGGAGGAGGTGGCGGCGGTGGCTGTGCTGCCCGCG 300
QY 301 CCAAGGGAGGCTGCGGACCCCGGACCTGGGATGTGGGGGCAACAGAGGCGCTGGCGGCCAG 360
DB 301 CCAAGGGAGGCTGCGGACCCCGGACCTGGGATGTGGGGGCAACAGAGGCGCTGGCGGCCAG 360
QY 361 GAGCGCTGGCCAGAGGCTGCGGATGTGGGGGCAACAGAGGCGCTGGCGGCCAG 420
DB 361 GAGCGCTGGCCAGAGGCTGCGGATGTGGGGGCAACAGAGGCGCTGGCGGCCAG 420
QY 421 CTGCAACAGTGAGCTTCCAGCGCGCGTGTCTAGCGGAGGCGGATGAACCTCAGCTGGCA 480
DB 421 CTGCAACAGTGAGCTTCCAGCGCGCGTGTCTAGCGGAGGCGGATGAACCTCAGCTGGCA 480
QY 481 GCGGCCACACAGATGGGCGCTCAGAGAGACCGCCCTGTCTCAGGCGCCCGGGGGCGG 540
DB 481 GCGGCCACACAGATGGGCGCTCAGAGAGACCGCCCTGTCTCAGGCGCCCGGGGGCGG 540
QY 541 CACAGGACCTGAGGCTCAACTTTGTGGCAGGTGGCTGGAGCGCCCAAGGCGCCCTGGCC 600
DB 541 CACAGGACCTGAGGCTCAACTTTGTGGCAGGTGGCTGGAGCGCCCAAGGCGCCCTGGCC 600
QY 601 CTAGAGCGCTGCTGAGAGGCGCTGCGCGGCTTCTCATTTGCCAGCTTTCAGGAGCTG 660
DB 601 CTAGAGCGCTGCTGAGAGGCGCTGCGCGGCTTCTCATTTGCCAGCTTTCAGGAGCTG 660
QY 661 GAGCAGCGCTGAGACACCCCGTGAAGGCGGAGCGAGCGAGCTTCCATGCTTCATC 720
DB 661 GAGCAGCGCTGAGACACCCCGTGAAGGCGGAGCGAGCGAGCTTCCATGCTTCATC 720
QY 721 TCTACTGGGGTGCAGAGATCGGACAGAGATCCGAAAGATCAGGACTGTTCCACTGC 780
DB 721 TCTACTGGGGTGCAGAGATCGGACAGAGATCCGAAAGATCAGGACTGTTCCACTGC 780

DB 721 TCTACTGGGGTGCAGAGATCGGACAGAGATCCGAAAGATCAGGACTGTTCCACTGC 780
QY 781 CAGCTCTTCCGTTTTCGACAGAGAGAGGCGCGCTCGGGGCGCTTCGACAGCTGCA 840
DB 781 CAGCTCTTCCGTTTTCGACAGAGAGAGGCGCGCTCGGGGCGCTTCGACAGCTGCA 840
QY 841 CAGCAGAGCCAGAGCTGACAGGAGTCTCGGGGAGACAGAGCGGTTCTTGAGCAGGTG 900
DB 841 CAGCAGAGCCAGAGCTGACAGGAGTCTCGGGGAGACAGAGCGGTTCTTGAGCAGGTG 900
QY 901 CTAGGCGCGGTGCTGACAGTCTGCTCCGCCACAGGCGAGGTGCAGGTCCACAAGATGAAGGCC 960
DB 901 CTAGGCGCGGTGCTGACAGTCTGCTCCGCCACAGGCGAGGTGCAGGTCCACAAGATGAAGGCC 960
QY 961 GTGTACTGTCGCTGAAACAGAGTGCAGGTGAGACACACGACAGTGCCTCATTTGCCGAG 1020
DB 961 GTGTACTGTCGCTGAAACAGAGTGCAGGTGAGACACACGACAGTGCCTCATTTGCCGAG 1020
QY 1021 GCCTGGTGTCTGTCGAGACCTGCGCGCTCGAGGAGGCGCTTCGCGGACAGCTCGATG 1080
DB 1021 GCCTGGTGTCTGTCGAGACCTGCGCGCTTCGAGGAGGCGCTTCGCGGACAGCTCGATG 1080
QY 1081 GAGGAGGAGTGAAGTCCGCTGCTCACCGCATCCCTTCGCGGACATGCCCCCACAATC 1140
DB 1081 GAGGAGGAGTGAAGTCCGCTGCTCACCGCATCCCTTCGCGGACATGCCCCCACAATC 1140
QY 1141 ATCCGACCAACCGCTTACGCGGAGTTCGAGGCGATCTGATGCTTACGGCGTGGGC 1200
DB 1141 ATCCGACCAACCGCTTACGCGGAGTTCGAGGCGATCTGATGCTTACGGCGTGGGC 1200
QY 1201 CGCTACCGAGAGTCAACCGCTGCTCACCATCATCATCATCATCATCATCATCATCAT 1260
DB 1201 CGCTACCGAGAGTCAACCGCTGCTCACCATCATCATCATCATCATCATCATCATCAT 1260
QY 1261 GTGATGTTCCGGGATGTGGGCGACGCGCTCATGTTCTTCTTTCGCGCTGGCCATGCTC 1320
DB 1261 GTGATGTTCCGGGATGTGGGCGACGCGCTCATGTTCTTCTTTCGCGCTGGCCATGCTC 1320
QY 1321 CTTGCGGAGAACCGACCGGTGTAAAGCGCGGAGAACAGAGATCTGGCAGACTTTCTTC 1380
DB 1321 CTTGCGGAGAACCGACCGGTGTAAAGCGCGGAGAACAGAGATCTGGCAGACTTTCTTC 1380
QY 1381 AGGGGCGCTTACCTGCTCTGCTTATGGGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 1440
DB 1381 AGGGGCGCTTACCTGCTCTGCTTATGGGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 1440
QY 1441 AACGAGTGTCTTCAAGTGGCGCACAGCATCTTCCCTTCGCGCTGGAGTGTGGCGCCATG 1500
DB 1441 AACGAGTGTCTTCAAGTGGCGCACAGCATCTTCCCTTCGCGCTGGAGTGTGGCGCCATG 1500
QY 1501 GCCAACAGTCTGGCTGGAGTGTGATGATTCCTGGCCACAGCATCTTCCCTTCGCGCTGGAT 1560
DB 1501 GCCAACAGTCTGGCTGGAGTGTGATGATTCCTGGCCACAGCATCTTCCCTTCGCGCTGGAT 1560
QY 1561 CCCAACGTCAACGGTGTCTTCTGGGACCTACCGCTTGGCATCGATCTTATTTGGAGC 1620
DB 1561 CCCAACGTCAACGGTGTCTTCTGGGACCTACCGCTTGGCATCGATCTTATTTGGAGC 1620
QY 1621 CTGGCTGCCAACCACTTGAAGTCTTCTCAACTCTTCAAGATGAAGATGTCGTCATCTG 1680
DB 1621 CTGGCTGCCAACCACTTGAAGTCTTCTCAACTCTTCAAGATGAAGATGTCGTCATCTG 1680
QY 1681 GCGCTGTCGATGCGCTTTGGGGTGGTCTTCGAGTCTTCAACACAGCTGCACTTTGGC 1740
DB 1681 GCGCTGTCGATGCGCTTTGGGGTGGTCTTCGAGTCTTCAACACAGCTGCACTTTGGC 1740
QY 1741 CAGAGGCAACCGGCTGCTGGAGAGCTGCCGAGCTCACCTTCTGCTGGGACTTCTTC 1800
DB 1741 CAGAGGCAACCGGCTGCTGGAGAGCTGCCGAGCTCACCTTCTGCTGGGACTTCTTC 1800
QY 1801 GGTTCCTGCTGTTCTTAGTCACTCAAGTGTGTGTCTGTGGGTGCGCAGGCGCGCC 1860
DB 1801 GGTTCCTGCTGTTCTTAGTCACTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860

Qy	1861	TCGCCAGCATCTCATCACTTCATCAACATGTTCTCTTCTCCACAGCCCCAGCAAC	1920
Db	1861	TCGCCAGCATCTCTCATCACTTCATCAACATGTTCTCTTCTCCACAGCCCCAGCAAC	1920
Qy	1921	AGGCTGCTCTACCCCGGCAAGGAGTGGTCCAGGCCACGCTGGTGTCTCTGGCCTTGGCC	1980
Db	1921	AGGCTGCTCTACCCCGGCAAGGAGTGGTCCAGGCCACGCTGGTGTCTCTGGCCTTGGCC	1980
Qy	1981	ATGTGCGCCATCTGTCTGTGGCACACCCCTGCACTGTGTGCACCGCCACCGCCGCCGC	2040
Db	1981	ATGTGCGCCATCTGTCTGTGGCACACCCCTGCACTGTGTGCACCGCCACCGCCGCCGC	2040
Qy	2041	CTCGGAGGAGGCCCGCTGACCGACAGGAGGAAAAAACAAGGCCGGTGTGTGACCTTGCCT	2100
Db	2041	CTCGGAGGAGGCCCGCTGACCGACAGGAGGAAAAAACAAGGCCGGTGTGTGACCTTGCCT	2100
Qy	2101	GACGCATCTGTGAATGGCTGGAGTCCGATGAGGAAAAAGCAGGGGCGCTGGATGATGAA	2160
Db	2101	GACGCATCTGTGAATGGCTGGAGTCCGATGAGGAAAAAGCAGGGGCGCTGGATGATGAA	2160
Qy	2161	GAGGAGCCGAGCTCGTCCCTCCGAGGTGCTCATGCACAGAGGCATCCACACCATCGAG	2220
Db	2161	GAGGAGCCGAGCTCGTCCCTCCGAGGTGCTCATGCACAGAGGCATCCACACCATCGAG	2220
Qy	2221	TTCTGCTGGGCTGCGTCTCCAAACACCGCCTCTACTGTGGCGCTGTGGGCGCTGAGCCTG	2280
Db	2221	TTCTGCTGGGCTGCGTCTCCAAACACCGCCTCTACTGTGGCGCTGTGGGCGCTGAGCCTG	2280
Qy	2281	GCCACGCGCAGCTGTCGAGGTTCTGTGGGCCATGATGATGCGCATAGGCCCTGGGCGCTG	2340
Db	2281	GCCACGCGCAGCTGTCGAGGTTCTGTGGGCCATGATGATGCGCATAGGCCCTGGGCGCTG	2340
Qy	2341	GGCCGGAGGTGGCGGTGGCGGTGTGGTCTGGTCTCCCATCTTTGCGCGCTTTGCGGTG	2400
Db	2341	GGCCGGAGGTGGCGGTGGCGGTGTGGTCTGGTCTCCCATCTTTGCGCGCTTTGCGGTG	2400
Qy	2401	ATGACGCTGGCTATCTGTGTGTGATGGAGGACTCTCAGCCTTCTGTGCACGCGCTTCGG	2460
Db	2401	ATGACGCTGGCTATCTGTGTGTGATGGAGGACTCTCAGCCTTCTGTGCACGCGCTTCGG	2460
Qy	2461	CTGCACCTGGGTGGAATTCAGAAACAAGTTCTACTCAGGCAAGGGCTACAGCTGAGTCCC	2520
Db	2461	CTGCACCTGGGTGGAATTCAGAAACAAGTTCTACTCAGGCAAGGGCTACAGCTGAGTCCC	2520
Qy	2521	TTCACTTTCGCTGCCACAGATGACTAGGGGCCACTGCAGGTCTCTGCCAGACCTCTTCCT	2580
Db	2521	TTCACTTTCGCTGCCACAGATGACTAGGGGCCACTGCAGGTCTCTGCCAGACCTCTTCCT	2580
Qy	2581	GACCTCTGAGGCAAGGAGGAGNATAAGACGGTCCGCGCTTGGCAAAAAAATAAAAAA	2640
Db	2581	GACCTCTGAGGCAAGGAGGAGNATAAGACGGTCCGCGCTTGGCAAAAAAATAAAAAA	2640

RESULT 7

RESULT 7
 US-10-843-641A-2737
 ; Sequence 2737, Application US/10843641A
 ; Publication No. US20050064454A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Avalon Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
 ; TITLE OF INVENTION: Signature Gene Sets
 ; FILE REFERENCE: 68290-189
 ; CURRENT APPLICATION NUMBER: US/10/843,641A
 ; CURRENT FILING DATE: 2004-05-12
 ; PRIOR APPLICATION NUMBER: US/09/873,367
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US/09/954,531
 ; PRIOR FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: US/09/954,456
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: US/09/962,436
 ; PRIOR FILING DATE: 2001-09-25

721 TCCTACTGGGTGAGCAGATCGGACAGAGATCCGCAAGATCA CGGACTGCTTCCACTGC 780
721 TCCTACTGGGTGAGCAGATCGGACAGAGATCCGCAAGATCA CGGACTGCTTCCACTGC 780
781 CACGCTCTCCGCTTCTGACAGCAGAGAGAGCCCGCTCGGGGCCCTGACAGCTGCA 840
781 CACGCTCTCCGCTTCTGACAGCAGAGAGAGCCCGCTCGGGGCCCTGACAGCTGCA 840
841 CAGCAGAGCCAGAGCTGACAGAGAGTCTCGGGGAGACAGAGCGGTTCCTGAGCCAGGTG 900
841 CAGCAGAGCCAGAGCTGACAGAGAGTCTCGGGGAGACAGAGCGGTTCCTGAGCCAGGTG 900
901 CTAGCCCGGTGCTGACAGCTGCTGCCCGCAGGAGAGTGCACAGATGAAGGCC 960
901 CTAGCCCGGTGCTGACAGCTGCTGCCCGCAGGAGAGTGCACAGATGAAGGCC 960
961 GTGTACTGGCCCTGAACAGTGCAGCGTGAGCACCACGACAGTGCCTCATTTGCCGAG 1020
961 GTGTACTGGCCCTGAACAGTGCAGCGTGAGCACCACGACAGTGCCTCATTTGCCGAG 1020
1021 GCCTGTGCTCTGTGCGAGACCTGCCCGCTGACAGAGGCCCTGCGGGACAGCTCGATG 1080
1021 GCCTGTGCTCTGTGCGAGACCTGCCCGCTGACAGAGGCCCTGCGGGACAGCTCGATG 1080
1081 GAGGAGGAGTGAAGTGCCTGAGTCCAGCATCCCTGCGGGACATGCCCGCCACACTC 1140
1081 GAGGAGGAGTGAAGTGCCTGAGTCCAGCATCCCTGCGGGACATGCCCGCCACACTC 1140
1141 ATCCGACCAACCGCTTACAGGCGCAGCTTCCAGGGCATCGTGGATCGCTACGGGTGGC 1200
1141 ATCCGACCAACCGCTTACAGGCGCAGCTTCCAGGGCATCGTGGATCGCTACGGGTGGC 1200
1201 CGCTACAGAGAGTCAACCGCGTCCCTACACCATCATCACTTCCCTTCTGTTTGTCT 1260
1201 CGCTACAGAGAGTCAACCGCGTCCCTACACCATCATCACTTCCCTTCTGTTTGTCT 1260
1261 GTGATGTTCCGGGATGTTGGGCGACAGGCTGCTCATGTTCTTCCGCTGGCCATGGTC 1320
1261 GTGATGTTCCGGGATGTTGGGCGACAGGCTGCTCATGTTCTTCCGCTGGCCATGGTC 1320
1321 CTTGCGGAGAACCGACCGCTGTGAAGCGCGCAGAGACGAGATCTGGCAGACTTCTTC 1380
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1381 AGGGCGCGCTACCTGCTCTGCTTATGGGCTGTTTCTCATCTACACCGGCTTCATCTAC 1440
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1441 AACGAGTGTCTCAGTCCGCGCACAGCATCTTCCCTCGGGCTGGAGTGGCGGCCATG 1500
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1501 GCCAACGAGTCTGCTGAGTGTGATTCCTTCCGCGCACAGCATCTTCCCTCGGGCTGGAGTGGCGGCCATG 1560
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1561 CCCAACGTCACCGGTGTTCTTCTGGGACCTTACCCCTTTGGCATTCGATTCATTTGGAGC 1620
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1621 CTGGCTGCCAACCATTTGAGCTTCTCAACTCTTCAAGATGAAGTTCGGTCACTTC 1680
1681 GCGGTCTGTCACATGGCTTTGGGTGGTCTCGAGTCTTCAACACGCTGCACTTTGGC 1740
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1741 CAGAGGACCGGTGCTGCTGGAGACGCTCCCGAGCTCACTTCTGCTGGGACTCTTC 1800
1741 CAGAGGACCGGTGCTGCTGGAGACGCTCCCGAGCTCACTTCTGCTGGGACTCTTC 1800
1801 GGTACTCTGTTCTTCTAGTCACTACAGTGGCTGTGTCTGGGCTGCCAGGGCGGCC 1860

1801 GGTACTCTGTTCTTCTAGTCACTACAGTGGCTGTGTCTGGGCTGCCAGGGCGGCC 1860
1861 TCGCCAGCATCTCTCATCCATTCATCAACATGTTCTTCTTCTCCACAGCCCCAGCAAC 1920
1861 TCGCCAGCATCTCTCATCCATTCATCAACATGTTCTTCTTCTCCACAGCCCCAGCAAC 1920
1921 AGGCTGCTCTACCCCCCGGACAGAGTGGTCCAGGCCACGCTGTGTGTCTTGGCTTGGCC 1980
1921 AGGCTGCTCTACCCCCCGGACAGAGTGGTCCAGGCCACGCTGTGTGTCTTGGCTTGGCC 1980
1981 ATGCTGCCCATCTGCTGCTTGGCACACCTCTGACCTGCTGCAACCGCCACCGCGCGCC 2040
1981 ATGCTGCCCATCTGCTGCTTGGCACACCTCTGACCTGCTGCAACCGCCACCGCGCGCC 2040
2041 CTGCGAGGAGGCCCGCTGACCCGACAGAGAGAAAAAAGGCGCGGTGTCTGGACCTGCCT 2100
2041 CTGCGAGGAGGCCCGCTGACCCGACAGAGAGAAAAAAGGCGCGGTGTCTGGACCTGCCT 2100
2101 GACGATCTGTGAATGCTGAGCTCCGATGAGGAAAAAGGAGGGGCTGGATGATGAA 2160
2101 GACGATCTGTGAATGCTGAGCTCCGATGAGGAAAAAGGAGGGGCTGGATGATGAA 2160
2161 GAGGAGCCGAGCTCGTCCCTCCGAGGTGCTCATGACACAGGCCATCCACACCATCGAG 2220
2161 GAGGAGCCGAGCTCGTCCCTCCGAGGTGCTCATGACACAGGCCATCCACACCATCGAG 2220
2221 TTCTGCTGGCTGCGCTCTCAACACACCGCTCTTACCTGCGGCTGTGGGCTCGAGCTG 2280
2221 TTCTGCTGGCTGCGCTCTCAACACACCGCTCTTACCTGCGGCTGTGGGCTCGAGCTG 2280
2281 GCCACGCCCAGCTGTCCGAGGTTCTGTGGGCTCATGCTGATGCGCATAGGCTGGGCTG 2340
2281 GCCACGCCCAGCTGTCCGAGGTTCTGTGGGCTCATGCTGATGCGCATAGGCTGGGCTG 2340
2341 GCGCGGAGTGGGCTGGGCTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
2341 GCGCGGAGTGGGCTGGGCTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
2401 ATGACCTGCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
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2461 CTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
2461 CTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
2521 TTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
2521 TTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
2581 GACCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640
2581 GACCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2640

RESULT 8

US-10-843-641A-6682
; Sequence 6682, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: Signature Gene Sets
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25

RESULT 11

US-11-126-866-1
; Sequence 1, Application US/11126866
; Publication No. US20050220789A1
; GENERAL INFORMATION:
; APPLICANT: UTUKU, et al., NALAN
; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS TO
; FILE REFERENCE: 1472/71099-2A/JPW/AG
; CURRENT APPLICATION NUMBER: US/11/126,866
; CURRENT FILING DATE: 2005-05-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 2488
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (537)..(2378)
US-11-126-866-1

Query Match 78.3%; Score 2068; DB 13; Length 2488;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2105; Conservative 0; Mismatches 40; Indels 3; Gaps 1;
QY 496 GGGGCTCAGAGGAGGAGCCCTGCTCCAGGCCCCCGGGGGCCGCAACAGGACCTGAGG 555
DB 327 GGGGGCTGCTGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 386
QY 556 GTCAACTTTGTGGCAGGTCGCTGGAGCCGACCAAGGCCCCCTGCTAGAGGCGCTGCTC 615
DB 387 GCCAGCTTTGTGGCAGGTCGCTGGAGCCGACCAAGGCCCCCTGCTAGAGGCGCTGCTC 446
QY 616 TGGAGGCGCTGCGGGCTTCTCAATGTCAGCTTCAGGAGCTGAGAGCAGCGCTGGAG 675
DB 447 TGGAGGCGCTGCGGGCTTCTCAATGTCAGCTTCAGGAGCTGAGAGCAGCGCTGGAG 506
QY 676 CACCCGTGACGGGGAGGAGCCAGCTGATGACCTTCTCATCTCTCTACTTGGGGTGAG 735
DB 507 CACCCGTGACGGGGAGGAGCCAGCTGATGACCTTCTCATCTCTCTACTTGGGGTGAG 566
QY 736 CAGATCGGACAGAGATCCGCAAGATCAGGAGCTGCTTCCACTGCCACGCTCTTCCCGTTT 795
DB 567 CAGATCGGACAGAGATCCGCAAGATCAGGAGCTGCTTCCACTGCCACGCTCTTCCCGTTT 626
QY 796 CTGACGAGGAGGAGGCGCCCTCGGGCCCTGCGAGAGCTGCAAGAGCTGCAACAGAGGAGGAG 855
DB 627 CTGACGAGGAGGAGGCGCCCTCGGGCCCTGCGAGAGCTGCAAGAGCTGCAACAGAGGAGGAG 686
QY 856 CTGACGAGGAGGAGGCGCCCTCGGGCCCTGCGAGAGCTGCAAGAGCTGCAAGAGGAGGAGGAG 915
DB 687 CTGACGAGGAGGAGGCGCCCTCGGGCCCTGCGAGAGCTGCAAGAGCTGCAAGAGGAGGAGGAG 746
QY 916 CAGCTGCTGCCCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 975
DB 747 CAGCTGCTGCCCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 806
QY 976 AACAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1035
DB 807 AACAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 866
QY 1036 CAGAGCTGCCCGCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1095
DB 867 CAGAGCTGCCCGCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 926
QY 1096 GCGGTGGCTCAGCGATCCCTGCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1155
DB 927 GCGGTGGCTCAGCGATCCCTGCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 986
QY 1156 TTCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1215
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DB 1167 CCGGCTGTGAAGCGCGCAGAACAGAGATCTGGCAGATCTTTCAGGGGCGCTACCTG 1226
QY 1396 CTCCTGCTTATGGGCTGTTCTCCATCTACACGGCTTCTCATCAACAGAGTCTTCACT 1455
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QY 1873 CTATCTCATCTCAATGTTCTCTTCTCCACAGCCCGCAGCAACAGGCTGTCTTAC 1932
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DB 1887 CCGCTGACCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1946
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DB 1947 AATGCTGAGGCTCCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2006
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DB 2307 GAATTCAGAACAAAGTTCTACTCAGGACCGGCTTACAGCTGAGTCCCTTACCTTCGCT 2366
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DB 2427 AGGAGGGAATAAGAGCGTCCGCTGGCGGCTGGGCAAAAAAAAAAAAAA 2474

RESULT 12
US-11-126-841A-1
; Sequence 1, Application US/11126841A
; Publication No. US20050271659A1
; GENERAL INFORMATION:
; APPLICANT: UTU, et al., NALAN
; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS TO
; FILE OF INVENTION: AN EXTRACELLULAR DOMAIN OF A TIRC7 MEMBRANE PROTEIN
; FILE REFERENCE: 1472/71099-ZB/JPW/AG
; CURRENT APPLICATION NUMBER: US/11/126,841A
; CURRENT FILING DATE: 2005-05-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 2488
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (537)..(2378)
US-11-126-841A-1

Query Match 78.3%; Score 2068; DB 15; Length 2488;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2105; Conservative 0; Mismatches 40; Indels 3; Gaps 1;

QY 496 GGGGCTCAGAGGAGCGCCCTGCTCCAGGCCCCCGGGGGCGCGCACAGGACCTGAGG 555
DB 327 GGGGGCTGTGGGGAGGCGAGGAGGTTGGAGCAGCCCTGCCCCCGCGTGGCC 386
QY 556 GTCACTTTGTGCGAGGTGCGGTGGAGCCGCCACAGGCCCCCTGCGCTAGAGCGCTGCTC 615
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QY 616 TGGAGGCGCTGCGCGCTTCTCATTTGCGAGCTTACAGGAGCTGGAGCAGCGCTGGAG 675
DB 447 TGGAGGCGCTGCGCGCTTCTCATTTGCGAGCTTACAGGAGCTGGAGCAGCGCTGGAG 506
QY 676 CACCCGTGACGGGCGAGCGAGCGACCGTGTGATGACCTTCTCATCTCTACTGGGGTGAG 735
DB 507 CACCCGTGACGGGCGAGCGAGCGACCGTGTGATGACCTTCTCATCTCTACTGGGGTGAG 566
QY 736 CAGATCGGACAGAGATCCGCAAGATCA CGGACTGCTTCCACTGCCACGCTTCCCGCTTT 795
DB 567 CAGATCGGACAGAGATCCGCAAGATCA CGGACTGCTTCCACTGCCACGCTTCCCGCTTT 626
QY 796 CTCGACGAGGAGGCGCGCTTCCGCGGCTTCCAGAGCTTCCAGAGCTTCCAGAGGCGCAGGAG 855

DB 627 CTGACGACGAGGAGGAGGCGCGCTTGGGGCCCTTGACGAGCTGCAACAGCAGAGAGCCAGAG 686
QY 856 CTGACGAGAGTCTCTCGGGGAGACAGAGCGGTTCCTGAGCCAGAGTGTCTAGGCGGGGTGCTG 915
DB 687 CTGACGAGAGTCTCTCGGGGAGACAGAGCGGTTCCTGAGCCAGAGTGTCTAGGCGGGGTGCTG 746
QY 916 CAGCTGCTGCGGCGAGGCGAGGTGCAAGATGCAAGATGCAAGCGGTGTACTGCGGCTG 975
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QY 976 AACGAGTGCAGCGTGCAGCACACGACCAAGTGCCTCATTTGCGGAGGCTGTGTGCTCTGTG 1035
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DB 867 CGAGACCTGCGCGCTTGCAGGAGGCGCTTGCAGGACAGCTCGATGAGGAGGAGTGA 926
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QY 1216 AACCGCGCTCCCTTACACCATCATCACCTTCCCTTCTGTTGCTGTGATGTTTCGGGAT 1275
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DB 1467 TTGAGCTTCTCAACTCTTCAAGATGAAAGTGTGCGTATCTTGGGCGCTGTGCAATG 1526
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QY 1756 CTGCTGGAGACGCTGCGGAGCTCAGCTTCTGCTGGGACTCTTTCGGGTTACCTGCTGTTTC 1815
DB 1587 CTGCTGGAGACGCTGCGGAGCTCAGCTTCTGCTGGGACTCTTTCGGTTCCTGCTGTTTC 1646
QY 1816 CTAGTCACTTCAAGTGGCTGTGTGCTGGGCTGCCAGGCGCGCTG --- CCGAGCATC 1872
DB 1647 CTAGTCACTTCAAGTGGCTGTGTGCTGGGCTGCCAGGCGCGCTG --- CCGAGCATC 1706
QY 1873 CTCATCCACTTCACTCAACTGTTCTTCTTCCACAGCCCCAGGAGGCTGCTCTAC 1932
DB 1707 CTCATCCACTTCACTCAACTGTTCTTCTTCCACAGCCCCAGGAGGCTGCTCTAC 1766

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1933 CCCCGCAGAGGTGTTCCAGGCGACGCTGGTGGTCTCTGCGCCTTGGCCATGTTGCCCATC 1992
1767 CCCCGCAGAGGTGTTCCAGGCGACGCTGGTGGTCTCTGCGCCTTGGCCATGTTGCCCATC 1826
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1827 CTGCTGCTTGGCAGACCCCTGCACCTGCTGCACCGCCACCGCGCCGCTGCGGAGGAGG 1886
2053 CCGCTGACCGACAGAGGAGAAACAGAGCGGGTTGCTGGACCTGCTGACGATCTGTG 2112
1887 CCGCTGACCGACAGAGGAGAAACAGAGCGGGTTGCTGGACCTGCTGACGATCTGTG 1946
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2007 CTCGTCCTCCGAGGTGCTCATGACACAGGCGCATCCACACCATCGAGTTCTGCTGGGC 2066
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2293 CTGTCGAGGTTCTGTGGGCCATGTTGATGCGCATAGGCGCTGCGGCTGCGGCGGAGGTG 2352
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2353 GCGGTGGGCGCTGTGTTGCTGCCCATCTTTTGGCGCTTTTGGCGCTGATGACCGTGGCT 2412
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2247 ATCTGCTGGTGTATGAGGAGCTCTAGCGCTTCTGCGCGCTTCTGCGCGCTGACCTGGGTG 2306
2473 GAATTCAGAACAAAGTTCTACTCAGGACGGGCTACAAGCTCAGTCCCTTCACTTCGCT 2532
2307 GAATTCAGAACAAAGTTCTACTCAGGACGGGCTACAAGCTCAGTCCCTTCACTTCGCT 2366
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2367 GCCACAGATGACTAGGGCCCACTGACAGGTCTGCGCAGACCTCTTCTGACCTCTGAGGC 2426
2593 AGGAGAGGATGAAGACGCTCGCCCTGCGCAAAAAAAAAAAAAAAAAAAAA 2640
2427 AGGAGAGGATGAAGACGCTCGCCCTGCGCAAAAAAAAAAAAAAAAAAAAA 2474
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RESULT 13
US-10-145-012-12
; Sequence 12, Application US/10145012
; Publication No. US20030124614A1
; GENERAL INFORMATION:
; APPLICANT: UTU et al.
; TITLE OF INVENTION: T-CELL MEMBRANE PROTEIN (TIRC7), PEPTIDES AND ANTIBODIES DERIVED
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 4400-0105P
; CURRENT APPLICATION NUMBER: US/10/145,012
; CURRENT FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 2488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (537)..(2378)
US-10-145-012-12
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Query Match 78.3%; Score 2066.4; DB 7; Length 2488;

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Best Local Similarity 98.0%; Pred. No. 0;
Matches 2104; Conservative 0; Mismatches 41; Indels 3; Gaps 1;
QY 496 GGGGCTCAGAGAGACGCCCTCTGTCAGAGGCCCGGGGGCCCGCAGGACCTTGAGG 555
DB 327 GGGGCGCTGGTGGGGAGGAGGAGGAGGAGGTTGGAGCAGCCCTGCCCAGCCCGTGGCC 386
QY 556 GTCAACTTTGTGGCAGGTGCGGTGAGAGCCCAAGAGCCCTTGCCTTAGAGGCGCTGCTC 615
DB 387 GCCAGCTTTGTGGCAGGTGCGGTGAGAGCCCAAGAGCCCTTGCCTTAGAGGCGCTGCTC 446
QY 616 TGGAGGCGCTGCGCGGCTTCTCATGTCAGCTTTCAGGAGCTGAGCAGCGCTGGAG 675
DB 447 TGGAGGCGCTGCGCGGCTTCTCATGTCAGCTTTCAGGAGCTGAGCAGCGCTGGAG 506
QY 676 CACCCCGTGAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 735
DB 507 CACCCCGTGAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 566
QY 736 CAGATCGGACAGAGATCGGCAAGATCAGGAGCTGCTTCCACTGCGACGCTCTTCCGTTT 795
DB 567 CAGATCGGACAGAGATCGGCAAGATCAGGAGCTGCTTCCACTGCGACGCTCTTCCGTTT 626
QY 796 CTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 855
DB 627 CTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 586
QY 856 CTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 915
DB 687 CTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 746
QY 916 CAGCTGCTGCGCGCAGGCGAGGTCAGGTCACAGATGAGGCGCTGCTACCTTGGCCCTG 975
DB 747 CAGCTGCTGCGCGCAGGCGAGGTCAGGTCACAGATGAGGCGCTGCTACCTTGGCCCTG 806
QY 976 AACAGTGCAGGTCAGGACCAAGTGCCTCATTTGCCAGGCGCTTGGTCTGCTG 1035
DB 807 AACAGTGCAGGTCAGGACCAAGTGCCTCATTTGCCAGGCGCTTGGTCTGCTG 866
QY 1036 CGAGACTGCGCGCTCTGAGAGGCGCTTGGGAGCAGTCGATGAGAGGAGGAGT 1095
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QY 1096 GCGGTGGCTCAGCGATCCCTTGGCGGAGCAGTGGCCCGCAGCTATCCGCAACACCG 1155
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QY 1156 TTACGCGCAGCTTCCAGGCGATCGTGGATCGCTACGCGGTGGGCGCTTACCGAGGTC 1215
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DB 1047 AACCGGCTTCCATACCATCATCTTCCCTTCCCTTCTGTTGCTGATGTTGGGGAT 1106
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DB 1167 CCGGTGTGAAGCGCGCAGAGATCTGGGAGACTTTCTTCCAGGGCGCTACCTG 1226
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Db 1347 TGGAGTGATGATTCCTGGGCCAGCACACGATGCTTACCTGGATCCCAACGTCACCGGT 1406
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Db 1467 TTGAGCTTCTCAACTCTCTCAAGATGAAGATGTCGGTCATCTCTGGGGTGCTGCATG 1526
Qy 1696 GCCTTTGGGGTGCTCTCGAGTCTTCAACACACGTCGACTTTGGCCAGAGGACACCGCTG 1755
Db 1527 GCCTTTGGGGTGCTCTCGAGTCTTCAACACACGTCGACTTTGGCCAGAGGACACCGCTG 1586
Qy 1756 CTGCTGAGAGCTGCGCGAGCTCACCTTCTGCTGGGACTCTTTCGGTTACCTCTGTTTC 1815
Db 1587 CTGCTGAGAGCTGCGCGAGCTCACCTTCTGCTGGGACTCTTTCGGTTACCTCTGTTTC 1646
Qy 1816 CTAGTCATACAGTGGCTGTGTGCTGGGCTGCCAGGGCGGCTCG---CCAGCATC 1872
Db 1647 CTAGTCATACAGTGGCTGTGTGCTGGGCTGCCAGGGCGGCTCGGGCCCCAGCATC 1706
Qy 1873 CTCATCCACTTTCATCAACATGTTCTCTTCTCCACAGCCCGACCAACAGGCTGCTCTAC 1932
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Db 1767 CCCCAGAGGCTGTCAGGACACGCTGGTGTCTTGGCTCTGGCCATGTTGCCCATC 1826
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Db 1827 CTGCTGCTGGCACACCCCTGACCTCTGTCACCGCCACACCGCCCGCTGCGGAGAGG 1886
Qy 2053 CCGCTGACCGACAGGAGGAAAAAAGCCGGGTGCTGACCTGCTGACGCACTGTG 2112
Db 1887 CCGCTGACCGACAGGAGGAAAAAAGCCGGGTGCTGACCTGCTGACGCACTGTG 1946
Qy 2113 AATGGCTGAGCTCCGATGAGGAAAAAGCAGGGGCTCGATGATGAAGAGGAGGCGGAG 2172
Db 1947 AATGGCTGAGCTCCGATGAGGAAAAAGCAGGGGCTCGATGATGAAGAGGAGGCGGAG 2006
Qy 2173 CTGCTCCCTCCGAGGCTCATGACCGGCTGTGGGCCCTGAGCCTGGGCCACGCGCCAG 2232
Db 2007 CTGCTCCCTCCGAGGCTCATGACCGGCTGTGGGCCCTGAGCCTGGGCCACGCGCCAG 2066
Qy 2233 TGCGCTTCCAAACACCGCTCTACCTGCGCTGTGGGCCCTGAGCCTGGGCCACGCGCCAG 2292
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Db 2247 ATCTCTGTGTGATGAGGAGCTCTCAGCCTTCTGACCGCTTCTGACCGCTTGGGCTGCACTGGTG 2306
Qy 2473 GAATTCAGAACTTCTACTCAGGACCGGCTTACAGCTGAGTCCCTTTCACCTTCGCT 2532
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Db 2427 AGGAGAGGAATAAAGAGCGTCCGCCCTTGGCAAAAAA 2474

RESULT 14

US-11-126-866-12
; Sequence 12, Application US/111126866
; Publication No. US20050220789A1
; GENERAL INFORMATION:
; APPLICANT: UTOKU, et al., NALAN
; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS
; FILE REFERENCE: 1472/71099-2A/JPW/AG
; CURRENT APPLICATION NUMBER: US/11/126,866
; CURRENT FILING DATE: 2005-05-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 2488
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; NAME/KEY: CDS
; LOCATION: (537) .. (2378)
US-11-126-866-12

Query Match 78.3%; Score 2066.4; DB 13; Length 2488;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 2104; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

Qy 496 GGGGCTTCAGAGAGGACGCCCCCTGCTCCAGGCCCCGGGGGGCGCACACGAGACCTGAGG 555
Db 327 GGGGGGCTGTGTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 386
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Db 387 GCCAGCTTTTGTGGAGGTGCGGTGGAGCCCAAGAGCCCTGCTCTAGAGCGCTGCTC 446
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Search completed: June 30, 2006, 06:17:08
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ACCESSION AR577091
VERSION AR577091.1 GI:56579543
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

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AUTHORS Scashenko, P. and Li, Y.-P.
TITLE Osteoclast proton pump subunit
JOURNAL Patent: US 677537-A 1 17-AUG-2004;
Forsyth Dental Infirmary for Children; Boston, MA;
WOX;

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source Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AR270531
LOCUS AR270531 2655 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1094 from patent US 6500938.
ACCESSION AR270531
VERSION AR270531.1 GI:29701765
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2655)
AUTHORS Au-Young, J. and Seilhamer, J. J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1094 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
WOX;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 2640; DB 2; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CGGCTGTGCGGACGCGGACGAGCGGAGCGCGGCGAGCACACCCGGGGACCATG 60
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DB 61 GGTCCATGTTCCGGAGCGAGGAGTGGCCCTGTGCTTCTGCCCCACAGCGGT 120
QY 121 GCCTACACTGGCTGAGTGGCTGGCGAGCTGGGCTCTGAGGATTCAGAGACCTCAAC 180
DB 121 GCCTACACTGGCTGAGTGGCTGGCGAGCTGGGCTCTGAGGATTCAGAGACCTCAAC 180
QY 181 GCTCGGTGAGCGCTTCCAGAGCGCTTGTGTGTTGATGTTGTGGCTGTGAGGAGCTG 240
DB 181 GCTCGGTGAGCGCTTCCAGAGCGCTTGTGTGTTGATGTTGTGGCTGTGAGGAGCTG 240
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DB 241 GAGAAAGCTTTCACCTTCTCTGAGGAGAGGTGCGGCGGCTGGGCTGTGCTTGTGCCCCG 300
QY 301 CCAAGGGAGGCTGCGGCAACCCCAACCGGAGCTGCTGCGCATCCAGAGAGAGCG 360
DB 301 CCAAGGGAGGCTGCGGCAACCCCAACCGGAGCTGCTGCGCATCCAGAGAGAGCG 360
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DB 361 GAGCGCTTGGCCACGAGCTGCGGATGTGCGGGCAACAGAGGCGCTTGGCGGCCAG 420
QY 421 CTGCAACAGCTGCACTCCACGCGCTGTCTAGCCAGGGCCATGAACCTCAGCTGGCA 480
DB 421 CTGCAACAGCTGCACTCCACGCGCTGTCTAGCCAGGGCCATGAACCTCAGCTGGCA 480
QY 481 GCGGCCCCACAGATGGGGCTTCAGAGAGAGCGCCCTGCTCCAGGCCCCCGGGGGCGG 540
DB 481 GCGGCCCCACAGATGGGGCTTCAGAGAGAGCGCCCTGCTCCAGGCCCCCGGGGGCGG 540
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DB 541 CACAGGACCTTGAGGCTCAAATTTGTGGCAGGTGCGTGGAGGCCCAAGGCGCCCTGCG 600
QY 601 CTAGAGCGCTGCTCTGAGGCGCTGCGCGGCTTCTCATTTGCGAGCTTCAGGAGCTG 660
DB 601 CTAGAGCGCTGCTCTGAGGCGCTGCGCGGCTTCTCATTTGCGAGCTTCAGGAGCTG 660
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DB 661 GAGCAGCGCTGGAGCACCCCGTGCAGCGGCGAGCCAGCGTGCATGACCTTCTCATC 720

Db	2041																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
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Db	61	GGCTCCATGTTCCGAGCGAGAGGTGGCCCTGGTCCAGACTTTTCTGCCACAGCGGCT	120
Qy	121	GCCTACACCTCGTGAGTCGGCTGGCGAGCTGGGCCCTCGTGAGATTACAGACCTCAAC	180
Db	121	GCCTACACCTCGTGAGTCGGCTGGCGAGCTGGGCCCTCGTGAGATTACAGACCTCAAC	180
Qy	181	GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTGATTTGGCGCTGTGAGGAGCTG	240
Db	181	GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTGATTTGGCGCTGTGAGGAGCTG	240
Qy	241	GAGAGAGCTTTACCTTCTCGAGAGAGAGGTGCGCGGGCTGGGCTGCTCTGCCCCCG	300
Db	241	GAGAGAGCTTTACCTTCTCGAGAGAGAGGTGCGCGGGCTGGGCTGCTCTGCCCCCG	300
Qy	301	CCAAAGGGGAGGCTCCGGCACCCCCACCCCGGGACCTGCTCGCATCCAGAGAGAGCG	360
Db	301	CCAAAGGGGAGGCTCCGGCACCCCCACCCCGGGACCTGCTCGCATCCAGAGAGAGCG	360
Qy	361	GAGCGCTTGGCCCAAGAGCTGGGGATGTGCGGGCAACACAGAGGCCCTGCGGGCCAG	420
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Qy	421	CTGCACACAGCTGCAGCTCCACGCGCCGTGTACGCCAGGGCCATGAACCTCAGCTGGCA	480
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Qy	541	CACCAGAGCTGAGGCTCAACTTTGTGACAGTGCCTGGAGCCCCCAAGGCCCTGCG	600
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Qy	601	CTAGAGCGCTTGTCTGTGAGGGCCCTGCGCGGCTTCTCATTTGCCAGCTTCAAGGAGCTG	660
Db	601	CTAGAGCGCTTGTCTGTGAGGGCCCTGCGCGGCTTCTCATTTGCCAGCTTCAAGGAGCTG	660
Qy	661	GAGCAGCGCTGAGACACCCCGTGACGGGCGAGCCAGCCACGTGTGATGACCTTCTCATC	720
Db	661	GAGCAGCGCTGAGACACCCCGTGACGGGCGAGCCAGCCACGTGTGATGACCTTCTCATC	720
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Qy	781	CAGCTCTTCCGTTTCTGTGACGAGGAGGCCCGCCCTCGGGGCCCTCGAGCAGCTGCAA	840
Db	781	CAGCTCTTCCGTTTCTGTGACGAGGAGGCCCGCCCTCGGGGCCCTCGAGCAGCTGCAA	840
Qy	841	CAGCAGAGCCAGGAGCTGCAGGAGTCTTCGGGGAGACAGAGCGGTTCTCGAGCCAGGTG	900
Db	841	CAGCAGAGCCAGGAGCTGCAGGAGTCTTCGGGGAGACAGAGCGGTTCTCGAGCCAGGTG	900
Qy	901	CTAGGCCGGGTGTCTGACGTCTGCGCCGACGGGAGGTGTCAGGTCACAAGATGAAGGCC	960
Db	901	CTAGGCCGGGTGTCTGACGTCTGCGCCGACGGGAGGTGTCAGGTCACAAGATGAAGGCC	960
Qy	961	GTGTACTGGCCCTGAACCAAGTCAGCGTGAAGCACCAAGCAAGTGCCTCATTTGCCGAG	1020
Db	961	GTGTACTGGCCCTGAACCAAGTCAGCGTGAAGCACCAAGCAAGTGCCTCATTTGCCGAG	1020
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Db	1021	GCTTGTGTCTGTGCGAGACCTGCGCCCTGTGAGGAGGCCCTCGGGGACAGCTCGATG	1080
Qy	1081	GAGAGGAGGTGAGTGGCGTGGCTCAACGCATCCCTCGCGGGACATGCCCCCACTTC	1140
Db	1081	GAGAGGAGGTGAGTGGCGTGGCTCAACGCATCCCTCGCGGGACATGCCCCCACTTC	1140

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Db	241		300
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Db	301		360
		CAAAGGGGAGGCTGCCGGCACCCCCACACCCCGGGACCTGCTGCGCATCCAGGAGGAGACG	
Qy	361	GAGCGCTGGCCCAAGGAGCTGCGGGATGTGCGGGCAACCAAGAGGCCCTCTCGGGGCCAG	420
Db	361		420
		GAGCGCTGGCCCAAGGAGCTGCGGGATGTGCGGGCAACCAAGAGGCCCTCTCGGGGCCAG	
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Db	421		480
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Db	481		540
		GCCGCCCCACACAGATGGGGCTTCAAGAGGAGCGCCCTCTTCTCCAGGCCCCCGGGGGCCG	
Qy	541	CACCAGGACCTGAGGGTCAACTTTTGTGGCAGGTGCGTGGAGGCCCAAGGGCCCTTGC	600
Db	541		600
		CACCAGGACCTGAGGGTCAACTTTTGTGGCAGGTGCGTGGAGGCCCAAGGGCCCTTGC	
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		CTAGAGCGCTGCTCTGAGGGCCCTGCGCGGCTTCTCTCATTTGCCAGCTTCAGGAGCTG	
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		TCCTACTGGGTGAGCAGATCGGACAGAAATCCGCAAGATCACGGATGCTTCCACTGC	
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		CACGCTTCCCGTTTCTGCACGAGGAGGCGCGCTCGGGGCCCTGACAGCACTGCAAA	
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Qy	901	CTAGGCGGGTGTGCACTGCTGCCCGCAGGCGAGGTGCAAGTTCACAGATGAAGCC	960
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		CTAGGCGGGTGTGCACTGCTGCCCGCAGGCGAGGTGCAAGTTCACAGATGAAGCC	
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Db	961		1020
		GTGTACTTGGCCCTGAACCAAGTCAGCGTGAACACAGCAAGTGCCTCATTTGCCGAG	
Qy	1021	GCCTGGTGTCTGTGCGAGACCTGCCCGCCTGACGAGGCGCTTCGGGACAGCTCGATG	1080
Db	1021		1080
		GCCTGGTGTCTGTGCGAGACCTGCCCGCCTGACGAGGCGCTTCGGGACAGCTCGATG	
Qy	1081	GAGGAGGAGTGAGTGGCTGGCTACCGCATCCCTTCGCGGACATGCCCCCACAATC	1140
Db	1081		1140
		GAGGAGGAGTGAGTGGCTGGCTACCGCATCCCTTCGCGGACATGCCCCCACAATC	
Qy	1141	ATCCGACCAACCGCTTTCAGGGCCAGTTCAGGGGCATCTGTGGATCGCTACGGCGGGC	1200
Db	1141		1200
		ATCCGACCAACCGCTTTCAGGGCCAGTTCAGGGGCATCTGTGGATCGCTACGGCGGGC	
Qy	1201	CGCTACCAAGGAGTCAACCCCGCTTACACCATCATCTTCCCTTCTTGTGTGCT	1260
Db	1201		1260
		CGCTACCAAGGAGTCAACCCCGCTTACACCATCATCTTCCCTTCTTGTGTGCT	
Qy	1261	GTGATGTTGGGATGTGGGCCACGGGCTGCTCATGTTCTTCTGCGCCCTGGCCATGGTC	1320
Db	1261		1320
		GTGATGTTGGGATGTGGGCCACGGGCTGCTCATGTTCTTCTGCGCCCTGGCCATGGTC	

Qy	1321	CTTGGCGAGAACCGACCGGCTGTGAAGCCGCCGAGAACAGATCTGGCAGACTTTCTTC	1380
Db	1321	CTTGGCGAGAACCGACCGGCTGTGAAGCCGCCGAGAACAGATCTGGCAGACTTTCTTC	1380
Qy	1381	AGGGCCGCCTACCTGCTCTCTGTATTATGGCCCTGTTCTCCATCTACACCGGCTTCATCTAC	1440
Db	1381	AGGGCCGCCTACCTGCTCTCTGTATTATGGCCCTGTTCTCCATCTACACCGGCTTCATCTAC	1440
Qy	1441	AACGAGTGCTTCAGTGGCGCCAACCAAGCATCTTCCCCTCGGGCTGGAGTGTGGCGCCCATG	1500
Db	1441	AACGAGTGCTTCAGTGGCGCCAACCAAGCATCTTCCCCTCGGGCTGGAGTGTGGCGCCCATG	1500
Qy	1501	GCCAAACCAGTCTGGCTGGAGTGATGCATCTTCGBCCCAGCACACGATGCTTACCCCTGGAT	1560
Db	1501	GCCAAACCAGTCTGGCTGGAGTGATGCATCTTCGBCCCAGCACACGATGCTTACCCCTGGAT	1560
Qy	1561	CCCAAACGTCACCGGTGTCTTCTCTGGGACCCCTACCCCTTGGGATCGATCCTATTTCGGAGC	1620
Db	1561	CCCAAACGTCACCGGTGTCTTCTCTGGGACCCCTACCCCTTGGGATCGATCCTATTTCGGAGC	1620
Qy	1621	CTGGCTGCCAACAATTGAGCTTCTCAACTCTTCAAGATGAAGATGTCOGTCACTCTG	1680
Db	1621	CTGGCTGCCAACAATTGAGCTTCTCAACTCTTCAAGATGAAGATGTCOGTCACTCTG	1680
Qy	1681	GGCGTCTGCACATGGCCCTTTGGGGTGTCTCTCGAGTCTTCAAACAAGTGAACCTTTGGC	1740
Db	1681	GGCGTCTGCACATGGCCCTTTGGGGTGTCTCTCGAGTCTTCAAACAAGTGAACCTTTGGC	1740
Qy	1741	CAGAGGCACCGGCTGCTCTGGAGACGCTGCCGGAGCTCACCTCTCTGCTGGGACCTTTC	1800
Db	1741	CAGAGGCACCGGCTGCTCTGGAGACGCTGCCGGAGCTCACCTCTCTGCTGGGACCTTTC	1800
Qy	1801	GTTACCTCGTGTCTTAGTCACTACAAAGTGGCTGTGTCTGGGCTGCCAGGGCCGCC	1860
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Qy	1921	AGGCTGCTCTACCCCGGCGAGAGTGTGTCAGGCCACAGCTGCTGGTGTCTGGCTTTGGCC	1980
Db	1921	AGGCTGCTCTACCCCGGCGAGAGTGTGTCAGGCCACAGCTGCTGGTGTCTGGCTTTGGCC	1980
Qy	1981	ATGTTGCCCATCTGCTCTTTGGCACACCCCTGCACTGCTGCA CGGCCACCGCCCGCCG	2040
Db	1981	ATGTTGCCCATCTGCTCTTTGGCACACCCCTGCACTGCTGCA CGGCCACCGCCCGCCG	2040
Qy	2041	CTGGGAGGAGCCCGCTGACCGACAGAGGAAAAA CAAGCCCGGGTTGTGACACTGGCT	2100
Db	2041	CTGGGAGGAGCCCGCTGACCGACAGAGGAAAAA CAAGCCCGGGTTGTGACACTGGCT	2100
Qy	2101	GACGCATCTGTGATGGCTGGAGCTCCGATGAGGAAAAGGCAAGGGGCTGTGATGATGA	2160
Db	2101	GACGCATCTGTGATGGCTGGAGCTCCGATGAGGAAAAGGCAAGGGGCTGTGATGATGA	2160
Qy	2161	GAGGAGGCGAGCTCGTCCCTCCGAGTGTCTATGCA CAGGCCATCCACACCATCGAG	2220
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Qy	2221	TTCTGCTGGGCTGCGTCTCAAACA CCGCTCTTACCTGCGCTGTGGGCCCTGAGCCCTG	2280
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Qy	2281	GCCACGCCCGAGCTGTCGAGGTTCTGTGGGCCATG GTGATGCGCATAGGCCCTGGGCCCTG	2340
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Qy	2341	GGCCGGGAGGTGGGCGTGGCGGCTGTGTGTGTGTG TGTGCTTTCGCGCTTTTGGCCG	2400
Db	2341	GGCCGGGAGGTGGGCGTGGCGGCTGTGTGTGTGTG TGTGCTTTCGCGCTTTTGGCCG	2400
Qy	2401	ATGACCGTGGCTATCCTGCTGGTGTGAGGAGGACT CTGAGCCCTTCTGACGCGCCCTGCGG	2460

Db 2401 ATGACCGTGGCTATCTGCTGGTATGGAGGACTCTCAGCCTTCTGACGCCCTGCGG 2460
Qy 2461 CTGCACTGGGTGAATTCAGAAACAAGTTCTACTAGGCAAGGGCTTACAAGCTGAGTCCC 2520
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Qy 2581 GACCTCTGAGGAGGAGAGAAATAAGACGGTCCGCCCTGGCAAAAAAAGAAAAA 2640
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AX410717
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DEFINITION Sequence 3364 from Patent WO229103.
ACCESSION AX410717
VERSION AX410717.1 GI:21443422

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
1
Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J. G.
Gene expression profiles in liver cancer
Patent: WO 0229103-A 3364 11-APR-2002;
GENE LOGIC INC (US)

FEATURES
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ORIGIN

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DEFINITION mRNA, complete cds.
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VERSION U45285.1 GI:1245045
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
Li, Y.-P., Chen, W. and Staehenko, P.
Molecular cloning and characterization of a putative novel human
osteoclast-specific 116-kDa vacuolar proton pump subunit
Biochem. Biophys. Res. Commun. 218 (3), 813-821 (1996)
REFERENCE 1 (bases 1 to 2655)
AUTHORS Li, Y.-P., Chen, W. and Staehenko, P.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-1996) Yi-Ping Li, Cytokine Biology, Forsyth
PUBMED Dental Center, 140 Fenway, Boston, MA 02115, USA
8579597 Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 2640; DB 5; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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VERSION	BC032465.1 GI:21619617
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REFERENCE	
AUTHORS	1 (bases 1 to 2722)
	Klausner,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hoptkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P., Diatchenko,L., Marusina,K., Farmer,A.K., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Donald,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Vitaloni,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywicki,M.I., Skalska,U., Smalls,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
CONSRMTM	Mammalian Gene Collection Program Team
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12477932
REFERENCE	2 (bases 1 to 2722)

CONSORTM TITLE	Scmeicn,A., Schenr,J.E., Jones,S.O. and Matra,M.A. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932
JOURNAL PUBMED	2 (bases 1 to 2722)
REFERENCE	NIH MGC Project
AUTHORS	Direct Submission
CONSORTM TITLE	Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
JOURNAL	NIH-MGC Project URL: http://mgc.nci.nih.gov
REMARK	Contact: MGC help desk
COMMENT	Email: cgabbs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigr.nih.gov
Akhtar N., Ayle K., Beckstrom-Sternberg, S.M., Benjamin, B.,
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Maduro, Q.J., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
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Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.		
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof		
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Qy	173	ACCTCAACGGCTCGGTGAGCGCCTTCAGAGACGCTTTGTGTTGATGTTTGGCGCTGTG	232
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Qy	233	AGGAGCTGGAGAGACCTTCACCTTCCTGACGAGGAGGTGCGGCGGCTGGGCTGGTCC	292
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Qy	293	TGCCCCCGCCAAAGGGGAGGCTGCGCGCAACCCCAACCCCGGACCTGCTCGCATCCAGG	352
Db	249	TGCCCCCGCCAAAGGGGAGGCTGCGCGCAACCCCAACCCCGGACCTGCTCGCATCCAGG	308
Qy	353	AGGAGACGAGCGCCTTGGCCAGAGCTGCGGATGTGCGGGGCAACACAGACGGCCTGTC	412
Db	309	AGGAGACGAGCGCCTTGGCCAGAGCTGCGGATGTGCGGGGCAACACAGACGGCCTGTC	368

Db	1449		CCGCCATGGCCAAACAGTCTGGCTGGAGTGATGCAATTCCTTGGGCCACACACGATGCTTA	1508
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Db	1509		CCCTGGATCCCAACGTCACCGGTGCTCTTCTGGGACCGCTACCCCTTTGGCATCGATCCTA	1568
Qy	1613		TTTGGAGCTGGCTGGCCAAACATTGAGCTTCTCAACTCTTCAAGATGAAGATGTCG	1672
Db	1569		TTTGGAGCTGGCTGGCCAAACATTGAGCTTCTCAACTCTTCAAGATGAAGATGTCG	1628
Qy	1673		TCATCTTGGGCGTCGTGCACATGSCCTTTGGGGTGGTCCCTCGAGTCTTCAAACAAGTGC	1732
Db	1629		TCATCTTGGGCGTCGTGCACATGSCCTTTGGGGTGGTCCCTCGAGTCTTCAAACAAGTGC	1688
Qy	1733		ACTTTGGCCAGAGGACACGGCTGCTGGAGACGCTGCCGGAGCTCACCTTCTGCTGCG	1792
Db	1689		ACTTTGGCCAGAGGACACGGCTGCTGGAGACGCTGCCGGAGCTCACCTTCTGCTGCG	1748
Qy	1793		GACTCTTGGGTACTCTGCTTCTAGTCACTACAAGTGGCTGTGTGTCTGGGCTGCCA	1852
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Qy	1853		GGGGCGGCTGG- ---CCAGAGATCTCATCACTTCAACAATGTTCTTCTTCCACACA	1909
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Qy	1910		GCCCCAGCAACAGGCTGCTTACCCCCGGCAGAGGTGGTCCAGGCCACACCTGGTGGTCC	1969
Db	1869		GCCCCAGCAACAGGCTGCTTACCCCCGGCAGAGGTGGTCCAGGCCACACCTGGTGGTCC	1928
Qy	1970		TGGCCTTTGGCCATGGTGGCCATCTGCTGTCTTGGCACACCCCTGCACCTGCTGCACCGCC	2029
Db	1929		TGGCCTTTGGCCATGGTGGCCATCTGCTGTCTTGGCACACCCCTGCACCTGCTGCACCGCC	1988
Qy	2030		ACCGCCCGGCTGGGAGGAGGCCCCGCTGACCGACAGAGAGAAAACAAGGCCGGGTTC	2089
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Db	2169		ACACCATCGAGTTCGCTGGGCTGCTCTCCAAACCGCTCTACTCTGCGCTGTGGG	2228
Qy	2270		CCCTGAGGCTGGGCCACGCCCGAGGTGTCGAGGTCTTGGGGCATTGGTGATGGGATAG	2329
Db	2229		CCCTGAGGCTGGGCCACGCCCGAGGTGTCGAGGTCTTGGGGCATTGGTGATGGGATAG	2288
Qy	2330		GCCTGGGCTGGGGCGGAGGTGGGCGTGGCGGTGGTGGTGGTGGTGGTGGTGGTGGG	2389
Db	2289		GCCTGGGCTGGGGCGGAGGTGGGCGTGGCGGTGGTGGTGGTGGTGGTGGTGGTGGG	2348
Qy	2390		CCTTTGCCGTGATGACCGTGGCTATCTGCTGGTGATGGAGGACCTCTACGCTTCTCTGC	2449
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Qy	2450		ACGCCCTGGCGCTGCATGGGTGGAAATTCAGAAACAAGTTCATCAGGACACGGGTACA	2509
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Qy	2510		AGCTGAGTCTCTTACCTCTGCTGCCACAGATGACTAGGGCCACCTGCAGTCTCTGCAG	2569
Db	2469		AGCTGAGTCTCTTACCTCTGCTGCCACAGATGACTAGGGCCACCTGCAGTCTCTGCAG	2528
Qy	2570		ACCTCTCTCTGACCTCTGAGGCGAGGAGGAATAAAGACGGTCCGCCCTGGCA	2623

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DEFINITION	Sequence 1 from Patent WO9911782.		
ACCESSION	A98501		
VERSION	A98501.1	GI:6781601	
KEYWORDS	.		
SOURCE	unidentified		
ORGANISM	unclassified		
REFERENCE	unclassified sequences.		
AUTHORS	1 (bases 1 to 2488)		
TITLE	Utku.N. and Milford.E.L.		
JOURNAL	T-CELL MEMBRANE PROTEIN (TIRC7), PEPTIDES AND ANTIBODIES DERIVED THEREFROM AND USES THEREOF		
FEATURES	Patent: WO 9911782-A 1 11-MAR-1999;		
source	UTKU NALAN (DE); BRIGHAM & WOMENS HOSPITAL (US)		
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Best Local Similarity	99.7%	Pred. No. 0;	
Matches 2077;	Conservative	0; Mismatches	3; Indels 3; Gaps 1;
Qy	561	CTTTGTGGCAGGTGCGGTGGAGCCCCACAAAGGCCCTTGCCCTAGAGCGCTGCTCTGGAG	620
Db	392	CTTTGTGGCAGGTGCGGTGGAGCCCCACAAAGGCCCTTGCCCTAGAGCGCTGCTCTGGAG	451
Qy	621	GGCCTGCGCGGGTTCCTCATTTGCCAGCTTCAGGAGCTGGAGCAGCGCTGGAGCACCC	680
Db	452	GGCCTGCGCGGGTTCCTCATTTGCCAGCTTCAGGAGCTGGAGCAGCGCTGGAGCACCC	511
Qy	681	CGTGACGGGCGGACGACGACGCGGTGACCTTCCTCATCTCCTACTTGGGGTGAGCAGAT	740
Db	512	CGTGACGGGCGGACGACGACGCGGTGACCTTCCTCATCTCCTACTTGGGGTGAGCAGAT	571
Qy	741	CGGACAGAAGATCCGCAAGATCATCGGACTGCTTCCACATGCCACGTCTTCCCGTTTCTGCA	800
Db	572	CGGACAGAAGATCCGCAAGATCATCGGACTGCTTCCACATGCCACGTCTTCCCGTTTCTGCA	631
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Db	632	GCAGGAGGAGGCCCGGCTCGGGGCCCTTGACGACGCTGCCAACAGCAGACCCAGAGCTGCA	691
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Qy	921	GCTGCCGCCCAGGCGAGGTGCGAGTCCACAAGATGAAGCGCGGTGTA CTTGCCCTGAACCA	980
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ACCESSION AX920850
VERSION AX920850.1 GI:40214620
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 unclassified sequences.
AUTHORS Utku,N., Gullans,S.R. and Milford,E.L.
TITLE T-cell membrane protein (TIRC7), gene encoding it and antibodies
JOURNAL against it and uses thereof
PATENT Patent: EP 1350848-A 1 08-OCT-2003;
UTKU, Nalan (DE); BRIGHAM AND WOMEN'S HOSPITAL (US)
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ORIGIN

Query Match	63.9%;	Score 1687;	DB 2;	Length 2488;
Best Local Similarity	99.7%;	Pred. No. 0;		
Mismatches	0;	Conservative	3;	Indels 3; Gaps 1;
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Qy	1761	GGAGACGCTGCGCGGAGCTCACCTTCTGCTGGAGCTCTTTCGGTTACTCTGTTCTTAGT	1820
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Qy	2118	CTGGAGCTCCGATGAGGAGAAAGGAGGCGCTTGGATGATGAAGAGGAGGCGGAGCTCGT	2177
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Db	2192	GCGGCTGTGGTGTCTGCTGCCCATCTTTGCGGCTTTCGCTGATGACCGTGTATCTCT	2251
Qy	2418	GCTGGTGTGAGGAGGACTCTGAGCTTCTGCAACCGCTTGGGCTGCACTGGGTGGAAT	2477
Db	2252	GCTGGTGTGAGGAGGACTCTGAGCTTCTGCAACCGCTTGGGCTGCACTGGGTGGAAT	2311
Qy	2478	CCAGAACAGTTCCTACTCAGGCAACGGGCTCAAGCTGAGTCCCTTCACTTCCCTGCCAC	2537
Db	2312	CCAGAACAGTTCCTACTCAGGCAACGGGCTCAAGCTGAGTCCCTTCACTTCCCTGCCAC	2371
Qy	2538	AGATGACTAGGCGCCACCTGCGAGGCTCTGCAAGCTCTTCTGACCTCTGAGGCGAGGAG	2597
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QY 2598 AGGATTAAGACGCTCCGCTTGCACAAAAA 2640
Db 2432 AGGATTAAGACGCTCCGCTTGCACAAAAA 2474

RESULT 14
BD080989
LOCUS
DEFINITION Novel T cell membrane protein (TIRC7), peptide, antibody
originating therein and utilization thereof.
ACCESSION BD080989
VERSION BD080989.1 GI:22626592
KEYWORDS JP 2001514852-A/1.
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 2488)
AUTHORS Utku,N., Gullans,S.R. and Milford,E.L.
TITLE Novel T cell membrane protein (TIRC7), peptide, antibody
originating therein and utilization thereof
JOURNAL Patent: JP 2001514852-A 1 18-SEP-2001;
NALAN UTKU, BRIGHAM AND WOMEN'S HOSPITAL INC
COMMENT OS Unidentified
PN JP 2001514852-A/1
PD 18-SEP-2001
PF 28-AUG-1998 JP 2000508792
PR 29-AUG-1997 DE 137 38 710.1,12-FEB-1998 DE 298 02 653.8 PI
PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
A61P29/00
PC A61P31/00,A61P35/00,A61P37/04,A61P37/06,A61P37/08,C07K14/705,
C07K16/28,
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CC Topology: Linear;
CC Novel T cell membrane protein (TIRC7), peptide, antibody CC
originating
therein and utilization thereof
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
source
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ORIGIN
Query Match 63.98; Score 1687; DB 2; Length 2488;
Best Local Similarity 99.74; Pred. No. 0;
Matches 2077; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
QY 561 CTTTGTGGCAGGTGCGTGGAGCCCAAGGCCCTGCGCTAGAGCGCTGCTCTGGAG 620
Db 392 CTTTGTGGCAGGTGCGTGGAGCCCAAGGCCCTGCGCTAGAGCGCTGCTCTGGAG 451
QY 621 GGCCTGCGCGGTTCCTCATTCGCAAGTTCAGGAGCTGGAGCAGCCGCTGGAGCACCC 680
Db 452 GGCCTGCGCGGTTCCTCATTCGCAAGTTCAGGAGCTGGAGCAGCCGCTGGAGCACCC 511
QY 681 CGTGAGGGCGAGCCAGCCAGCTGGATGACCTTCCTCATCTCTCTAGTGGGGTGGAGCAT 740
Db 512 CGTGAGGGCGAGCCAGCCAGCTGGATGACCTTCCTCATCTCTCTAGTGGGGTGGAGCAT 571
QY 741 CGGACAGAGATCCGCAAGATCACGGACTGCTTCCACTGCGACGCTTCCTGTTCTGCA 800
Db 572 CGGACAGAGATCCGCAAGATCACGGACTGCTTCCACTGCGACGCTTCCTGTTCTGCA 631
QY 801 GCAGGAGGAGCCCGCTCGGGGCCCTGCGAGCTGTCACAGCAGCCAGGAGCTGCA 860
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QY 861 GGAGGTCTCTCGGGGAGACAGAGCGGTTCCTGAGCCAGGTGCTAGGCCGGGTGCTGAGCT 920

Db 692 GGAGGTCTCTCGGGGAGACAGAGCGGTTCCTGAGCCAGGTGCTAGGCCGGGTGCTGCAGCT 751
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Db 752 GCTGCCGCCAGGGCAGGTGCGAGTCCACAAGATGAAGGCCCGGTACCTGGCCCTGCAACCA 811
QY 981 GTGAGCGGTGAGACACAGCAAGTGCCTCATTTGCCAGGCCCTGGTGTCTCTGTGCGAGA 1040
Db 812 GTGAGCGGTGAGACACAGCAAGTGCCTCATTTGCCAGGCCCTGGTGTCTCTGTGCGAGA 871
QY 1041 CTTGCCGCCCTGCGAGGAGCCCTGCGGACAGCTCGATGAGGAGGAGGTGAGTGCCTG 1100
Db 872 CTTGCCGCCCTGCGAGGAGCCCTGCGGACAGCTCGATGAGGAGGAGGTGAGTGCCTG 931
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QY 1161 GGCGAGTTCGAGGGGATCGTGATCGCTACGGGCTGGGCGCTACAGAGAGTCAACCC 1220
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QY 1281 CCACGGGCTGCTCATGTTCTCTTCGCCCTGGCCATGCTCTTCGCGGAGAACCCAGCCGGC 1340
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Db 1172 TGTGAAAGCCGCGAGAACAGAGATCTGGGAGACTTTCTTCAGGGGCGCTACCTGCTCT 1231
QY 1401 GCTTATGGGCTGTTCTCCATCTACACCGGCTTCATCTACAGAGTGTCTCAGTCCGGC 1460
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QY 1461 CACCAGCATCTTCCCTCGGGCTGGAGTGGGCGCCATGCGCAACAGAGTCTGCTGGAG 1520
Db 1292 CACCAGCATCTTCCCTCGGGCTGGAGTGGGCGCCATGCGCAACAGAGTCTGCTGGAG 1351
QY 1521 TGATGATTCCTGGCCAGCACAGATGCTTACCTGGATCCCAACCTACCGGTGCTT 1580
Db 1352 TGATGATTCCTGGCCAGCACAGATGCTTACCTGGATCCCAACCTACCGGTGCTT 1411
QY 1581 CTTGGGACCTACCCCTTTTGGCATCGATCCTATTTGGAGCTGCTGCCAACCACTTGAG 1640
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QY 1641 CTTTCTCAACTCTCTTCAAGATGAAGATGTCCTGCATCCTCGGGGCTCGTGCACATGGCTT 1700
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QY 1701 TGGGGTGGTCTCGGAGTCTTCAACCAAGTGCATTTTGGCCAGAGGCAACCGGTGCTGCT 1760
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QY 1761 GGAAGCGCTGCGGAGCTCACCTTCTGCTGGGACTTTCGTTTACCTCGTGTCTTCTAGT 1820
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QY 1821 CATCTCAAGTGGCTGTGTGTCTGGGCTGCAGGGCGCCCTCGGCCCCAGCATCTCAT 1877
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QY 1878 CCACTTCAACAACATGTTCTTCTTCCCAAGCCCCAGCAACAGGCTGCTTACCCCCG 1937
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QY 1938 GCAGGAGGTGGTCCAGGCCAGCTGTTGCTTGGCTTGGCCATGTCATGTCCTTCTGCT 1997

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 05:24:06 ; Search time 1622 Seconds
(without alignments)
11348.173 Million cell updates/sec

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Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 1

Total number of hits satisfying chosen parameters: 10489196

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2640	100.0	2640	2 AAV04529	AAV04529 Human OC-
2	2640	100.0	2640	6 ABN86735	ABN86735 Human OC-
3	2640	100.0	2640	13 ADR44118	ADR44118 Human 116
4	2640	100.0	2640	14 ADY92605	ADY92605 Human 116
5	2640	100.0	2655	6 ABL64400	ABL64400 Stomach c
6	2640	100.0	2655	6 ABL68345	ABL68345 Kidney ca
7	2640	100.0	2655	6 ABK84337	ABK84337 Human cdn
8	2640	100.0	2655	6 ABN96866	ABN96866 Gene #336
9	2640	100.0	2655	10 ACAS6496	ACAS6496 Human sig
10	2640	100.0	2655	11 ADI31590	ADI31590 Human cdn
11	2640	100.0	2655	12 ADI56292	ADI56292 Human pol
12	2640	100.0	2655	13 ADS83657	ADS83657 Human lym
13	2142	81.1	2700	12 ADI28819	ADI28819 Human mod
14	2142	81.1	2700	12 ADP10401	ADP10401 Reference
15	2142	81.1	2700	13 ACN39267	ACN39267 Tumour-as
16	2090	79.2	2676	13 ADQ86432	ADQ86432 Human tum
17	2090	79.2	2676	13 ADQ83344	ADQ83344 Human psy
18	2046	77.5	2493	14 ADV43978	ADV43978 Human psy

19	2039	77.2	2676	12	ADQ85289	Adq85289 Human tum
20	1742	66.0	2561	12	ADH22582	Adh22582 CDNA enco
21	1687	63.9	2488	2	AAx24912	AAx24912 T-cell me
22	1670	63.3	2480	13	ACN39268	ACN39268 Tumour-as
23	1640	62.1	2762	13	ACN43472	ACn43472 Human dia
24	1636	62.0	2488	2	AAx24913	AAx24913 T-cell me
25	1449	54.9	1845	14	ADV43979	Adv43979 Human psy
26	1304	49.4	3104	6	ABQ54601	Abq54601 Human ova
27	612	23.2	612	10	ADD27224	Add27224 Human adi
28	442	16.7	493	6	ABL68797	AbL68797 Kidney ca
29	442	16.7	493	6	ABL82832	AbL82832 Human ova
30	442	16.7	493	6	ABN94793	ABn94793 Gene #129
31	373	14.1	373	10	ADD27651	Add27651 Human adi
32	350	13.3	425	9	ACH49178	Ach49178 Human tes
33	302	11.4	434	6	ABL81465	AbL81465 Human ova
34	288	10.9	414	9	ACH29799	Ach29799 Human tes
35	238	9.0	238	4	AAI29251	Aai29251 Colon tum
36	238	9.0	238	8	ABZ33437	Abz33437 Human col
37	221	8.4	15941	10	ADC64674	Adc64674 Human TCI
38	179	6.8	189	12	ACH92650	Ach92650 Human gen
39	179	6.8	532	12	ACH78950	Ach78950 Human gen
40	179	6.8	3269	4	AAK69047	Aak69047 Human imm
41	176	6.7	570	6	ABL80219	AbL80219 Human ova
42	166	6.3	419	6	ABL81517	AbL81517 Human ova
43	138	5.2	561	6	ABL82854	AbL82854 Human ova
44	124	4.7	568	13	ADU14483	Adu14483 Solid tum
45	110	4.2	151	2	AAQ72536	Aaq72536 Osteoclas

ALIGNMENTS

RESULT 1

AAV04529 standard; cDNA; 2640 BP.

XX AAV04529;
AC AAV04529;

XX 02-JUL-1998 (first entry)

XX Human OC-116 kDa cDNA sequence.

XX Osteoclast; human; OC-116 kDa; screening; cell surface marker; probe; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 58..2523

XX /*tag= a

XX /product= "OC-116 kDa"

XX /note= "no stop codon given"

XX WO9803651-AL.

XX 29-JAN-1998.

XX 10-JUL-1997; 97WO-US012569.

XX 19-JUL-1996; 96US-00684932.

XX (FORS-) FORSYTH DENTAL INFIRMARY FOR CHILDREN.

XX Stashenko P, Li Y, Wucherpfennig AL;

XX WPI; 1998-120776/11.

XX P-PSDB; AAW41943.

XX Osteoclast specific or related DNA sequence - useful as probe to screen genomic DNA or cDNA library, or as osteoclast cell surface marker.

XX Example 8; Page 58-61; 75pp; English.

XX The present sequence represents the human OC-116 kDa cDNA sequence which

Db	1381	AGGGCGCGCTACCTGCTCCTGCTTATGGGCGCTGTTCTTCCTCATCTATACACCGGGCTTCATCTAC	1444
Qy	1441	AACGAGTGCTTCAGTTCGCGCCACACGACATCTTCCCTCTCGGCTGGAGTGTGGCGCCCATG	1500
Db	1441	AACGAGTGTTCAGTTCGCGCCACACGACATCTTCCCTCGGCTGGAGTGTGGCGCCCATG	1500
Qy	1501	GCCAAACAGTCTGGCTCGAGTGATGCAATTCCTGGCGCCAGCACAGATGCTTACCCCTGGAT	1560
Db	1501	GCCAAACAGTCTGGCTCGAGTGATGCAATTCCTGGCGCCAGCACAGATGCTTACCCCTGGAT	1560
Qy	1561	CCCAACGTCAACGGTGTCTTCTCGGACCCCTACCCCTTGGCATCGATCTCTATTGTGGAGC	1620
Db	1561	CCCAACGTCAACGGTGTCTTCTCGGACCCCTACCCCTTGGCATCGATCTCTATTGTGGAGC	1620
Qy	1621	CTGGCTGCCAACACATTTGAGCTTCTCTCAATCTTCAAGATGAAGATGTCCGTCACTCTTG	1680
Db	1621	CTGGCTGCCAACACATTTGAGCTTCTCTCAATCTTCAAGATGAAGATGTCCGTCACTCTTG	1680
Qy	1681	GGCGTCGTGCACATGGCTTTGGGGTGGTCTCTCGGAGTCTTCAACACAGCTGCATTTGGC	1740
Db	1681	GGCGTCGTGCACATGGCTTTGGGGTGGTCTCTCGGAGTCTTCAACACAGCTGCATTTGGC	1740
Qy	1741	CAGAGGCAACGGCTGTCTGTGGAGACGCTGCGGAGTCACTTCCTGTCTGGAGCTCTTTC	1800
Db	1741	CAGAGGCAACGGCTGTCTGTGGAGACGCTGCGGAGTCACTTCCTGTCTGGAGCTCTTTC	1800
Qy	1801	GGTTACCTCGTGTCTTAGTGCATCTAACAAGTGGCTGTGCTCTGGGCTGCCAGGCGCGCC	1860
Db	1801	GGTTACCTCGTGTCTTAGTGCATCTAACAAGTGGCTGTGCTCTGGGCTGCCAGGCGCGCC	1860
Qy	1861	TCGCCCAGCATCTCATCCACTTCAACACATGTTCTCTTCTCCACAGCCCCAGCAAC	1920
Db	1861	TCGCCCAGCATCTCATCCACTTCAACACATGTTCTCTTCTCCACAGCCCCAGCAAC	1920
Qy	1921	AGGCTGTCTACCCCGGCGAGGAGTGGTCAGGCGCACGCTGTGTGTCCTGTGGCTTGGCC	1980
Db	1921	AGGCTGTCTACCCCGGCGAGGAGTGGTCAGGCGCACGCTGTGTGTCCTGTGGCTTGGCC	1980
Qy	1981	ATGCTGCCCATCTCTGTCTTGGCACACCCCTGCACCTGTGTGCACGCGCACCGCGCGCGC	2040
Db	1981	ATGCTGCCCATCTCTGTCTTGGCACACCCCTGCACCTGTGTGCACGCGCACCGCGCGCGC	2040
Qy	2041	CTGCGGAGGAGCCCGCTGACCGACAGGAGAAACAAAGCCGGTGTCTGGACCTGCGCT	2100
Db	2041	CTGCGGAGGAGCCCGCTGACCGACAGGAGGAAACAAAGCCGGTGTCTGGACCTGCGCT	2100
Qy	2101	GACGCATCTGTAATGCTGGAGCTCCGATGAGGAAAGACAGGGGCGCTGGATGATGAA	2160
Db	2101	GACGCATCTGTAATGCTGGAGCTCCGATGAGGAAAGACAGGGGCGCTGGATGATGAA	2160
Qy	2161	GAGGAGCCGAGTCTGTCCTCCGAGGTGCTCATGCAACGAGGCATCCACACCATCGAG	2220
Db	2161	GAGGAGCCGAGTCTGTCCTCCGAGGTGCTCATGCAACGAGGCATCCACACCATCGAG	2220
Qy	2221	TTCTGCTGGGCTGGCTCTCCACACCGCTCTTACCTGGCGCTGTGGGCGCTGAGGCTG	2280
Db	2221	TTCTGCTGGGCTGGCTCTCCACACCGCTCTTACCTGGCGCTGTGGGCGCTGAGGCTG	2280
Qy	2281	GCCACGCGCAGCTGTCTGGGCTGTGGGCGATGGTGTATGCGCATAGCGCTGGGCGCTG	2340
Db	2281	GCCACGCGCAGCTGTCTGGGCTGTGGGCGATGGTGTATGCGCATAGCGCTGGGCGCTG	2340
Qy	2341	GGCCGGAGGTGGCGTGGCGGTGTGGTGTCTGGTCCCGCATCTTTTGCCGCTTTTGCCGTG	2400
Db	2341	GGCCGGAGGTGGCGTGGCGGTGTGGTGTCTGGTCCCGCATCTTTTGCCGCTTTTGCCGTG	2400
Qy	2401	ATGACCTGGGCTATCCCTGCTGTGATGGAGGACCTCTCAGCTTCTGCAAGCCCTGCGG	2460
Db	2401	ATGACCTGGGCTATCCCTGCTGTGATGGAGGACCTCTCAGCTTCTGCAAGCCCTGCGG	2460
Qy	2461	CTGCATCTGGGTGGAAATTCCAGAACAAAGTTCTTACTCAGGCGACGGGCTACAAGCTGAGTCCC	2520
Db	2461	CTGCATCTGGGTGGAAATTCCAGAACAAAGTTCTTACTCAGGCGACGGGCTACAAGCTGAGTCCC	2520

QY	2521	TTACCTTCGGTGGCCACAGATGACTAGGGCCCACTGCAGGTCTCGCCAGACCTCCTTCCT	2580			
Db	2521	TTACCTTCGGTGGCCACAGATGACTAGGGCCCACTGCAGGTCTCGCCAGACCTCCTTCCT	2580			
QY	2581	GACCTCTGAGGCAGGAGGAGGAAATAAGACGGTCCGCCCTGGCAAAAAAAAAAAAAA	2640			
Db	2581	GACCTCTGAGGCAGGAGGAGGAAATAAGACGGTCCGCCCTGGCAAAAAAAAAAAAAA	2640			
RESULT 4						
ADY92605						
ID	ADY92605 standard; cDNA; 2640 BP.					
XX						
AC	ADY92605;					
XX						
DT	02-JUN-2005 (first entry)					
XX						
DE	Human 116 kD osteoclast proton pump OC-116 subunit cDNA.					
XX						
KW	cloning; osteopathic; antiarthritic; gene therapy;					
XX						
KW	osteoclast proton pump; bone disease; osteoporosis; osteoarthritis; gene;					
XX						
OS	Homo sapiens.					
XX						
FH	Key	Location/Qualifiers				
FT	CDS	58..2547				
FT	/*tag= a					
FT	/product= "116 kD osteoclast proton pump subunit"					
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FN	US2005064448-A1.					
XX						
PD	24-MAR-2005.					
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PF	20-FEB-2004; 2004US-00783519.					
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PR	22-FEB-1996; 96US-00605378.					
PR	18-JUL-2000; 2000US-00618304.					
XX						
PA	(STAS/) STASHENKO P.					
PA	(LIYY/) LI Y.					
PI	Stashenko P, Li Y;					
XX						
DR	WPI; 2005-241271/25.					
DR	P-PSDB; ADY92606.					
PT	New isolated genes and encoded human 116-kDa osteoclast proton pump					
PT	subunit polypeptides useful for treating bone mass disorders associated					
PT	with aberrant rate of bone degradation (e.g. osteoporosis or					
PT	osteoarthritis).					
XX						
PS	Claim 3; SEQ ID NO 1; 17pp; English.					
XX						
CC	The invention relates to an isolated gene encoding a polypeptide which is					
CC	a human 116-KD osteoclast proton pump subunit. The composition and					
CC	methods are useful for treating bone mass disorders characterized by					
CC	aberrant rate of bone degradation (e.g. osteoporosis or osteoarthritis).					
CC	The protein may also be used as cell surface markers for osteoclasts.					
CC	This sequence corresponds to the cDNA encoding the novel proton pump					
CC	subunit. The cDNA was isolated by differential screening of a human					
CC	osteoclastoma cDNA library.					
XX						
SQ	Sequence 2640 BP; 445 A; 885 C; 824 G; 486 T; 0 U; 0 Other;					
Query Match 100.0%; Score 2640; DB 14; Length 2640;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	CGGCGTGGCGGACGGGCAGCAGCAGCGGAGCGCGCGCAGCACACCCGGGACCATG	60			
Db	1	CGGCGTGGCGGACGGGCAGCAGCAGCGGAGCGCGCGCAGCACACCCGGGACCATG	60			

QY 61 GGCCTCCATGTTCCGGAGCGAGGAGGTGGCCCTGGTCCAGCTCTTTCTGCCCCACAGCGGCT 120
Db 61 GGCCTCCATGTTCCGGAGCGAGGAGGTGGCCCTGGTCCAGCTCTTTCTGCCCCACAGCGGCT 120
QY 121 GCCTACACCTCGGTGAGTCGGCTGGGCGAGCTGGGCCCTCGTGGAGTTCAGAGACCTCAAC 180
Db 121 GCCTACACCTCGGTGAGTCGGCTGGGCGAGCTGGGCCCTCGTGGAGTTCAGAGACCTCAAC 180
QY 181 GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGTGTTGATGTTTGGCGCTGTGAGAGCTG 240
Db 181 GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGTGTTGATGTTTGGCGCTGTGAGAGCTG 240
QY 241 GAGAGACCTTCACTTCTTCAGAGAGAGGTGGCGGGCTGGGCTGGTCTGCCCCCG 300
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Db 301 CCAAGAGGGAGGCTGCGGGCACCCCCACCCCGGACCTGCTGCGCATCCAGAGAGAGACG 360
QY 361 GAGCGCTGGCCCAAGAGCTCGGGATGTGCGGGCAACCAAGCAGGCCCTGCGGGCCCGAG 420
Db 361 GAGCGCTGGCCCAAGAGCTCGGGATGTGCGGGCAACCAAGCAGGCCCTGCGGGCCCGAG 420
QY 421 CTGCACAGCTGCAGCTCCAGCGCCGCTGTACGCCAGGGCCATGAACCTCAGCTGGCA 480
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QY 541 CACAGGACCTGAGGGTCAACTTTGTGGAGGTGCGGTGGAGGCCCAAGGCCCTGCCC 600
Db 541 CACAGGACCTGAGGGTCAACTTTGTGGAGGTGCGGTGGAGGCCCAAGGCCCTGCCC 600
QY 601 CTAGAGCGCTGCTCGAGGGCTGCGGGCTTCTCATTTGCGAGCTTCAGGAGCTG 660
Db 601 CTAGAGCGCTGCTCGAGGGCTGCGGGCTTCTCATTTGCGAGCTTCAGGAGCTG 660
QY 661 GAGCAGCGCTGGAGCACCCCGTGCACGGCGGAGCAGCCAGCTGGATGACCTTCTCATC 720
Db 661 GAGCAGCGCTGGAGCACCCCGTGCACGGCGGAGCAGCCAGCTGGATGACCTTCTCATC 720
QY 721 TCCTACTGGGGTGAGCAGATCGGACAGAGATCCGCAAGATCACGGACTGCTTCACTGC 780
Db 721 TCCTACTGGGGTGAGCAGATCGGACAGAGATCCGCAAGATCACGGACTGCTTCACTGC 780
QY 781 CAGCTCTTCCGTTTCTGACAGCAGGAGAGGCGCCGCTCGGGCCCTGCGAGCAGCTGAA 840
Db 781 CAGCTCTTCCGTTTCTGACAGCAGGAGAGGCGCCGCTCGGGCCCTGCGAGCAGCTGAA 840
QY 841 CAGCAGAGCAGGAGCTGACAGGAGTCTCGGGGAGACAGAGCGGTTCTTGAGCCAGGTG 900
Db 841 CAGCAGAGCAGGAGCTGACAGGAGTCTCGGGGAGACAGAGCGGTTCTTGAGCCAGGTG 900
QY 901 CTAGGCGGGTGCTGACAGCTGCTGCGCCAGGGCAGGTGACAGTCCCAAGATGAAGGCC 960
Db 901 CTAGGCGGGTGCTGACAGCTGCTGCGCCAGGGCAGGTGACAGTCCCAAGATGAAGGCC 960
QY 961 GTGTACTGGCCCTGAACAGTGCAGCGTGAAGCAACAGCAAGTGCCTCATTTGCCGAG 1020
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QY 1261 GTGATGTTGCGGGAGTGGGCCACGGGCTGCTCATGTTTCTTCTGCGCCCTGCCCATGGTC 1320
Db 1261 GTGATGTTGCGGGAGTGGGCCACGGGCTGCTCATGTTTCTTCTGCGCCCTGCCCATGGTC 1320
QY 1321 CTTGCGGAGAACCCAGCGGCTGTGAAGCGCGCAGAACAGAGATGTGCAGACTTCTTC 1380
Db 1321 CTTGCGGAGAACCCAGCGGCTGTGAAGCGCGCAGAACAGAGATGTGCAGACTTCTTC 1380
QY 1381 AGGGCGCGCTACCTGCTCTCTTATGGGCTGTTCCTCATCTACACCGGCTTCATCTAC 1440
Db 1381 AGGGCGCGCTACCTGCTCTCTTATGGGCTGTTCCTCATCTACACCGGCTTCATCTAC 1440
QY 1441 AACGAGTGTTCAGTTCGCGGCCACGAGCATTTTCCCTCGGGCTGGAGTGTGGCCCATG 1500
Db 1441 AACGAGTGTTCAGTTCGCGGCCACGAGCATTTTCCCTCGGGCTGGAGTGTGGCCCATG 1500
QY 1501 GCCAACAGCTGTGCTGAGTGTGATGCTTCTGCGCCAGCACAGATGCTTACCTGAT 1560
Db 1501 GCCAACAGCTGTGCTGAGTGTGATGCTTCTGCGCCAGCACAGATGCTTACCTGAT 1560
QY 1561 CCCAAAGCTACCGGTGTCTTCTGGGACCTTACCCCTTTGGGATCGATCTATTTGGAGC 1620
Db 1561 CCCAAAGCTACCGGTGTCTTCTGGGACCTTACCCCTTTGGGATCGATCTATTTGGAGC 1620
QY 1621 CTGCTGCCAACCACTTGTAGCTTCTCAACTCTTCAAGATGAAGATGTCCGCTCATCTG 1680
Db 1621 CTGCTGCCAACCACTTGTAGCTTCTCAACTCTTCAAGATGAAGATGTCCGCTCATCTG 1680
QY 1681 GCGGTCGTGCACATGGGCTTTGGGGTGGTCTCGGAGTCTTCAACCAAGCTGCTTGGC 1740
Db 1681 GCGGTCGTGCACATGGGCTTTGGGGTGGTCTCGGAGTCTTCAACCAAGCTGCTTGGC 1740
QY 1741 CAGAGGACCGGCTGTGCTGGAGCGCTGCGGAGCTCACTTCTGCTGGGACTCTTC 1800
Db 1741 CAGAGGACCGGCTGTGCTGGAGCGCTGCGGAGCTCACTTCTGCTGGGACTCTTC 1800
QY 1801 GGTTCACCTCGTGTTCCTAGTCACTACAAGTGGTGTGTGCTGGGCTGCGAGGCGGCC 1860
Db 1801 GGTTCACCTCGTGTTCCTAGTCACTACAAGTGGTGTGTGCTGGGCTGCGAGGCGGCC 1860
QY 1861 TCGCCAGCATCTCATCTCACTTCAACATGTTCTTCTTCTCCCAAGCCCCAGCAAC 1920
Db 1861 TCGCCAGCATCTCATCTCACTTCAACATGTTCTTCTTCTCCCAAGCCCCAGCAAC 1920
QY 1921 AGGCTGCTTACCCCGGCGAGGAGTGTGTCAGGCGCAGCTGTGTGCTGCGGCTTGGCC 1980
Db 1921 AGGCTGCTTACCCCGGCGAGGAGTGTGTCAGGCGCAGCTGTGTGCTGCGGCTTGGCC 1980
QY 1981 ATGCTGCCCATCTGCTGTGGCAACCCCTGCACTGTGTGCAACCGGCGGCTGCTGGACTGCT 2040
Db 1981 ATGCTGCCCATCTGCTGTGGCAACCCCTGCACTGTGTGCAACCGGCGGCTGCTGGACTGCT 2040
QY 2041 CTTGCGAGGAGGCGCGCTGACCCGACAGAGAGAAACAAAGGCGGGTGTGCTGGACTGCT 2100
Db 2041 CTTGCGAGGAGGCGCGCTGACCCGACAGAGAGAAACAAAGGCGGGTGTGCTGGACTGCT 2100
QY 2101 GAGCATCTGTGAATGCTGAGCTCCGAGTCCGAGTGAAGAAAGCAGGGGCTGAGATGA 2160
Db 2101 GAGCATCTGTGAATGCTGAGCTCCGAGTCCGAGTGAAGAAAGCAGGGGCTGAGATGA 2160
QY 2161 GAGGAGGCGGAGCTGCTCCCTCCGAGGCTGTCTATGCAACAGGCGCATCCACACCATCGAG 2220
Db 2161 GAGGAGGCGGAGCTGCTCCCTCCGAGGCTGTCTATGCAACAGGCGCATCCACACCATCGAG 2220
QY 2221 TTCTGCTGGGCTGCGTCTCCAAACACCGGCTCTCTA CTTGCGGCTGTGCGGCGCTGAGCGCTG 2280

QY	241	GAGAGACCTTTCACCTTCTCTGCAGAGAGAGGTGCGCGGGCTGGGCTGGTCTGTCGCCCG	300
DB	241	GAGAGACCTTTCACCTTCTCTGCAGAGAGAGGTGCGCGGGCTGGGCTGGTCTGTCGCCCG	300
QY	301	CCAAAGGGAGGCTGCCGGCACCCACCCCGGGACCTGCTGCGCATCCAGAGAGAGACG	360
DB	301	CCAAAGGGAGGCTGCCGGCACCCCAACCCCGGACCTGCTGCGCATCCAGAGAGAGACG	360
QY	361	GAGCGCTTGCCCAAGAGCTGGGGATGTGGGGGCAACCAAGCAGGCCCTCGGGGCCAG	420
DB	361	GAGCGCTTGCCCAAGAGCTGGGGATGTGGGGGCAACCAAGCAGGCCCTCGGGGCCAG	420
QY	421	CTGCACCAAGCTGACGCTCCAGCGCGCTGTACGCCAGGGGCATGAACCTTAGCTGGCA	480
DB	421	CTGCACCAAGCTGACGCTCCAGCGCGCTGTACGCCAGGGGCATGAACCTTAGCTGGCA	480
QY	481	GCCGCCACACAGATGGGGCCTCAGAGAGAGCGCCCTGCTCCAGGCCCGCGGGGGCGG	540
DB	481	GCCGCCACACAGATGGGGCCTCAGAGAGAGCGCCCTGCTCCAGGCCCGCGGGGGCGG	540
QY	541	CACAGAGACTGAGGGTCAACTTTGTGGCAGGTGCCGTGGAGCCCCCAAGGCCCTTGCC	600
DB	541	CACCAGGACCTGAGGGTCAACTTTGTGGCAGGTGCCGTGGAGCCCCCAAGGCCCTTGCC	600
QY	601	CTAGAGCGCTGCTCTGAGAGGCGCTGCGCGGCTTCCTCATTGCAGCTTCAGGAGCTG	660
DB	601	CTAGAGCGCTGCTCTGAGAGGCGCTGCGCGGCTTCCTCATTGCAGCTTCAGGAGCTG	660
QY	661	GAGCAGCGCTGAGACACCCCGTGCACGGGCGAGCCAGCCACGTGGATGACCTTCTCATC	720
DB	661	GAGCAGCGCTGAGACACCCCGTGCACGGGCGAGCCAGCCACGTGGATGACCTTCTCATC	720
QY	721	TCCTACTGGGTGAGCAGATCGGACAGAAGATCCGCAAGATCACGGACTGCTTCCACTGC	780
DB	721	TCCTACTGGGTGAGCAGATCGGACAGAAGATCCGCAAGATCACGGACTGCTTCCACTGC	780
QY	781	CACGTCCTCCGTTTCTGCACAGAGAGAGAGCCCGCTCGGGGCGCTGCAGCAGCTGCMA	840
DB	781	CACGTCCTCCGTTTCTGCACAGAGAGAGAGCCCGCTCGGGGCGCTGCAGCAGCTGCMA	840
QY	841	CAGCAGCCAGGAGCTGCAGGAGTCTCTCGGGGAGACAGAGCGGTTCTCAGCAGAGTG	900
DB	841	CAGCAGCCAGGAGCTGCAGGAGTCTCTCGGGGAGACAGAGCGGTTCTCAGCAGAGTG	900
QY	901	CTAGCCGGGTGCTGCAGCTGTCGCGCAAGGCAAGGTGCAGGTCCACAAGATGAAGGCC	960
DB	901	CTAGCCGGGTGCTGCAGCTGTCGCGCAAGGCAAGGTGCAGGTCCACAAGATGAAGGCC	960
QY	961	GTGTACTGGCCCTGAAACCAAGTCAGCTGAGCACCAGCACAGTGCCTCATTTGCCGAG	1020
DB	961	GTGTACTGGCCCTGAAACCAAGTCAGCTGAGCACCAGCACAGTGCCTCATTTGCCGAG	1020
QY	1021	GCCTGGTGCTCTGTGCGAGACCTGCCCCCTGCAGGAGGCCCTTCGCGGACAGCTCGATG	1080
DB	1021	GCCTGGTGCTCTGTGCGAGACCTGCCCCCTGCAGGAGGCCCTTCGCGGACAGCTCGATG	1080
QY	1081	GAGAGGGAGTGAGTGGCGGTCAACCGCATCCCTGCGGGGACATGCCCCCACAATC	1140
DB	1081	GAGAGGGAGTGAGTGGCGGTCAACCGCATCCCTGCGGGGACATGCCCCCACAATC	1140
QY	1141	ATCCGCAACCAACCGCTTACCGGCCAGCTTCAGGGCATCGTGGATCGCTACGGCGTGGCC	1200
DB	1141	ATCCGCAACCAACCGCTTACCGGCCAGCTTCAGGGCATCGTGGATCGCTACGGCGTGGCC	1200
QY	1201	CGCTACCAAGAGGTCAACCCCGCTCCCTTACACCATCATCTTTCCTCTCTTTTGCT	1260
DB	1201	CGCTACCAAGAGGTCAACCCCGCTCCCTTACACCATCATCTTTCCTCTCTTTTGCT	1260
QY	1261	GTGATGTCGGGGATGTGGGCCACGGGTGCTCATGTTCTCTTTGCGCCATGGCT	1320
DB	1261	GTGATGTCGGGGATGTGGGCCACGGGTGCTCATGTTCTCTTTGCGCCATGGCT	1320

QY	1321	CTTGGCGAGAACCGACGGCTGTGAAGCCGCGCAGAAACGAGATCTGGCAGACTTTCTTC	1380
DB	1321	CTTGGCGAGAACCGACGGCTGTGAAGCCGCGCAGAAACGAGATCTGGCAGACTTTCTTC	1380
QY	1381	AGGGGCGCTACCTGCTCCTGCTTATGGGCGTGTCTCCATCTACACGGCTTCATCTAC	1440
DB	1381	AGGGGCGCTACCTGCTCCTGCTTATGGGCGTGTCTCCATCTACACGGCTTCATCTAC	1440
QY	1441	AACGAGTGTCTCAGTTCGCGCCACACGACATCTCCCTCGGGCTGAGATGTGGCCGCCATG	1500
DB	1441	AACGAGTGTCTCAGTTCGCGCCACACGACATCTCCCTCGGGCTGAGATGTGGCCGCCATG	1500
QY	1501	GCCAACAGTCTGGCTGGAGTATGCAATTCCTGGGCCAGACACGATGCTTACCTTGAT	1560
DB	1501	GCCAACAGTCTGGCTGGAGTATGCAATTCCTGGGCCAGACACGATGCTTACCTTGAT	1560
QY	1561	CCCAACGTCAACGGTGTCTTCCTGGGACCTTACCCTTTGGCATTCGATCTATTTTGGAGC	1620
DB	1561	CCCAACGTCAACGGTGTCTTCCTGGGACCTTACCCTTTGGCATTCGATCTATTTTGGAGC	1620
QY	1621	CTGGCTGCCAACCACTTGAGCTTCTCAACTCCTTCAAGATGAAGATGTCGTCATCCTG	1680
DB	1621	CTGGCTGCCAACCACTTGAGCTTCTCAACTCCTTCAAGATGAAGATGTCGTCATCCTG	1680
QY	1681	GGGTCGTGGACATATGGCTTTTGGGTGGTCTCTGGAGCTTTCAAACAGTGCACTTTGGC	1740
DB	1681	GGGTCGTGGACATATGGCTTTTGGGTGGTCTCTGGAGCTTTCAAACAGTGCACTTTGGC	1740
QY	1741	CAGAGCACGGCTGTCTGGAGACGCTGCCGGAGCTCACTTCCTGCTGGGACTCTTC	1800
DB	1741	CAGAGCACGGCTGTCTGGAGACGCTGCCGGAGCTCACTTCCTGCTGGGACTCTTC	1800
QY	1801	GGTTACTCTGTTTCTAGTCACTTCAACAGTGGCTGTGTCTGGGCTGCCAGGGCCGCC	1860
DB	1801	GGTTACTCTGTTTCTAGTCACTTCAACAGTGGCTGTGTCTGGGCTGCCAGGGCCGCC	1860
QY	1861	TCGCCAGCATCTCATCCACTTCAACAATGTTCTTCTCCACAGCCACGACCAAC	1920
DB	1861	TCGCCAGCATCTCATCCACTTCAACAATGTTCTTCTCCACAGCCACGACCAAC	1920
QY	1921	AGGCTGCTCTACCCCGGAGGAGTGTCCAGGCCACGTGGTGGTCTGGCCTTGCC	1980
DB	1921	AGGCTGCTCTACCCCGGAGGAGTGTCCAGGCCACGTGGTGGTCTGGCCTTGCC	1980
QY	1981	ATGGTGCCCATCTGCTGTGGCAACCCCTGCACCTGTGCACCGCCACCGCGCGCC	2040
DB	1981	ATGGTGCCCATCTGCTGTGGCAACCCCTGCACCTGTGCACCGCCACCGCGCGCC	2040
QY	2041	CTGGGAGAGCCCGCTCACGACAGGAGGAAACAAAGCCCGGTTGTGGACCTGCCT	2100
DB	2041	CTGGGAGAGCCCGCTCACGACAGGAGGAAACAAAGCCCGGTTGTGGACCTGCCT	2100
QY	2101	GACGCATCTGTGAATGGCTGGAGCTCCGATAGAGAAAGGAGGGGGCTTGATGATGA	2160
DB	2101	GACGCATCTGTGAATGGCTGGAGCTCCGATAGAGAAAGGAGGGGGCTTGATGATGA	2160
QY	2161	GAGGAGGCGAGCTGCTGCCCTCCGAGGTGCTCATGCACAGGCCATCCACACCATCGAG	2220
DB	2161	GAGGAGGCGAGCTGCTGCCCTCCGAGGTGCTCATGCACAGGCCATCCACACCATCGAG	2220
QY	2221	TTCTGCTGGGCTGCTCTCAACACCGCTCTACCTGCGCTGTGGGGCTTGAGCCTG	2280
DB	2221	TTCTGCTGGGCTGCTCTCAACACCGCTCTACCTGCGCTGTGGGGCTTGAGCCTG	2280
QY	2281	GCCACAGCCAGCTGTCCGAGTTCTGTGGGCCATGTTGATGCGCATAGGCTCGGGCTG	2340
DB	2281	GCCACAGCCAGCTGTCCGAGTTCTGTGGGCCATGTTGATGCGCATAGGCTCGGGCTG	2340
QY	2341	GSCCGGGAGGTGGGGCTGGCGTGTGGTCTGGTCCCATCTTTGGCGCTTTGGCGTG	2400
DB	2341	GSCCGGGAGGTGGGGCTGGCGTGTGGTCTGGTCCCATCTTTGGCGCTTTGGCGTG	2400
QY	2401	ATGACCGTGGCTATCTCTGCTGGTGAATGGAGGACTCTCAGCCTTCTGGCAGCCCTGGG	2460

Qy	901	CTAGGCCGGGTGCTGCAGCTGCTGCCGCCACGGCAGGTGCAGGTGCCACAAGATGAAGCC	960
Db	901		
Qy	901	CTAGGCCGGGTGCTGCAGCTGCTGCCGCCACGGCAGGTGCAGGTGCCACAAGATGAAGCC	960
Db	901		
Qy	961	GTGTACCTGGCCCTGAAACAGTGCAGCTGAGACCAACGCAAGTGCCTCATTTGCCGAG	1020
Db	961		
Qy	961	GTGTACCTGGCCCTGAAACAGTGCAGCTGAGACCAACGCAAGTGCCTCATTTGCCGAG	1020
Db	961		
Qy	1021	GCCTGGTGCTCTGTGTCGAGACCTTGCCTGCCCTGACGAGGGCCCTGCGGACAGCTCGATG	1080
Db	1021		
Qy	1021	GCCTGGTGCTCTGTGTCGAGACCTTGCCTGCCCTGACGAGGGCCCTGCGGACAGCTCGATG	1080
Db	1021		
Qy	1081	GAGGAGGAGTGAAGTGCCTGGCTTCAACGGCTCACCGCATCCCTTCCCGGACATGCCCCCACATC	1140
Db	1081		
Qy	1081	GAGGAGGAGTGAAGTGCCTGGCTTCAACGGCTCACCGCATCCCTTCCCGGACATGCCCCCACATC	1140
Db	1081		
Qy	1141	ATCCGCACAAACCGCTTCAACGGCCAGCTTCCAGGGCATCGTGGATCGTACGGCGTGGGC	1200
Db	1141		
Qy	1141	ATCCGCACAAACCGCTTCAACGGCCAGCTTCCAGGGCATCGTGGATCGTACGGCGTGGGC	1200
Db	1141		
Qy	1201	CGCTACCAAGGAGTCAACCCCGCTCCCTTACACCATCATCACTTCCCTTCTCTTTGCT	1260
Db	1201		
Qy	1201	CGCTACCAAGGAGTCAACCCCGCTCCCTTACACCATCATCACTTCCCTTCTCTTTGCT	1260
Db	1201		
Qy	1261	GTGATGTTCCGGGATGTGGGCCACCGGGCTGCTCATGTTCTTCTTCCCTTGGCCATGGTC	1320
Db	1261		
Qy	1261	GTGATGTTCCGGGATGTGGGCCACCGGGCTGCTCATGTTCTTCTTCCCTTGGCCATGGTC	1320
Db	1261		
Qy	1321	CTTCGGGAGAACCGACCGGCTGTGAAGCGCGCAGAACAGAGATCTGGCAGACTTCTTC	1380
Db	1321		
Qy	1321	CTTCGGGAGAACCGACCGGCTGTGAAGCGCGCAGAACAGAGATCTGGCAGACTTCTTC	1380
Db	1321		
Qy	1381	AGGGCCCGCTACCTGCTCCTGCTTATGGGCTGTTCCTCATCTACACGGCTCATCTAC	1440
Db	1381		
Qy	1381	AGGGCCCGCTACCTGCTCCTGCTTATGGGCTGTTCCTCATCTACACGGCTCATCTAC	1440
Db	1381		
Qy	1441	AACGAGTGTCTTCAGTGCGGCCACACAGCATCTTCCCTCGGGCTGGAGTGGCGCCCATG	1500
Db	1441		
Qy	1441	AACGAGTGTCTTCAGTGCGGCCACACAGCATCTTCCCTCGGGCTGGAGTGGCGCCCATG	1500
Db	1441		
Qy	1501	GCCAAACAGTCTGGCTGGAGTGATGTCATCTCTGCGCCACGACAGATGCTTACCTGGAT	1560
Db	1501		
Qy	1501	GCCAAACAGTCTGGCTGGAGTGATGTCATCTCTGCGCCACGACAGATGCTTACCTGGAT	1560
Db	1501		
Qy	1561	CCCAAAGTACCGGTGCTTCTCGGGACCTTACCCCTTGGCATCGATCTTATTTGGAGC	1620
Db	1561		
Qy	1561	CCCAAAGTACCGGTGCTTCTCGGGACCTTACCCCTTGGCATCGATCTTATTTGGAGC	1620
Db	1561		
Qy	1621	CTGGCTGCCAACCACTTTGAGCTTCTTCAACTCTTCAAGATGAAGATGTCGTCATCTTG	1680
Db	1621		
Qy	1621	CTGGCTGCCAACCACTTTGAGCTTCTTCAACTCTTCAAGATGAAGATGTCGTCATCTTG	1680
Db	1621		
Qy	1681	GGCGTCTGTCACATGGCCCTTTGGGGTGGTCTCGGAGTCTTCAAACAGTGGCTTGGC	1740
Db	1681		
Qy	1681	GGCGTCTGTCACATGGCCCTTTGGGGTGGTCTCGGAGTCTTCAAACAGTGGCTTGGC	1740
Db	1681		
Qy	1741	CAGAGGACACCGGCTGCTGGAGACGCTGCGGAGCTCACTTCTGCTGGGACTTCTTC	1800
Db	1741		
Qy	1741	CAGAGGACACCGGCTGCTGGAGACGCTGCGGAGCTCACTTCTGCTGGGACTTCTTC	1800
Db	1741		
Qy	1801	GTTTAACTCTGTGTTCTTAGTCACTTCAAGTGGCTGTGTCTGGGCTGCCAGGGCGGCC	1860
Db	1801		
Qy	1801	GTTTAACTCTGTGTTCTTAGTCACTTCAAGTGGCTGTGTCTGGGCTGCCAGGGCGGCC	1860
Db	1801		
Qy	1861	TCGCCACGATCTCATCTTCACTTCAACATGTTCTTCTTCTCCACAGCCCCAGCAAC	1920
Db	1861		
Qy	1861	TCGCCACGATCTCATCTTCACTTCAACATGTTCTTCTTCTCCACAGCCCCAGCAAC	1920
Db	1861		
Qy	1921	AGGCTGCTTACCCCCGGCAGGAGTGGTCCAGGCCACGCTGGTGGTCTTGGCTTGGCC	1980
Db	1921		
Qy	1921	AGGCTGCTTACCCCCGGCAGGAGTGGTCCAGGCCACGCTGGTGGTCTTGGCTTGGCC	1980
Db	1921		

RECIT E O

ABN96866
917053

ABN96866
ID ABN96866 standard: DNA: 2655 BP.

XX

AC ABN96866;

XX

DT 13-AUG-2002 (first entry)

[illegible]

DE
XX
GENE #3304 USED TO DIAGNOSE LIVER CANCER.

Gene: liver cancer: ds: hepatocellular carcinoma: hepatotropic:

KW metastatic 1

KW disease prog

XX

OS Homo sapiens.

2000

FN
YY
W0200229103-A2.

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QY 1741 CAGAGCACCAGGCTGCTGCTGGAGAGCTGCCGAGCTCACCTTCCTGCTGGAGCTTTC 1800
Db 1741 CAGAGCACCAGGCTGCTGCTGGAGAGCTGCCGAGCTCACCTTCCTGCTGGAGCTTTC 1800
QY 1801 GGTACCTCGTGTCTAGTCACTACAGTGGCTGTGTCTGGGCTGCCAGGCGGCC 1860
Db 1801 GGTACCTCGTGTCTAGTCACTACAGTGGCTGTGTCTGGGCTGCCAGGCGGCC 1860
QY 1861 TCGCCAGCATCTCATCTCACTCAATCAATGTTCTCTTCTCCACAGCCCGAGCAAC 1920
Db 1861 TCGCCAGCATCTCATCTCACTCAATCAATGTTCTCTTCTCCACAGCCCGAGCAAC 1920
QY 1921 AGGCTGCTACCCCGGAGGAGGTGTCAGGCGACGCTGGTGTCTGCTGGCTTGGCC 1980
Db 1921 AGGCTGCTACCCCGGAGGAGGTGTCAGGCGACGCTGGTGTCTGCTGGCTTGGCC 1980
QY 1981 ATGGTGCCCATCTGCTGCTGGCACACCCCTGCACCTGTGCACCCGCCACCGCGCGC 2040
Db 1981 ATGGTGCCCATCTGCTGCTGGCACACCCCTGCACCTGTGCACCCGCCACCGCGCGC 2040
QY 2041 CTGGGAGGAGGCGCGCTGACCGACAGGAGGAAACAAAGCCCGGTTGCTGGACCTGCCT 2100
Db 2041 CTGGGAGGAGGCGCGCTGACCGACAGGAGGAAACAAAGCCCGGTTGCTGGACCTGCCT 2100
QY 2101 GAGCATCTGTAATGGCTGAGCTCCGATGAGGAAAGGAGGAGGAGGAGGAGGAGGAGG 2160
Db 2101 GAGCATCTGTAATGGCTGAGCTCCGATGAGGAAAGGAGGAGGAGGAGGAGGAGGAGG 2160
QY 2161 GAGGAGGCGAGCTGCTGCTCCGAGTGTCTATGACACGAGGCAATCCACCATCGAG 2220
Db 2161 GAGGAGGCGAGCTGCTGCTCCGAGTGTCTATGACACGAGGCAATCCACCATCGAG 2220
QY 2221 TTCTGCTGGGCTGCTGCTCAACACCGCTCTCTTACCTGCGCTGTGGGCGCTGAGCGTG 2280
Db 2221 TTCTGCTGGGCTGCTGCTCAACACCGCTCTCTTACCTGCGCTGTGGGCGCTGAGCGTG 2280
QY 2281 GCCACGCGCAGCTGCTGAGGTTCTGAGGCGCATGATGCGCATAGGCTGAGCGCTG 2340
Db 2281 GCCACGCGCAGCTGCTGAGGTTCTGAGGCGCATGATGCGCATAGGCTGAGCGCTG 2340
QY 2341 GGCGGAGGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Db 2341 GGCGGAGGAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
QY 2401 ATGACCGTGCTATCTGCTGCTGATGAGGAGTCTTACGCTTCTGTCAGCGCTGCGG 2460
Db 2401 ATGACCGTGCTATCTGCTGCTGATGAGGAGTCTTACGCTTCTGTCAGCGCTGCGG 2460
QY 2461 CTGCACTGGGTGGAATTCAGAACAGTTCTACTCAGGCGAGGCTACAGCTGAGTCCC 2520
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QY 2521 TTCACTCTGCTGCCACAGATGACTAGGCGCCACTGCGAGTCTTCTGCGACACCTCTTCT 2580
Db 2521 TTCACTCTGCTGCCACAGATGACTAGGCGCCACTGCGAGTCTTCTGCGACACCTCTTCT 2580
QY 2581 GACCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
Db 2581 GACCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
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RESULT 9

ACA56496
ID ACA56496 standard; cDNA; 2655 BP.

XX
AC ACA56496;

XX
DT 06-JUN-2003 (first entry)

XX
DE Human signalling pathway polynucleotide probe SEQ ID NO 1094.

XX
KW Human; probe; ss; array element; Parkinson's disease;

XX
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;

KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX Homo sapiens.
XX US6500938-B1.
XX 31-DEC-2002.
XX 30-JAN-1998; 98US-00016434.
XX 30-JAN-1998; 98US-00016434.
XX (INCY-) INCYTE GENOMICS INC.
XX Au-Young J, Seilhamer JJ;
XX WPI; 2003-352189/33.
XX
XX Combination of polynucleotide probes, useful as array elements in a
XX microarray for monitoring the expression of a number of target
XX polynucleotides.
XX
XX Claim 1; SEQ ID NO 1094; 65pp; English.

XX The invention relates to a combination which, comprises a number of
XX polynucleotide probes comprising a sequence selected from one of the 1490
XX sequences mentioned in the specification. The combination is useful as an
XX array element in a microarray for monitoring the expression of a number
XX of target polynucleotides. The microarray is particularly useful in the
XX diagnosis and treatment of cancer and immunopathology and neuropathology.
XX The microarray is useful in diagnostics and treatment regimens, drug
XX discovery and development, toxicological and carcinogenicity studies,
XX forensics and pharmacogenomics. The microarray is also useful for
XX monitoring progression of diseases and for developing sophisticated
XX profiles for the effects of currently available therapeutic drugs. The
XX combination is also useful for purifying a subpopulation of mRNAs, cDNAs
XX and genomic fragments and in research and diagnostic applications. The
XX array can detect changes in expression in a large number of genes coding
XX for different signaling pathway populations which can be used to diagnose
XX various diseases including cancer e.g. adenocarcinoma and leukaemia,
XX immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
XX and Parkinson's disease. The present sequence represents a polynucleotide
XX probe of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=06500938B1

XX Sequence 2655 BP; 460 A; 885 C; 824 G; 486 T; 0 U; 0 Other;

Query Match 100.0%; Score 2640; DB 10; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCTGCGGAGCGGCGAGCGAGCGAGCGGCGGCGGCGGCGAGCACACCGGGAGCATG 60
Db 1 CGCGCTGCGGAGCGGCGAGCGAGCGAGCGGCGGCGGCGGCGAGCACACCGGGAGCATG 60
QY 61 GGCTCCATGTTCCGAGCGAGGAGGTGGCCCTGGTCCAGCTCTTTCGCCACAGCGGCT 120
Db 61 GGCTCCATGTTCCGAGCGAGGAGGTGGCCCTGGTCCAGCTCTTTCGCCACAGCGGCT 120
QY 121 GCCTACACCTGCTGAGTGGCTGGCGAGCTGGGCTCTGTGAGTTTCAGAGCTCAAC 180
Db 121 GCCTACACCTGCTGAGTGGCTGGCGAGCTGGGCTCTGTGAGTTTCAGAGCTCAAC 180
QY 181 GCCTCGGTGAGCGCTTCCAGACCGCTTGTGTTGATGTTTGGCGCTGTGAGAGCTG 240
Db 181 GCCTCGGTGAGCGCTTCCAGACCGCTTGTGTTGATGTTTGGCGCTGTGAGAGCTG 240
QY 241 GAGAAGACCTTACCTTCTTCCAGAGGAGGAGTGGCGGCGCTGGGCTGTGCTGCCCGC 300
Db 241 GAGAAGACCTTACCTTCTTCCAGAGGAGGAGTGGCGGCGCTGGGCTGTGCTGCCCGC 300

Db 901 CTAGCGGGGTGCTGCAGCTGCTGCCGCCAGGCGAGGTGCAGGTCCACAAGATGAAGGCC 960
Qy 961 GTGTACTCTGGCCCTGAACAGGTGCAGGTGAGACCAACGACAAAGTGCCTCATTTGCCGAG 1020
Db 961 GTGTACTCTGGCCCTGAACAGGTGCAGGTGAGACCAACGACAAAGTGCCTCATTTGCCGAG 1020
Qy 1021 GCTGTGTGCTCTGTGCGAGACTTGGCCCGCTTCAGAGAGGCCCTTCGGGGACAGCTCGATG 1080
Db 1021 GCTGTGTGCTCTGTGCGAGACTTGGCCCGCTTCAGAGAGGCCCTTCGGGGACAGCTCGATG 1080
Qy 1081 GAGGAGGAGTGTAGTGCCTGCTACCGGATTCCTTCGCGGAGCAATGCCCCCAACATC 1140
Db 1081 GAGGAGGAGTGTAGTGCCTGCTACCGGATTCCTTCGCGGAGCAATGCCCCCAACATC 1140
Qy 1141 ATCCGACCAACCGCTTTCAGCGGAGCTTCCAGGCGATCGTGGATCGCTACGGCGTGGC 1200
Db 1141 ATCCGACCAACCGCTTTCAGCGGAGCTTCCAGGCGATCGTGGATCGCTACGGCGTGGC 1200
Qy 1201 CGCTACAGGAGGTCAACCCCGCTCCCTACACCATCATCACCTTCCCTCTTCTGTTTGT 1260
Db 1201 CGCTACAGGAGGTCAACCCCGCTCCCTACACCATCATCACCTTCCCTCTTCTGTTTGT 1260
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Db 1261 GTGATTTTCGGGATGTGGGCAACGGGCTGCTCATGTTCTCTTCCGCTTGGCCATGCTC 1320
Qy 1321 CTTGCGGAGAACGACCGGCTGTGAAGCGCGGAGAACGAGATCTGGCAGACTTCTTTC 1380
Db 1321 CTTGCGGAGAACGACCGGCTGTGAAGCGCGGAGAACGAGATCTGGCAGACTTCTTTC 1380
Qy 1381 AGGGGCGGCTACTCTGCTCTGCTTATGGGCTGTTCTTCATCTACACCGGCTTCATCTAC 1440
Db 1381 AGGGGCGGCTACTCTGCTCTGCTTATGGGCTGTTCTTCATCTACACCGGCTTCATCTAC 1440
Qy 1441 AACGAGTGTTCAGTTCGCGCACACGATCTTCCCTCGGGCTGGAGTGTGGCGGCATG 1500
Db 1441 AACGAGTGTTCAGTTCGCGCACACGATCTTCCCTCGGGCTGGAGTGTGGCGGCATG 1500
Qy 1501 GCCAACAGTCTGGCTGGAGTGTATGATCTTCCCTGGGCGGAGCACAGATGCTTACCTGGAT 1560
Db 1501 GCCAACAGTCTGGCTGGAGTGTATGATCTTCCCTGGGCGGAGCACAGATGCTTACCTGGAT 1560
Qy 1561 CCCAACGTCACCGGTGTCTTCTGGGACCCCTACCCCTTTGGCATCGATCTATTTGGAGC 1620
Db 1561 CCCAACGTCACCGGTGTCTTCTGGGACCCCTACCCCTTTGGCATCGATCTATTTGGAGC 1620
Qy 1621 CTGGCTGCGCAACCACTTGAAGTTCCTCAACTCTTCAAGATGAAGATGTCGGTCACTCTG 1680
Db 1621 CTGGCTGCGCAACCACTTGAAGTTCCTCAACTCTTCAAGATGAAGATGTCGGTCACTCTG 1680
Qy 1681 GCGTCTGTGCACATGCGCTTTGGGGTGTCTCGGAGTCTTCAACCACTGCACTTTGGC 1740
Db 1681 GCGTCTGTGCACATGCGCTTTGGGGTGTCTCGGAGTCTTCAACCACTGCACTTTGGC 1740
Qy 1741 CAGAGGACACCGGTGTCTGTGGAGACGCTGCCGAGCTCACCTTCTCTGTGGAGCTCTTTC 1800
Db 1741 CAGAGGACACCGGTGTCTGTGGAGACGCTGCCGAGCTCACCTTCTCTGTGGAGCTCTTTC 1800
Qy 1801 GGTACTCTGTGTTCCTAGTCACTAACAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860
Db 1801 GGTACTCTGTGTTCCTAGTCACTAACAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860
Qy 1861 TGGCCAGAGATCTCATCCACTTTCATCAATGTTCTCTTCTTCCACAGCCGCCAGCAAC 1920
Db 1861 TGGCCAGAGATCTCATCCACTTTCATCAATGTTCTCTTCTTCCACAGCCGCCAGCAAC 1920
Qy 1921 AGGCTCTCTTACCCCCGAGGAGGTGGTCCAGGCCACGCTGTGTGTCTTGGCTTTGGCC 1980
Db 1921 AGGCTCTCTTACCCCCGAGGAGGTGGTCCAGGCCACGCTGTGTGTCTTGGCTTTGGCC 1980
Qy 1981 ATGGTCCCATCTCTGTCTTGGCACACCCCTGCACTGTGTGACCGCCACCGCCGCCG 2040
Db 1981 ATGGTCCCATCTCTGTCTTGGCACACCCCTGCACTGTGTGACCGCCACCGCCGCCG 2040

Qy 2041 CTGCGGAGGAGCCCGCTGACCCGACGAGGAGGAAAACAAGCCGGGTTGCTGGACCTGCCT 2100
Db 2041 CTGCGGAGGAGCCCGCTGACCCGACGAGGAGGAAAACAAGCCGGGTTGCTGGACCTGCCT 2100
Qy 2101 GACGATCTGTGAATGGCTGGAGCTCCGATGAGGAAAAGCAGGGGGCTTGGATGATGAA 2160
Db 2101 GACGATCTGTGAATGGCTGGAGCTCCGATGAGGAAAAGCAGGGGGCTTGGATGATGAA 2160
Qy 2161 GAGGAGGCGGAGCTGTGCTCCCTCCGAGGTGCTCATGCAACAGGCCATCCACCATCGAG 2220
Db 2161 GAGGAGGCGGAGCTGTGCTCCCTCCGAGGTGCTCATGCAACAGGCCATCCACCATCGAG 2220
Qy 2221 TTCTGCTCGGGCTGGCTCTCCAAACCGCTCTTACCTGCGCTGTGGGCGCTTGAGCCTG 2280
Db 2221 TTCTGCTCGGGCTGGCTCTCCAAACCGCTCTTACCTGCGCTGTGGGCGCTTGAGCCTG 2280
Qy 2281 GCCACGCCCCAGCTGTCCGAGGTTTGTGGGCGCATGGTGATGCGCATAGGCCCTGGGCTG 2340
Db 2281 GCCACGCCCCAGCTGTCCGAGGTTTGTGGGCGCATGGTGATGCGCATAGGCCCTGGGCTG 2340
Qy 2341 GGC CGGAGGTGGCGTGGCGCTGTGTGCTGTGTCCTTTCGCGCTTTTGGCGCTG 2400
Db 2341 GGC CGGAGGTGGCGTGGCGCTGTGTGCTGTGTCCTTTCGCGCTTTTGGCGCTG 2400
Qy 2401 ATGACCGTGGCTATCTCTGCTGTGTGATGGAGGACTCTCAGCCCTTCTGCAAGCTGAGTCCC 2460
Db 2401 ATGACCGTGGCTATCTCTGCTGTGTGATGGAGGACTCTCAGCCCTTCTGCAAGCTGAGTCCC 2460
Qy 2461 CTGCACTGGGTGGAATTCAGAACAAAGTTCTACTCAGGCAACGGGCTTACAGCTGAGTCCC 2520
Db 2461 CTGCACTGGGTGGAATTCAGAACAAAGTTCTACTCAGGCAACGGGCTTACAGCTGAGTCCC 2520
Qy 2521 TTCACTTCTGCTGCCACAGATGACTAGGGCCCACTGAGGTCCTTGCAGACCTCTTCTCT 2580
Db 2521 TTCACTTCTGCTGCCACAGATGACTAGGGCCCACTGAGGTCCTTGCAGACCTCTTCTCT 2580
Qy 2581 GACCTCTGAGGCGAGAGGAAATAAGACGGTCCGCTTGGCAAAAAA 2640
Db 2581 GACCTCTGAGGCGAGAGGAAATAAGACGGTCCGCTTGGCAAAAAA 2640

RESULT 11

ADI56292
ID ADI56292 standard; DNA; 2655 BP.
XX
AC ADI56292;
XX
DT 22-APR-2004 (first entry)
XX
Human polynucleotide probe #1094.
XX
DE
XX
KW Human; probe; ss; receptor-like polypeptide; transducing polypeptide; effector-like polypeptide; cancer; immunopathology; neuropathology;
KW drug development; toxicology; carcinogenicity;
KW signalling pathway polypeptide; adrenal gland; bladder; bone;
KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX
OS Homo sapiens.
XX
PN US2004010136-A1.
XX
PD 15-JAN-2004.
XX
PF 26-NOV-2002; 2002US-00305720.
XX
PR 30-JAN-1998; 98US-00016434.
XX (INCY-) INCYTE GENOMICS INC.
XX Au-Young J, Seilhamer JJ;

XX WPI; 2004-090520/09.
XX New composition comprising polynucleotide probes, useful as array
PT elements in a microarray for monitoring the expression of target
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
PT fragments.
XX
XX Claim 6; SEQ ID NO 1094; 73pp; English.
XX
XX The invention relates to a composition of polynucleotide probes
CC comprising first polynucleotide probes comprising at least a portion of a
CC gene encoding a receptor-like polypeptide, second polynucleotide probes
CC comprising at least a portion of a gene encoding a transducing
CC polypeptide and third polynucleotide probes comprising at least a portion
CC of a gene encoding an effector-like polypeptide. The probes of the
CC composition are useful as array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray is useful in the
CC diagnosis and treatment of cancer, an immunopathology or a
CC neuropathology. It can also be used for drug discovery and development,
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.
CC Microarrays can also be used for monitoring the progression of diseases
CC that may be associated with the altered expression of signalling pathway
CC polypeptides. The composition can also be used to purify a subpopulation
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
CC epilepsy, Alzheimer's disease or depression. This sequence represents a
CC human polynucleotide probe of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 2655 BP; 460 A; 885 C; 824 G; 486 T; 0 U; 0 Other;

Query Match 100.0%; Score 2640; DB 12; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCGTCCGCGGACGGGACGACGAGCGGCGGCGGACACACCGGGGACCATG 60
DB 1 CGGCGTCCGCGGACGGGACGACGAGCGGCGGCGGACACACCGGGGACCATG 60
QY 61 GGCTCCATGTTCCGAGCGAGGAGGTGGCCCTGGTCCAGCTCTTTCTGCCACAGCGGCT 120
DB 61 GGCTCCATGTTCCGAGCGAGGAGGTGGCCCTGGTCCAGCTCTTTCTGCCACAGCGGCT 120
QY 121 GCCTACACCTGCGTGGTGGGCGAGCTGGGCGCTCTGGTCCAGCTCTTTCTGCCACAGCGGCT 180
DB 121 GCCTACACCTGCGTGGTGGGCGAGCTGGGCGCTCTGGTCCAGCTCTTTCTGCCACAGCGGCT 180
QY 181 GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTCATGTTTGGCGCTGTGAGGAGCTG 240
DB 181 GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTCATGTTTGGCGCTGTGAGGAGCTG 240
QY 241 GAGAAGACCTTACCTTCTCCAGGAGGAGGTGCGGCGGCTGGGCTGGTCTGCCCCCG 300
DB 241 GAGAAGACCTTACCTTCTCCAGGAGGAGGTGCGGCGGCTGGGCTGGTCTGCCCCCG 300
QY 301 CCAAGGGGAGGCTGCGGACACCCCGGAGCTGCGGCGGCTGGGCTGGTCTGCCCCCG 360
DB 301 CCAAGGGGAGGCTGCGGACACCCCGGAGCTGCGGCGGCTGGGCTGGTCTGCCCCCG 360
QY 361 GAGCGCTGCGGCGGAGCTGCGGATGTGCGGCGGCAACAGCAGGCGCTGCGGCGGCGG 420
DB 361 GAGCGCTGCGGCGGAGCTGCGGATGTGCGGCGGCAACAGCAGGCGCTGCGGCGGCGG 420
QY 421 CTCACACAGCTGAGCTTCAACCGCGCGCTGCTACGCCAGGCGGCAATGAACCTCAGCTGGCA 480
DB 421 CTCACACAGCTGAGCTTCAACCGCGCGCTGCTACGCCAGGCGGCAATGAACCTCAGCTGGCA 480

QY 481 GCGCCCCACACAGATGGGGCTCAGAGAGGAGCGCCCTGCTCCAGGCGCCCGGGGGCGG 540
DB 481 GCGCCCCACACAGATGGGGCTCAGAGAGGAGCGCCCTGCTCCAGGCGCCCGGGGGCGG 540
QY 541 CACCAGGACCTGAGGGTCAACTTTGTGGCAGGTGCGGTGGAGGCGCCCAAGAGGCGCTGCC 600
DB 541 CACCAGGACCTGAGGGTCAACTTTGTGGCAGGTGCGGTGGAGGCGCCCAAGAGGCGCTGCC 600
QY 601 CTAGAGCGCTGCTCTGAGAGGGCTGCGGGGCTTCTCTCATTTGCCAGCTTCAGGAGCTG 660
DB 601 CTAGAGCGCTGCTCTGAGAGGGCTGCGGGGCTTCTCTCATTTGCCAGCTTCAGGAGCTG 660
QY 661 GAGCAGCGCTGGAGCACCCCGTACCGGGGAGCAGCAGCTGGATGACCTTCTCATC 720
DB 661 GAGCAGCGCTGGAGCACCCCGTACCGGGGAGCAGCAGCTGGATGACCTTCTCATC 720
QY 721 TCCTACTGGGTGAGCAGATCGGACAGAAGATCCGAAAGATCACGGATGCTTCCACTGC 780
DB 721 TCCTACTGGGTGAGCAGATCGGACAGAAGATCCGAAAGATCACGGATGCTTCCACTGC 780
QY 781 CAGCTCTTCCGTTTCTGACAGGAGGAGGCGCCCTCGGGGCGCTTCGAGCAGCTGCAA 840
DB 781 CAGCTCTTCCGTTTCTGACAGGAGGAGGCGCCCTCGGGGCGCTTCGAGCAGCTGCAA 840
QY 841 CAGCAGAGCAGGAGCTGACAGGAGTCTCGGGGAGACAGAGCGGTTCTCGAGCAGGCTG 900
DB 841 CAGCAGAGCAGGAGCTGACAGGAGTCTCGGGGAGACAGAGCGGTTCTCGAGCAGGCTG 900
QY 901 CTAGGCGGGTGTGACAGCTGCTGCCCGAGGCGGAGTGCAGATCAACAGATCAAGGCC 960
DB 901 CTAGGCGGGTGTGACAGCTGCTGCCCGAGGCGGAGTGCAGATCAACAGATCAAGGCC 960
QY 961 GTGTACTGCGCTGAAACCAAGTGCAGCTGAGCAACGACCAAGTGCCTCATTTGCCGAG 1020
DB 961 GTGTACTGCGCTGAAACCAAGTGCAGCTGAGCAACGACCAAGTGCCTCATTTGCCGAG 1020
QY 1021 GCCTGCTGCTCTGCGAGAGCTGCGCGCGCTGCGAGAGGCGCTGCGGACAGCTCGATG 1080
DB 1021 GCCTGCTGCTCTGCGAGAGCTGCGCGCGCTGCGAGAGGCGCTGCGGACAGCTCGATG 1080
QY 1081 GAGGAGGAGTGTGCTGCGGTGCTACCGCATCCCTGCGGGGACATGCCCCCAGCATC 1140
DB 1081 GAGGAGGAGTGTGCTGCGGTGCTACCGCATCCCTGCGGGGACATGCCCCCAGCATC 1140
QY 1141 ATCCGACCAACCGCTTACGCGGACGCTTCCAGGACATCGTGGATCGCTAGCGGTGGG 1200
DB 1141 ATCCGACCAACCGCTTACGCGGACGCTTCCAGGACATCGTGGATCGCTAGCGGTGGG 1200
QY 1201 CGCTACAGAGAGTCAACCGCGCTTCCAGCATCATCTTCCCTTCTCGGCTTCTGTTGCT 1260
DB 1201 CGCTACAGAGAGTCAACCGCGCTTCCAGCATCATCTTCCCTTCTCGGCTTCTGTTGCT 1260
QY 1261 GTGATGTTGGGGATGTGGGCGACGCGCTGCTCATGTTCTTCTGCGGCTGGCCATGTC 1320
DB 1261 GTGATGTTGGGGATGTGGGCGACGCGCTGCTCATGTTCTTCTGCGGCTGGCCATGTC 1320
QY 1321 CTTGCGGAGAACCGGCTGTGAAGCGCGCAGAACGAGATCTGGCAGACTTCTTTC 1380
DB 1321 CTTGCGGAGAACCGGCTGTGAAGCGCGCAGAACGAGATCTGGCAGACTTCTTTC 1380
QY 1381 AGGGGCGCTTACCTGCTGCTTATGGGCTGTCTTCATCTACACCGGCTTCTATC 1440
DB 1381 AGGGGCGCTTACCTGCTGCTTATGGGCTGTCTTCATCTACACCGGCTTCTATC 1440
QY 1441 AACGAGTGTTCAGTTCGCGCACAGCATCTTCCCTCGGGCTGGAGTGGCGGCGCATG 1500
DB 1441 AACGAGTGTTCAGTTCGCGCACAGCATCTTCCCTCGGGCTGGAGTGGCGGCGCATG 1500
QY 1501 GCCAACAGCTGTGGCTGAGTGCATTCCTGGCGGAGCAGCATGCTTACCTCGAT 1560
DB 1501 GCCAACAGCTGTGGCTGAGTGCATTCCTGGCGGAGCAGCATGCTTACCTCGAT 1560
QY 1561 CCCAACGTCACCGGTGTCTTCTGCGGACCGCTACGCCCTTGTGGCATCGATCTATTTGAGC 1620

Db	1561		CCCAACGTCACCGGTGTCCTTCCTGGGACCTTACCCCTTGGCATCGATCTATTTGGAGC	1620
Qy	1621	CTGGCTGCGCAACCACTTCAGCTTCTCAACTCCCTTCAAGATGAAGATGTCGTCATCCTG	1680	
Db	1621	CTGGCTGCGCAACCACTTCAGCTTCTCAACTCCCTTCAAGATGAAGATGTCGTCATCCTG	1680	
Qy	1681	GGCGTCGTGCACATGGCCCTTTGGGTGGTCTCCGAGTCTTCAACCACTGCACTTTGGC	1740	
Db	1681	GGCGTCGTGCACATGGCCCTTTGGGTGGTCTCCGAGTCTTCAACCACTGCACTTTGGC	1740	
Qy	1741	CAGAGGCACCGGCTGCTCTGGAGACGCTGCCGAGCTCACCTTCCTCTGGGACTTCTC	1800	
Db	1741	CAGAGGCACCGGCTGCTCTGGAGACGCTGCCGAGCTCACCTTCCTCTGGGACTTCTC	1800	
Qy	1801	GTTTACCTTCGTGTTCTTAGTCATCTACAAGTGGCTGTGTGTCGGGCTGCCAGGCGCGC	1860	
Db	1801	GTTTACCTTCGTGTTCTTAGTCATCTACAAGTGGCTGTGTGTCGGGCTGCCAGGCGCGC	1860	
Qy	1861	TCGCCAGCATCTCATCCACTTCATCAACATGTTCTCTTCTCCACAGCCCCAGCAAC	1920	
Db	1861	TCGCCAGCATCTCATCCACTTCATCAACATGTTCTCTTCTCCACAGCCCCAGCAAC	1920	
Qy	1921	AGGCTGCTCTACCCCGGCGAGGAGGTGTCAGGCGCACGCTGGTGTCTTGGCTTTGGCC	1980	
Db	1921	AGGCTGCTCTACCCCGGCGAGGAGGTGTCAGGCGCACGCTGGTGTCTTGGCTTTGGCC	1980	
Qy	1981	ATGDTGCCCATCTCTGCTGCTTGGCACACCCCTGCACCTGTGTGCACGCCACCGCGCGCGC	2040	
Db	1981	ATGDTGCCCATCTCTGCTGCTTGGCACACCCCTGCACCTGTGTGCACGCCACCGCGCGCGC	2040	
Qy	2041	CTGCGGAGGAGCGCCGTGACCCGACAGGAGAAAACAAGCGCGGTTGTGTGGACCTGCGCT	2100	
Db	2041	CTGCGGAGGAGCGCCGTGACCCGACAGGAGAAAACAAGCGCGGTTGTGTGGACCTGCGCT	2100	
Qy	2101	GACGCATCTGTGAATGGCTGAGACTCCGATGAGAGAAAAGGACGGGGCCCTGGATGATGA	2160	
Db	2101	GACGCATCTGTGAATGGCTGAGACTCCGATGAGAGAAAAGGACGGGGCCCTGGATGATGA	2160	
Qy	2161	GAGGAGCCGAGCTCGTCCCTCCGAGGTGCTCATGCACAGGCCATCCACACCATCGAG	2220	
Db	2161	GAGGAGCCGAGCTCGTCCCTCCGAGGTGCTCATGCACAGGCCATCCACACCATCGAG	2220	
Qy	2221	TTCTGCTGGGCTCGTCTCAACAACCGCCTCTTACTGCGCCTGTGGGCCCTGAGCCTG	2280	
Db	2221	TTCTGCTGGGCTCGTCTCAACAACCGCCTCTTACTGCGCCTGTGGGCCCTGAGCCTG	2280	
Qy	2281	GCCACGCCACAGCTCCGAGTTCTGTGGCCATGGTGAATGCGCATAGGCTTGGGCTG	2340	
Db	2281	GCCACGCCACAGCTCCGAGTTCTGTGGCCATGGTGAATGCGCATAGGCTTGGGCTG	2340	
Qy	2341	GGCCGGAGGTGGGCGCTGTGGTGTGCTGCCCTCTTTGCGCGCTTTGCGCGTG	2400	
Db	2341	GGCCGGAGGTGGGCGCTGTGGTGTGCTGCCCTCTTTGCGCGCTTTGCGCGTG	2400	
Qy	2401	ATGACCGTGGCTATCTCTGTGGTGAATGAGAGGACTCTCAGCCCTTCTGCACGCCCTGCGG	2460	
Db	2401	ATGACCGTGGCTATCTCTGTGGTGAATGAGAGGACTCTCAGCCCTTCTGCACGCCCTGCGG	2460	
Qy	2461	CTGCACCTGGGTGGAAATTCAGAAACAAGTTTACTCAGGCAAGGCTACAGCTGAGTCCC	2520	
Db	2461	CTGCACCTGGGTGGAAATTCAGAAACAAGTTTACTCAGGCAAGGCTACAGCTGAGTCCC	2520	
Qy	2521	TTCACTTTCGTGCCACAGATGAATAGGCGGCCACTGCGAGGTCTCTGCCAGACCTCTTCCT	2580	
Db	2521	TTCACTTTCGTGCCACAGATGAATAGGCGGCCACTGCGAGGTCTCTGCCAGACCTCTTCCT	2580	
Qy	2581	GACCTCTGAGCGCAGAGAGGAATAAGACGGTCCGCCCTGGCAAAAAAATAAAAAA	2640	
Db	2581	GACCTCTGAGCGCAGAGAGGAATAAGACGGTCCGCCCTGGCAAAAAAATAAAAAA	2640	

Qy 241 GAGAAAGACCTTACCTTCTCGAGGAGGAGTGCGGGGCTGGGCTGGTCTGCTCCCGG 300
Db 241 GAGAAAGACCTTACCTTCTCGAGGAGGAGTGCGGGGCTGGGCTGGTCTGCTCCCGG 300
Qy 301 CCAAAGGGAGGCTGCGGGACCCCGCACCCCGGAGACTGCTGCGCATCCAGAGAGAGCG 360
Db 301 CCAAAGGGAGGCTGCGGGACCCCGCACCCCGGAGACTGCTGCGCATCCAGAGAGAGAGCG 360
Qy 361 GAGCGCTGGCCAGGAGCTCGGGATGTGGGGCAACAGAGAGGCTGCTGGGGCCAG 420
Db 361 GAGCGCTGGCCAGGAGCTCGGGATGTGGGGCAACAGAGAGGCTGCTGGGGCCAG 420
Qy 421 CTGACACAGCTGAGCTCCAGCGCGCTGTACGCCAGGGCCATGAACCTCAGCTGGCA 480
Db 421 CTGACACAGCTGAGCTCCAGCGCGCTGTACGCCAGGGCCATGAACCTCAGCTGGCA 480
Qy 481 GCCGCCACACAGATGGGGCTCAGAGAGAGCGCCCTGTCTCCAGGGCCCGGGGGCGG 540
Db 481 GCCGCCACACAGATGGGGCTCAGAGAGAGCGCCCTGTCTCCAGGGCCCGGGGGCGG 540
Qy 541 CACAGAGACTGAGGGTCACTTTGTGGCAGGTGGCGTGGAGCCCGCACAGGGCCCTGCC 600
Db 541 CACAGAGACTGAGGGTCACTTTGTGGCAGGTGGCGTGGAGCCCGCACAGGGCCCTGCC 600
Qy 601 CTAGAGCGCTGCTTGAGGGCTGCGCGGCTTCTCTCATTTGCCAGCTTCAGGGAGCTG 660
Db 601 CTAGAGCGCTGCTTGAGGGCTGCGCGGCTTCTCTCATTTGCCAGCTTCAGGGAGCTG 660
Qy 661 GAGCAGCGCTGAGAGACCCCGTGAACGGGCGAGCGAGCCAGCTGGATGACCTTCTCATC 720
Db 661 GAGCAGCGCTGAGAGACCCCGTGAACGGGCGAGCGAGCCAGCTGGATGACCTTCTCATC 720
Qy 721 TCCTACTGGGTGAGCAGATCGGACAGAGATCCGCAAGATCAAGGACTGCTTCACATGC 780
Db 721 TCCTACTGGGTGAGCAGATCGGACAGAGATCCGCAAGATCAAGGACTGCTTCACATGC 780
Qy 781 CACGTCTCCGTTTCTGACAGAGAGGAGCGCGCTCGGGGCGCTGACAGCTGCAAGTCGAA 840
Db 781 CACGTCTCCGTTTCTGACAGAGAGGAGCGCGCTCGGGGCGCTGACAGCTGCAAGTCGAA 840
Qy 841 CAGCAGAGCCAGGAGCTGAGGAGTCTCGGGGAGACAGAGCGTTCCTGAGCAGGTG 900
Db 841 CAGCAGAGCCAGGAGCTGAGGAGTCTCGGGGAGACAGAGCGTTCCTGAGCAGGTG 900
Qy 901 CTAGGCGGGTGTGAGCTGCTGCGCGCAGGGCAGGTGCAAGTCCACAGATGAAGGCC 960
Db 901 CTAGGCGGGTGTGAGCTGCTGCGCGCAGGGCAGGTGCAAGTCCACAGATGAAGGCC 960
Qy 961 GTGTACCTGGCCCTGAAACCAAGTGCAGCGTGAACCAAGTGCCTCATTTGCCGAG 1020
Db 961 GTGTACCTGGCCCTGAAACCAAGTGCAGCGTGAACCAAGTGCCTCATTTGCCGAG 1020
Qy 1021 GCCTGTGCTCTGTGCGAGACTGCGCGCTCGAGGAGCGCTGCGGACAGCTCGATG 1080
Db 1021 GCCTGTGCTCTGTGCGAGACTGCGCGCTCGAGGAGCGCTGCGGACAGCTCGATG 1080
Qy 1081 GAGAGGAGGTGAGTGCCTGGTCAACCGATCCCTGCGGGGACATGCCCCCACACTC 1140
Db 1081 GAGAGGAGGTGAGTGCCTGGTCAACCGATCCCTGCGGGGACATGCCCCCACACTC 1140
Qy 1141 ATCGCACCAACCGCTTTCAGGGCAGCTTCAGGGGATGCTGGATGCTGAGCGGTGGG 1200
Db 1141 ATCGCACCAACCGCTTTCAGGGCAGCTTCAGGGGATGCTGGATGCTGAGCGGTGGG 1200
Qy 1201 CGCTACAGAGGTCAACCCCGCTCTACACCATCATCACTTCCCTTCTCTGTTGCT 1260
Db 1201 CGCTACAGAGGTCAACCCCGCTCTCTACACCATCATCACTTCCCTTCTCTGTTGCT 1260
Qy 1261 GTGATGTTGGGATGTGGGCAAGGGCTGCTCATGTTCTTTCGCCCTGGCCATGGTC 1320
Db 1261 GTGATGTTGGGATGTGGGCAAGGGCTGCTCATGTTCTTTCGCCCTGGCCATGGTC 1320
Qy 1321 CTTGCGGAGAACCGACCGGCTGTGAAGCGCGCAGAACGAGATCTGGCAGACTTTCTTC 1380

Db 1321 CTTGCGGAGAACCGACCGGCTGTGAAGCGCGCAGAACGAGATCTGGCAGACTTTCTTC 1380
Qy 1381 AGGGCCCGCTACCTGCTCTGCTTATGGGCTGTCTCCATCTACACGGCTTCATCTAC 1440
Db 1381 AGGGCCCGCTACCTGCTCTGCTTATGGGCTGTCTCCATCTACACGGCTTCATCTAC 1440
Qy 1441 AACGAGTGTTCAGTTCGCGCCACAGCATCTTCCCTCGGGTGGAGTGGCCGCCATG 1500
Db 1441 AACGAGTGTTCAGTTCGCGCCACAGCATCTTCCCTCGGGTGGAGTGGCCGCCATG 1500
Qy 1501 GCCAACCACTGCTGGCTGGAGTGCATTCCTGCGCCACAGCATCTTCCCTCGGGTGGAGT 1560
Db 1501 GCCAACCACTGCTGGCTGGAGTGCATTCCTGCGCCACAGCATCTTCCCTCGGGTGGAGT 1560
Qy 1561 CCCAACGTACCGGTGTCTTCTGCGGACCTTACCCTTTGGCATCGATCTTATTTGGAGC 1620
Db 1561 CCCAACGTACCGGTGTCTTCTGCGGACCTTACCCTTTGGCATCGATCTTATTTGGAGC 1620
Qy 1621 CTGGCTGCAACCACTTGGAGTTCCTCAACTCTTCAAGATGAAGATGCTGCTCATCTG 1680
Db 1621 CTGGCTGCAACCACTTGGAGTTCCTCAACTCTTCAAGATGAAGATGCTGCTCATCTG 1680
Qy 1681 GGCGTGTGCACATGGGCTTTGGGGTGTCTCGAGTCTTCAACCACTGCACTTTGGC 1740
Db 1681 GGCGTGTGCACATGGGCTTTGGGGTGTCTCGAGTCTTCAACCACTGCACTTTGGC 1740
Qy 1741 CAGAGGCAACCGGCTGCTGAGAGCGCTGCGGAGCTCACTTCTCTGCTGGAGCTTTC 1800
Db 1741 CAGAGGCAACCGGCTGCTGAGAGCGCTGCGGAGCTCACTTCTCTGCTGGAGCTTTC 1800
Qy 1801 GGTTCACCTGTTTCTAGTCACTCAAGTGGTGTGTGTCTGCGGCTGCCAGGCGCGC 1860
Db 1801 GGTTCACCTGTTTCTAGTCACTCAAGTGGTGTGTGTCTGCGGCTGCCAGGCGCGC 1860
Qy 1861 TCGCCAGCAGCTTCATCCACTTCAATGTTCTTCTTCTCCACAGCCCCCAGCAAC 1920
Db 1861 TCGCCAGCAGCTTCATCCACTTCAATGTTCTTCTTCTCCACAGCCCCCAGCAAC 1920
Qy 1921 AGGCTGTCTTACCCCGGCGAGGAGTGTCCAGGCGCAGCTGGTGTCTGCGCTTGGCC 1980
Db 1921 AGGCTGTCTTACCCCGGCGAGGAGTGTCCAGGCGCAGCTGGTGTCTGCGCTTGGCC 1980
Qy 1981 ATGTGCGCCATCTGCTGTGCGACACCCCTGCACTGCTGCAACCGCGCGCGC 2040
Db 1981 ATGTGCGCCATCTGCTGTGCGACACCCCTGCACTGCTGCAACCGCGCGCGC 2040
Qy 2041 CTGCGGAGGAGGCGCGCTGACCGAGAGGAGAAACAGGCGCGGTTGCTGGACCTGCT 2100
Db 2041 CTGCGGAGGAGGCGCGCTGACCGAGAGGAGAAACAGGCGCGGTTGCTGGACCTGCT 2100
Qy 2101 GAGCATCTGTGAATGCTGGAGCTCCGATGAGGAGAAAGGAGGCGCTGGATGATGA 2160
Db 2101 GAGCATCTGTGAATGCTGGAGCTCCGATGAGGAGAAAGGAGGCGCTGGATGATGA 2160
Qy 2161 GAGGAGCCGAGCTGCTCCCTCCGAGGTGCTATGCAACAGGCCATCCACACCATCGAG 2220
Db 2161 GAGGAGCCGAGCTGCTCCCTCCGAGGTGCTATGCAACAGGCCATCCACACCATCGAG 2220
Qy 2221 TTCTGCTGGCTGGCTGCTCCAAACCGCTCTTACCTGCGCTGTGGGCGCTGAGCGCTG 2280
Db 2221 TTCTGCTGGCTGGCTGCTCCAAACCGCTCTTACCTGCGCTGTGGGCGCTGAGCGCTG 2280
Qy 2281 GCCCACCCAGCTGCTCCGAGGTCTGTGGCCATGTGTATGCCATAGGCTGGGCTG 2340
Db 2281 GCCCACCCAGCTGCTCCGAGGTCTGTGGCCATGTGTATGCCATAGGCTGGGCTG 2340
Qy 2341 GGCGGAGGTGGCGCTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Db 2341 GGCGGAGGTGGCGCTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Qy 2401 ATGACCGTGGCTATCTGCTGGTGTGAGGAGCTCTAGGCTTCTGCGAGCGCTGGG 2460

Db 2401 ATGACCGTGCTATCTCTGCTGGTGATGGAGGACTCTCAGCCCTTCTGTCAGCGCCCTGCGG 2460
Qy 2461 CTGCACTGGGTGAATTCAGAACTTCTACTCAGGACAGGGCTTCAAGCTGAGTCCC 2520
Db 2461 CTGCACTGGGTGAATTCAGAACTTCTACTCAGGACAGGGCTTCAAGCTGAGTCCC 2520
Qy 2521 TTCACTTCTGCTGCCACAGATAGTGGGCCCACTGCAGTCTCTGCCAGACCTCTTCTT 2580
Db 2521 TTCACTTCTGCTGCCACAGATAGTGGGCCCACTGCAGTCTCTGCCAGACCTCTTCTT 2580
Qy 2581 GACCTCTGAGGACAGGAGAGGAATAAAGACGGTCCGCCCTGGCAAAAAA 2640
Db 2581 GACCTCTGAGGACAGGAGAGGAATAAAGACGGTCCGCCCTGGCAAAAAA 2640

RESULT 13

AD128819
ID AD128819 standard; cDNA; 2700 BP.

XX AC AD128819;

XX DT 22-APR-2004 (first entry)

XX DE Human modifier of p53 (MP53) gene TCIRG-1.

XX KW Human; MP53; modifier of p53; p53; cytosolic; gene therapy;

XX KW T-cell immune regulator 1; TCIRG-1; gene; ss.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT CDS 109..2601

XX FT /*tag= a

XX FT /product= "MP53 TCIRG-1"

XX WO2004004766-A1.

XX PD 15-JAN-2004.

XX PF 09-JUL-2003; 2003WO-US021378.

XX PR 10-JUL-2002; 2002US-0394992P.

XX PR 07-AUG-2002; 2002US-0401604P.

XX PR 16-SEP-2002; 2002US-0410988P.

XX PR 25-NOV-2002; 2002US-0428837P.

XX PA (EXEL-) EXELIXIS INC.

XX PI Costa MA, Maxwell ME, Lackner MR, Hung T, O'Brien CL, Jin Y;

XX PI Nicoll M, Hai B, Zhang H, Lickteig K, Amundsen CD;

XX DR WPI; 2004-142922/14.

XX DR P-PSDB; AD128834.

XX DR REFSEQ; NM_006019.2.

XX PT Identifying a candidate p53 pathway modulating agent for treating e.g.,
PT cancer, comprises contacting an assay system comprising a MP53
PT polypeptide or nucleic acid with a test agent and detecting a test agent-
PT biased activity.

XX PS Example 2; SEQ ID NO 10; 139pp; English.

XX CC In the present invention, genetic screens were designed to identify
CC modifiers of the p53 pathway in *Caenorhabditis elegans*, where a
CC homozygous p53 deletion mutant was used. Various specific genes were
CC silenced by RNA inhibition. Genes causing altered phenotypes in the worms
CC were identified as modifiers of the p53 pathway. Human orthologs, denoted
CC modifiers of p52 (MP53). Of these modifiers were identified. These
CC include the present sequence, characterized as encoding T-cell immune
CC regulator 1, ATPase, H⁺ transporting, or lysosomal V0 protein a isoform
CC 3. MP53 nucleic acids and polypeptides are attractive drug targets for
CC the treatment of pathologies associated with a defective p53 signalling
CC pathway, such as cancer. Methods for modulating MP53 function and/or the

CC p53 pathway in a mammalian cell involve contacting the cell with an agent
CC that specifically binds a MP53 polypeptide or nucleic acid. The agent may
CC be a small molecular modulator, a nucleic acid modulator or an antibody.

XX SQ Sequence 2700 BP; 451 A; 905 C; 850 G; 494 T; 0 U; 0 Other;

Query Match 81.1%; Score 2142; DB 12; Length 2700;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2582; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

Qy 38 GCGCAGCACACCCGGGACCATGGGCTCCATGTTCCGAGCGAGGAGGTGGCCCTGGTCC 97
Db 89 GCGCAGCACACCCGGGACCATGGGCTCCATGTTCCGAGCGAGGAGGTGGCCCTGGTCC 148

Qy 98 AGCTCTTTTGGCCACAGCGGCTGCTACACCTGCTGAGTGGCTGGGGGAGCTGGGCC 157
Db 149 AGCTCTTTTGGCCACAGCGGCTGCTACACCTGCTGAGTGGCTGGGGGAGCTGGGCC 208

Qy 158 TGTGGAGTTTCAGAGACCTCAACGCTCGTGGTGGCGCTTCCAGAGACGCTTTGTGTTG 217
Db 209 TGTGGAGTTTCAGAGACCTCAACGCTCGTGGTGGCGCTTCCAGAGACGCTTTGTGTTG 268

Qy 218 ATGTTTGGCGCTGTGAGGAGCTGGAGAGACCTTCACTTCTCTGAGGAGGAGTGGCGC 277
Db 269 ATGTTTGGCGCTGTGAGGAGCTGGAGAGACCTTCACTTCTCTGAGGAGGAGTGGCGC 328

Qy 278 GGGCTGGGCTGTGCTTGTGCCCCCGCCAAAGGGAGGCTGCGGACACCCACCCCGGAGC 337
Db 329 GGGCTGGGCTGTGCTTGTGCCCCCGCCAAAGGGAGGCTGCGGACACCCACCCCGGAGC 388

Qy 338 TGTGCGCATCCAGAGGAGAGCGGCGCTTGGCCAGGAGCTGCGGGAGTGTGCGGGCA 397
Db 389 TGTGCGCATCCAGAGGAGAGCGGCGCTTGGCCAGGAGCTGCGGGAGTGTGCGGGCA 448

Qy 398 ACCAGCAGCCCTTGGCGGCGCCAGCTGCACAGCTGCAGCTTCAACGCGCGCTTACGCC 457
Db 449 ACCAGCAGCCCTTGGCGGCGCCAGCTGCACAGCTGCAGCTTCAACGCGCGCTTACGCC 508

Qy 458 AGGGCCATGAACCTCAGCTGGCAGCGCGCCACACAGATGGGGCTCAGAGAGACGCCCC 517
Db 509 AGGGCCATGAACCTCAGCTGGCAGCGCGCCACACAGATGGGGCTCAGAGAGACGCCCC 568

Qy 518 TGTCTCAGGCCCCCGGGGGCGCGCACAGGACCTGAGGGTCAACTTTTGTGGCAGGTGCCG 577
Db 569 TGTCTCAGGCCCCCGGGGGCGCGCACAGGACCTGAGGGTCAACTTTTGTGGCAGGTGCCG 628

Qy 578 TGGAGCCCCCAAGGCCCTTGCCTTAGAGCGCTTGTCTGGAGGGCTGCGCGGCTTCC 637
Db 629 TGGAGCCCCCAAGGCCCTTGCCTTAGAGCGCTTGTCTGGAGGGCTGCGCGGCTTCC 688

Qy 638 TCATTGCCAGCTTCAGGAGCTGGAGCAGCGCTGGAGCACCCCTGACGGGGAGCCAG 697
Db 689 TCATTGCCAGCTTCAGGAGCTGGAGCAGCGCTGGAGCACCCCTGACGGGGAGCCAG 748

Qy 698 CCACGTGGATGACTTCTCTCATCTCTACTGGGGTGAGCAGATCGGACAGAGATCCGCA 757
Db 749 CCACGTGGATGACTTCTCTCATCTCTACTGGGGTGAGCAGATCGGACAGAGATCCGCA 808

Qy 758 AGATCACTGGACTGTCTTCCACTGCCAGCTTCCCGTTTCTGACGAGGAGGAGCCGCC 817
Db 809 AGATCACTGGACTGTCTTCCACTGCCAGCTTCCCGTTTCTGACGAGGAGGAGCCGCC 868

Qy 818 TGGGGCCCTTGCAGCAGCTTGCACAGCAGCAGGAGCTGCAGGAGGTCTCTGGGGAGA 877
Db 869 TGGGGCCCTTGCAGCAGCTTGCACAGCAGCAGGAGCTGCAGGAGGTCTCTGGGGAGA 928

Qy 878 CAGAGCGGTCTCTGACCCAGGTGCTAGGCGGGTGTCTGAGCTGTCTGCCAGGAGGAGG 937
Db 929 CAGAGCGGTCTCTGACCCAGGTGCTAGGCGGGTGTCTGAGCTGTCTGCCAGGAGGAGG 988

Qy 938 TGCAGTCCCAAGATGAAGGCGGTGTATCTGGCCCTGTAACCAAGTGCAGCGTGAACCA 997
Db 989 TGCAGTCCCAAGATGAAGGCGGTGTATCTGGCCCTGTAACCAAGTGCAGCGTGAACCA 1048

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Qy 998 CGCACAAGTGCTCATTTGCGAGGCGCTGGTGTCTGTGTCGAGACCTGCCCCCGCTGCAGG 1057
Db 1049 CGCACAAGTGCTCATTTGCGAGGCGCTGGTGTCTGTGTCGAGACCTGCCCCCGCTGCAGG 1108
Qy 1058 AGGCGCTTGCAGGACAGCTTCGATGAGAGGAGGAGTGAGTGCCTGGCTCACCGCATCCCTCT 1117
Db 1109 AGGCGCTTGCAGGACAGCTTCGATGAGAGGAGGAGTGAGTGCCTGGCTCACCGCATCCCTCT 1168
Qy 1118 GCCGGGACATGCCCGCCCAACATCATTCGCAACAAACCGCTTCAACCGGCAAGCTTCCAGGGCA 1177
Db 1169 GCCGGGACATGCCCGCCCAACATCATTCGCAACAAACCGCTTCAACCGGCAAGCTTCCAGGGCA 1228
Qy 1178 TCGTGGATCGCTACGGGCTGGGCGCTACACAGGAGGTCAACCCCGCTCCCTACACCATCA 1237
Db 1229 TCGTGGATCGCTACGGGCTGGGCGCTACACAGGAGGTCAACCCCGCTCCCTACACCATCA 1288
Qy 1238 TCACCTTCCCTTCTCTGTGCTGTGATGTTTCGGGGATGTGGGCCACCGGGCTGTCTCATGT 1297
Db 1289 TCACCTTCCCTTCTCTGTGCTGTGATGTTTCGGGGATGTGGGCCACCGGGCTGTCTCATGT 1348
Qy 1298 TCCTCTTTCGCGCTGGCCATGTCCTTTCGGGAGAACCGACCGGCTGTGAAAGCCGCGCAGA 1357
Db 1349 TCCTCTTTCGCGCTGGCCATGTCCTTTCGGGAGAACCGACCGGCTGTGAAAGCCGCGCAGA 1408
Qy 1358 ACGAGATCTGCGACACTTCTTTCAGGGGCGCTACCTGCTCTGCTTATGGGCGCTGTCT 1417
Db 1409 ACGAGATCTGCGACACTTCTTTCAGGGGCGCTACCTGCTCTGCTTATGGGCGCTGTCT 1468
Qy 1418 CCATCTACACCGGCTTTCATCTACAAACGAGTCTTTCAGTCGGCGCCACACAGCATCTTCCCT 1477
Db 1469 CCATCTACACCGGCTTTCATCTACAAACGAGTCTTTCAGTCGGCGCCACACAGCATCTTCCCT 1528
Qy 1478 CGGCTCGAGTGTGGCCCGCCATGCCAAACAGTCTGGCTGGAATGATGTCATTCCTGGGCC 1537
Db 1529 CGGCTCGAGTGTGGCCCGCCATGCCAAACAGTCTGGCTGGAATGATGTCATTCCTGGGCC 1588
Qy 1538 AGCACAGATGCTTACCTTGATCCCAACGTCACCGGTGCTTCTTGGGACCTTACCGCT 1597
Db 1589 AGCACAGATGCTTACCTTGATCCCAACGTCACCGGTGCTTCTTGGGACCTTACCGCT 1648
Qy 1598 TTGGCATCGATCTCTATTTGGAGCTGTGCTGCAACCACTTTCAGCTTCTCAACTCTTCTCA 1657
Db 1649 TTGGCATCGATCTCTATTTGGAGCTGTGCTGCAACCACTTTCAGCTTCTCAACTCTTCTCA 1708
Qy 1658 AGATGAAGATGTCGCTCATCTCGGCGCTGTGTCACATGCGCTTTGGGTGTCTCTCGAG 1717
Db 1709 AGATGAAGATGTCGCTCATCTCGGCGCTGTGTCACATGCGCTTTGGGTGTCTCTCGAG 1768
Qy 1718 TCTTCAACCAAGTGCATTTTGGCCAGAGGACACCGGCTGTCTGAGACGCTGCGGAGC 1777
Db 1769 TCTTCAACCAAGTGCATTTTGGCCAGAGGACACCGGCTGTCTGAGACGCTGCGGAGC 1828
Qy 1778 TCACCTTCTGCTGGGACTCTTTCGGTTACCTCGTGTTCCTAGTTCATCTACAAGTGGCTGT 1837
Db 1829 TCACCTTCTGCTGGGACTCTTTCGGTTACCTCGTGTTCCTAGTTCATCTACAAGTGGCTGT 1888
Qy 1838 GTGTCTGGGTGTCAGGCGCGCTCTG---CCAGCATCTCTCATCCACTTTCATCAACATGT 1894
Db 1889 GTGTCTGGGTGTCAGGCGCGCTCTG---CCAGCATCTCTCATCCACTTTCATCAACATGT 1948
Qy 1895 TCCTCTTCTCCACAGCCCAAGCAAGGCTGTCTACCCCGCGCAGAGAGTGTGTCAGG 1954
Db 1949 TCCTCTTCTCCACAGCCCAAGCAAGGCTGTCTACCCCGCGCAGAGAGTGTGTCAGG 2008
Qy 1955 CCAGCTGTGTGCTCTGGCTTGGCCATGTGGCCATCTGCTGTCTTGGCACACCCCTGC 2014
Db 2009 CCAGCTGTGTGCTCTGGCTTGGCCATGTGGCCATCTGCTGTCTTGGCACACCCCTGC 2068
Qy 2015 ACCTGTGACCCGACACCGCGCGCTGCGGAGAGGCGCGCTGACCGCAGCAGGAGAAA 2074
Db 2069 ACCTGTGACCCGACACCGCGCGCTGCGGAGAGGCGCGCTGACCGCAGCAGGAGAAA 2128
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Qy 2075 ACAGGCGCGGTTGCTGGACCTGCTGACGATCTGTGAATGGCTGGAGCTCCGATGAGG 2134
Db 2129 ACAGGCGCGGTTGCTGGACCTGCTGACGATCTGTGAATGGCTGGAGCTCCGATGAGG 2188
Qy 2135 AAAAGGACAGGGGCTGATGATGAAGAGAGGCGAGCTGTCCTCCCTCCGAGGTGCTCA 2194
Db 2189 AAAAGGACAGGGGCTGATGATGAAGAGAGGCGAGCTGTCCTCCCTCCGAGGTGCTCA 2248
Qy 2195 TGCAACAGGCGCATCCACACCATCGAGTTCCTGCTGGGCTGCTTCCAAACACCGCTCT 2254
Db 2249 TGCAACAGGCGCATCCACACCATCGAGTTCCTGCTGGGCTGCTTCCAAACACCGCTCT 2308
Qy 2255 ACCTGCGCTGTGGGCGCTGAGCTGCGCCACGCGCCAGCTCTCGAGGTTCCTGCGGCA 2314
Db 2309 ACCTGCGCTGTGGGCGCTGAGCTGCGCCACGCGCCAGCTCTCGAGGTTCCTGCGGCA 2368
Qy 2315 TGTGATGCGCATAGGCTGCGGCTTGGCGGAGGTGGGCGTGGCGCTGTGGTGTCTGG 2374
Db 2369 TGTGATGCGCATAGGCTGCGGCTTGGCGGAGGTGGGCGTGGCGCTGTGGTGTCTGG 2428
Qy 2375 TCCCATCTTTGCGGCTTTGCGGCTGATGACCGTGGCTATCTGCTGCTGATGAGGAGAC 2434
Db 2429 TCCCATCTTTGCGGCTTTGCGGCTGATGACCGTGGCTATCTGCTGCTGATGAGGAGAC 2488
Qy 2435 TCTCAGCTTCTCTGACGCGCTGCGCTGCACTGGTGGATTCAGAGAACAGTTCCTACT 2494
Db 2489 TCTCAGCTTCTCTGACGCGCTGCGCTGCACTGGTGGATTCAGAGAACAGTTCCTACT 2548
Qy 2495 CAGCACGGGCTACAGCTGATGCTTTCACCTTTCGCTGCCACAGATGACTAGGCGCCAC 2554
Db 2549 CAGCACGGGCTACAGCTGATGCTTTCACCTTTCGCTGCCACAGATGACTAGGCGCCAC 2608
Qy 2555 TGCAAGTCTCTGCCAGACCTCTTCTGACCTCTCAGGCGAGAGGAAATAAGACGGTCC 2614
Db 2609 TGCAAGTCTCTGCCAGACCTCTTCTGACCTCTCAGGCGAGAGGAAATAAGACGGTCC 2668
Qy 2615 GCCCTGGCA 2623
Db 2669 GCCCTGGCA 2677

RESULT 14
ADP10401
ID ADP10401 standard; DNA; 2700 BP.
XX
AC ADP10401;
XX
XX 12-AUG-2004 (first entry)
XX
DE Reference mRNA sequences for marker probe #78.
XX
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO2004042346-A2.
XX
XX 21-MAY-2004.
XX
XX 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
XX
XX 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX Rosenberg S;
XX
XX WPI; 2004-400724/37.
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX
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PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.

XX Claim 80; SEQ ID NO 410; 1762pp; English.

XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprising detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis
CC and monitoring of allograft rejection and other disorders.

XX Sequence 2700 BP; 451 A; 905 G; 850 C; 494 T; 0 U; 0 Other;

Query Match 81.1%; Score 2142; DB 12; Length 2700;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2592; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 38 GCGCAGCACACCCGGGAGCATTGGCTCCATGTTCCGAGCGAGGAGGTGGCCCTGGTCC 97

DB 89 GCGCAGCACACCCGGGAGCATTGGCTCCATGTTCCGAGCGAGGAGGTGGCCCTGGTCC 148

QY 98 AGCTCTTTTGTGCCACAGCGGCTGCTTACACCTGCGTGTAGTGGCTGGCGAGCTGGGC 157

DB 149 AGCTCTTTTGTGCCACAGCGGCTGCTTACACCTGCGTGTAGTGGCTGGCGAGCTGGGC 208

QY 158 TCGTGGAGTTCAGAGACCTCAACCGCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTG 217

DB 209 TCGTGGAGTTCAGAGACCTCAACCGCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTG 268

QY 218 ATGTTTGGCGCTGTGAGGAGCTGGAGAACCTTACCTTCTCTGAGGAGGAGGTGGCG 277

DB 269 ATGTTTGGCGCTGTGAGGAGCTGGAGAACCTTACCTTCTCTGAGGAGGAGGTGGCG 328

QY 278 GGCTCGGCTGTGCTGCCCGCCAAAGGGAGGCTGCGGCACCCCGCCAGCGGAGC 337

DB 329 GGCTCGGCTGTGCTGCCCGCCAAAGGGAGGCTGCGGCACCCCGCCAGCGGAGC 388

QY 338 TGTGCGCATCCAGGAGGAGACGAGCGCTTGGCCCGAGGAGCTGCGGGATGTGCGGGCA 397

DB 389 TGTGCGCATCCAGGAGGAGACGAGCGCTTGGCCCGAGGAGCTGCGGGATGTGCGGGCA 448

QY 398 ACCAGCAGGCGCTTGGCGGCGCAGCTGACACAGCTGAGCTTCCAGCGCGCGTGTACGCC 457

DB 449 ACCAGCAGGCGCTTGGCGGCGCAGCTGACACAGCTGAGCTTCCAGCGCGCGTGTACGCC 508

QY 458 AGGGCCATGAACCTCAGCTGGCAGCGCCGACACAGATGGGGCTCAGAGAGACGCCCC 517

DB 509 AGGGCCATGAACCTCAGCTGGCAGCGCCGACACAGATGGGGCTCAGAGAGACGCCCC 568

QY 518 TGTCTCAGCGCCCGCGGGGCGCGCACAGACTGAGGGTCAACTTTGTGGCAGGTGCGG 577

DB 569 TGTCTCAGCGCCCGCGGGGCGCGCACAGACTGAGGGTCAACTTTGTGGCAGGTGCGG 628

QY 578 TGGAGCCCCACAGGCGCTGCTAGAGCGCTGCTCTGAGGGCTGCGCGGCTTCC 637

DB 629 TGGAGCCCCACAGGCGCTGCTAGAGCGCTGCTCTGAGGGCTGCGCGGCTTCC 688

QY 638 TCATTGCCAGCTTCAGGAGCTGGAGCAGCGCTGAGCACCCTGAGCGGGGAGCCAG 697

DB 689 TCATTGCCAGCTTCAGGAGCTGGAGCAGCGCTGAGCACCCTGAGCGGGGAGCCAG 748

QY 698 CACAGTGGATGACCTTCTCATCTCTGAGGAGTGGAGATCGGACAGAGATCCGA 757

DB 749 CCACGTGGATGACCTTCTCTCATCTCTACTGCGGTGAGCAGATCGGACAGAGATCCGCA 808

QY 758 AGATCACGAGCTGCTTCCACTGCGCAGCTTCTCCGTTTCTGACGAGGAGGAGGCGCCGCC 817

DB 809 AGATCACGAGCTGCTTCCACTGCGCAGCTTCTCCGTTTCTGACGAGGAGGAGGCGCCGCC 868

QY 818 TCGGGCCCTCGCAGCAGCTGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 877

DB 869 TCGGGCCCTCGCAGCAGCTGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 928

QY 878 CAGAGCGGTCTCTGAGCAGCAGGTGCTAGGCGCGGTGCTGACAGCTGCTGCGCCAGGCGCAGG 937

DB 929 CAGAGCGGTCTCTGAGCAGCAGGTGCTAGGCGCGGTGCTGACAGCTGCTGCGCCAGGCGCAGG 988

QY 938 TCGAGGTCCACAAGATGAAGCGCGGTGCTGACCTGGCCCTGAACAGTGCAGCTGAGCAGCAGCA 997

DB 989 TCGAGGTCCACAAGATGAAGCGCGGTGCTGACCTGGCCCTGAACAGTGCAGCTGAGCAGCAGCA 1048

QY 998 CGCACAGTGCCTCATTTGCGCAGGCGCTGGTGTCTGTGCGAGACCTGCGCGCCCTGCAGG 1057

DB 1049 CGCACAGTGCCTCATTTGCGCAGGCGCTGGTGTCTGTGCGAGACCTGCGCGCCCTGCAGG 1108

QY 1058 AGGCCCTGCGGACAGCTCGATGGAGGAGGTGAGTGCCCTGCTGCTACCGCATCCCCCT 1117

DB 1109 AGGCCCTGCGGACAGCTCGATGGAGGAGGTGAGTGCCCTGCTGCTACCGCATCCCCCT 1168

QY 1118 GCGGGAGACATGCCCCCAGCAGCTCATCCGCGCAGCAACCGCTTACGGCGCAGCTTCCAGGGCA 1177

DB 1169 GCGGGAGACATGCCCCCAGCAGCTCATCCGCGCAGCAACCGCTTACGGCGCAGCTTCCAGGGCA 1228

QY 1178 TCGTGGATCGCTACCGCGTGGCGCGCTACACGAGGTCAACCCCGCTCCCTACACCATCA 1237

DB 1229 TCGTGGATCGCTACCGCGTGGCGCGCTACACGAGGTCAACCCCGCTCCCTACACCATCA 1288

QY 1238 TCACCTTCCCCCTTCTCTGTTTGTGTGATGTTTCGGGAGATGTGGGCCACCGGCTGCTCATGT 1297

DB 1289 TCACCTTCCCCCTTCTCTGTTTGTGTGATGTTTCGGGAGATGTGGGCCACCGGCTGCTCATGT 1348

QY 1298 TCTCTTGGCCCTGGCCATGGTCTTTCAGGGCGCGCTACTGCTCTGCTTATGGGCTGCTTCT 1357

DB 1349 TCTCTTGGCCCTGGCCATGGTCTTTCAGGGAGAACCGACCGCTGTGGAAGCGCGCAGA 1408

QY 1358 AGGAGATCTGGCAGACTTCTTTCAGGGCGCGCTACTGCTCTGCTTATGGGCTGCTTCT 1417

DB 1409 AGGAGATCTGGCAGACTTCTTTCAGGGCGCGCTACTGCTCTGCTTATGGGCTGCTTCT 1468

QY 1418 CCATCTACACCGGCTTCTTCAACAGAGTGTCTCAGTCGCGCCACACAGCATCTTCCCCCT 1477

DB 1469 CCATCTACACCGGCTTCTTCAACAGAGTGTCTCAGTCGCGCCACACAGCATCTTCCCCCT 1528

QY 1478 CGGGCTGGAGTGTGGCGCGCATGGCCACACAGTCTGGCTGGAGTGTGATTCCTTGGCCCC 1537

DB 1529 CGGGCTGGAGTGTGGCGCGCATGGCCACACAGTCTGGCTGGAGTGTGATTCCTTGGCCCC 1588

QY 1538 AGCACACAGTGTCTTACCTTGGATCCCAAGCTCACCGGTGTCTTCTGGGACCTTACCCCT 1597

DB 1589 AGCACACAGTGTCTTACCTTGGATCCCAAGCTCACCGGTGTCTTCTGGGACCTTACCCCT 1648

QY 1598 TTGGCATCGATCTTATTTGGAGCCTGGCTGCCAACAACCTTGTGAGCTTCTCAACTCTTCA 1657

DB 1649 TTGGCATCGATCTTATTTGGAGCCTGGCTGCCAACAACCTTGTGAGCTTCTCAACTCTTCA 1708

QY 1658 AGATGAAGATGTCCTCATCTCGGGGCTGTCACATGCGCTTGGGGTGGTCTCGGAG 1717

DB 1709 AGATGAAGATGTCCTCATCTCGGGGCTGTCACATGCGCTTGGGGTGGTCTCGGAG 1768

QY 1718 TCTTCAACACCACTGTCATTTGGCCAGAGGACACCGGTGTGCTGTGAGAGCGCTGCCGAGC 1777

DB 1769 TCTTCAACACCACTGTCATTTGGCCAGAGGACACCGGTGTGCTGTGAGAGCGCTGCCGAGC 1828

QY 1778 TCACCTTCTGCTGGAGCTCTTTGGGTTTACCTGTTTCTAGTCTATCATCAAGTGGCTGT 1837

DB 1829 TCACCTTCTGCTGGAGCTCTTTGGGTTTACCTGTTTCTAGTCTATCATCAAGTGGCTGT 1888

QY 1838 GTGTCCTGGCTGCCAGGCGCCCTCG----CCAGCATCCTCATTCACCTTCAATCAACATGT 1894
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QY 1889 GTGTCCTGGCTGCCAGGCGCCCTCGGCCCCAGCATCCTCATCCACTTCAATCAACATGT 1948
Db |||||
QY 1895 TCCTCTTCTCCACACAGCCCAAGCAAGCTGCTCTACCCCGGCGAGGAGTGTGTCAGG 1954
Db |||||
QY 1949 TCCTCTTCTCCACACAGCCCAAGCAAGCTGCTCTACCCCGGCGAGGAGTGTGTCAGG 2008
QY 1955 CCACGCTGGTGGTCTTGGCTTGGCCATGAGTGGCCATCCTGCTGTGGCCACACCCCTGC 2014
Db |||||
QY 2009 CCACGCTGGTGGTCTTGGCTTGGCCATGAGTGGCCATCCTGCTGTGGCCACACCCCTGC 2068
QY 2015 ACCTGCTGCCACCGCCACCGCCCGCTCGGAGAGGCCCGCTGACCGACAGAGGAA 2074
Db |||||
QY 2069 ACCTGCTGCCACCGCCACCGCCCGCTCGGAGAGGCCCGCTGACCGACAGAGGAA 2128
QY 2075 ACAAGGCGGGTGTCTGGACCTGCTGACGATCTGTGAATGGCTGGAGCTCCGATGAGG 2134
Db |||||
QY 2129 ACAAGGCGGGTGTCTGGACCTGCTGACGATCTGTGAATGGCTGGAGCTCCGATGAGG 2188
QY 2135 AAAAGGAGGGGGCTTGATGATGAAGAGGAGCGAGCTCGTCCCTCCGAGTGTCTCA 2194
Db |||||
QY 2189 AAAAGGAGGGGGCTTGATGATGAAGAGGAGCGAGCTCGTCCCTCCGAGTGTCTCA 2248
QY 2195 TGCACAGGCCATCCACACCATGAGTTCGCTGGGCTGGCTCTCCAAACACCGCCTCT 2254
Db |||||
QY 2249 TGCACAGGCCATCCACACCATGAGTTCGCTGGGCTGGCTCTCCAAACACCGCCTCT 2308
QY 2255 ACCTGCGCCTGTGGGCTTGAGCTGACGCTGACGCTGCTGCGAGTTCCTGGGCCA 2314
Db |||||
QY 2309 ACCTGCGCCTGTGGGCTTGAGCTGACGCTGACGCTGCTGCGAGTTCCTGGGCCA 2368
QY 2315 TGTGTATGCGCATAGGCTTGCGCTTGGGCTGGGCGGAGGTGGGCTGTGCTGTGG 2374
Db |||||
QY 2369 TGTGTATGCGCATAGGCTTGCGCTTGGGCTGGGCGGAGGTGGGCTGTGCTGTGG 2428
QY 2375 TCCCATCTTGGCGCTTGGCTGTGATGACCGTGGCTATCTGCTGTGATGAGGAC 2434
Db |||||
QY 2429 TCCCATCTTGGCGCTTGGCTGTGATGACCGTGGCTATCTGCTGTGATGAGGAC 2488
QY 2435 TCTCAGCTTCTTCCAGCCTCGGCTGCACTGGGTGGAATCCAGAACAAAGTTCTACT 2494
Db |||||
QY 2489 TCTCAGCTTCTTCCAGCCTCGGCTGCACTGGGTGGAATCCAGAACAAAGTTCTACT 2548
QY 2495 CAGCACGGGCTACAAGCTGAGTCCCTTACCTTCGCTGCGCACAGATGACTAGGCGCCAC 2554
Db |||||
QY 2549 CAGCACGGGCTACAAGCTGAGTCCCTTACCTTCGCTGCGCACAGATGACTAGGCGCCAC 2608
QY 2555 TGCAGGTCTTCCAGACCTCTTCTGACCTCTGAGGAGAGGAGGAAATGAAGCGTCC 2614
Db |||||
QY 2609 TGCAGGTCTTCCAGACCTCTTCTGACCTCTGAGGAGAGGAGGAAATGAAGCGTCC 2668
QY 2615 GCCCTGGCA 2623
Db |||||
QY 2669 GCCCTGGCA 2677

RESULT 15

ACN39267

ID ACN39267 standard; cDNA; 2700 BP.

XX

AC

XX

XX

XX

XX

18-NOV-2004 (first entry)

Tumour-associated antigenic target (TAT) cDNA DNA325509, SEQ ID NO:3304.

Tumour-associated antigenic target; TAT; human; overexpression; cancer;

tumour; diagnosis; cell proliferative disorder; breast cancer;

colorectal cancer; lung cancer; ovarian cancer; liver cancer;

central nervous system cancer; bladder cancer; pancreatic cancer;

cervical cancer; melanoma; leukaemia; hybridisation probe;

chromosome identification; chromosome mapping; gene mapping;
gene therapy; cytostatic; gene; ss.

Homo sapiens.

WO2004030615-A2.

15-APR-2004.

29-SEP-2003; 2003WO-US028547.

02-OCT-2002; 2002US-0414971P.

(GETH) GENENTECH INC.

Wu TD, Zhang Z, Zhou Y;

WPI; 2004-347921/32.

P-PSDB, ABM81281.

New tumor-associated antigenic target polypeptides and nucleic acids,
useful in preparing a medicament for treating or detecting a
proliferative disorder, e.g. breast, lung, colorectal, ovarian or
prostate cancer or tumor.

Claim 1; SEQ ID NO 3304; 7273pp; English.

The invention relates to human tumour-associated antigenic target (TAT)
polypeptides, and their related nucleic acids. The TAT polypeptides are
overexpressed in cancer tissues compared to normal tissues, and may thus
serve as effective targets for the diagnosis and treatment of cancer in
mammals. The invention also relates to nucleic acid and polypeptide
sequences at least 80% identical to the TAT nucleic acids and
polypeptides; expression vectors and host cells comprising a TAT nucleic
acid; an antibody specific for a TAT polypeptide; a peptide or organic
molecule which binds to a TAT polypeptide; fusion proteins comprising a
TAT polypeptide; and methods and compositions for the treatment or
diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
antibodies, antagonists, binding molecules and compositions are useful
for diagnosing or treating a cell proliferative disorder associated with
increased TAT expression, particularly cancers such as breast cancer,
colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
cancer, pancreatic cancer, cervical cancer, cancers of the central
nervous system, melanoma and leukaemia. TAT nucleic acids may further be
used as hybridisation probes, in chromosome and gene mapping, in
chromosome identification and in gene therapy. The present sequence
represents a TAT nucleic acid of the invention

Sequence 2700 BP; 451 A; 905 C; 850 G; 494 T; 0 U; 0 Other;

Query Match 81.1%; Score 2142; DB 13; Length 2700;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2582; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 38 GCGCAGCACACCGGGGACCATGGCTCCATGTCGAGGAGGAGGTGGCCCTGTGTC 97
Db |||||
QY 89 GCGCAGCACACCGGGGACCATGGCTCCATGTCGAGGAGGAGGTGGCCCTGTGTC 148
Db |||||
QY 98 AGCTCTTTCTGCCACAGCGGCTGCTACACCTGCGTGAGTTCGGCGAGCTGGGCC 157
Db |||||
QY 149 AGCTCTTTCTGCCACAGCGGCTGCTACACCTGCGTGAGTTCGGCGAGCTGGGCC 208
QY 158 TCGTGGAGTTTCAGAGACCTCAACGCTTCGGTGAGCGCTTCCAGAGACGCTTTGTGTTG 217
Db |||||
QY 209 TCGTGGAGTTTCAGAGACCTCAACGCTTCGGTGAGCGCTTCCAGAGACGCTTTGTGTTG 268
QY 218 ATGTTTGGCGCTGTGAGGAGCTGAGAAACCTTCACTTCTTCAGAGAGAGGTGGCGC 277
Db |||||
QY 269 ATGTTTGGCGCTGTGAGGAGCTGAGAAACCTTCACTTCTTCAGAGAGAGGTGGCGC 328
QY 278 GGCGTGGCTGGTTCCTGCCCCCCCCCAAGGGGAGGCTGCGGCAACCCCAACCCCGGACCC 337
Db |||||
QY 329 GGCGTGGCTGGTTCCTGCCCCCCCCCAAGGGGAGGCTGCGGCAACCCCAACCCCGGACCC 388

QY	338	TGCTGCGCATTCAGGAGGAGACGAGAGCGCTTGGCCGAGAGGAGCTGCGGGGCA	397
DB	389	TGCTGCGCATTCAGGAGGAGACGAGAGCGCTTGGCCGAGAGGAGCTGCGGGGCA	448
QY	398	ACACAGAGGCGCTGCGGGCCAGCTGCACACAGCTGCAGCTCCACGCCCGCTGCTACGCC	457
DB	449	ACACAGAGGCGCTGCGGGCCAGCTGCACACAGCTGCAGCTCCACGCCCGCTGCTACGCC	508
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Job time : 1631 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 05:44:05 ; Search time 12282 Seconds
(without alignments)
12019.788 Million cell updates/sec

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96473154

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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- 1: gb_est1.*
- 2: gb_est3.*
- 3: gb_est4.*
- 4: gb_est5.*
- 5: gb_est6.*
- 6: gb_est7.*
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- 8: gb_est9.*
- 9: gb_est10.*
- 10: gb_est11.*
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- 12: gb_est13.*
- 13: gb_est14.*
- 14: gb_est15.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1290	48.9	2493	14	AY407799 Homo sapi
3	838	31.7	1655	6	CR602058 full-leng
4	734	27.8	909	4	EX358008 BX358008
5	729	27.6	757	9	DN996103 TC110144
6	692	26.2	1070	4	EX332189 BX332189
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8	671	25.4	1088	3	BQ073186 AGENCOURT
9	620	23.5	664	3	BU732254 UI-E-CQ1-
10	619	23.4	619	4	CA425567 UI-H-PF0-
11	613	23.2	842	8	CR992406 CR992406
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15	599	22.7	619	3	BM976782 UI-H-FLO-
16	599	22.7	693	3	BM976782 UI-CF-EN1
17	599	22.7	703	4	CA307407 UI-H-FT1-
18	599	22.7	756	4	CA944661 UI-CF-FNO
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33	526	19.9	921	4	EX358007 BX358007
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ALIGNMENTS

CR594613 1864 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CSDD004YI18 of Neuroblastoma Cot
50-normalized of Homo sapiens (human).

CR594613
HTC; CNSLT_cDNA.

CR594613.1 GI:50475420

HTC; CNSLT_cDNA.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1864)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue

Genoscope.

2 (bases 1 to 1864)

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seque@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

Location/Qualifiers

1. 1864

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/mol_type="mRNA"

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Best Local Similarity 99.6%; Pred. No. 0;
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RESULT 2

AY407799

LOCUS

DEFINITION

Homo sapiens

AY407799

ACCESSION

AY407799

VERSION

AY407799.1

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

AY407799 2493 bp DNA linear GSS 15-DEC-2003
Homo sapiens TCR1G1 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY407799.1 GI:39763770
GSS.
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1. (bases 1 to 2493)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civeillo, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

Gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302

REFERENCE 2 (bases 1 to 2493)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Carroll, M.

TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

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Qy 2002 GGCACACCTCTGACCTGTGTCACCGCCACCGCGCGCTGCGGAGAGGCGCGCTGAC 2061

Db 1948 GGCACACCTCTGACCTGTGTCACCGCCACCGCGCGCTGCGGAGAGGCGCGCTGAC 2007

Qy 2062 CGACAGAGAGAAACAAGGCGGCTGCTGACCTGCTGACGATCTGTAAGTGGCTGG 2121

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CR602058      1655 bp      mRNA      linear      HTC 21-JUL-2004
LOCUS      full-length cDNA clone CS0DI059YF06 of Placenta Cot 25-normalized
DEFINITION      of Homo sapiens (human).
ACCESSION      CR602058
VERSION      CR602058.1 GI:50482865
KEYWORDS      HTC; CNSLT CDNA.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE      1 (bases 1 to 1655)
AUTHORS      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished
REMARK      Contact : Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Paraday Avenue
              2 (bases 1 to 1655)
REFERENCE      Genoscope.
AUTHORS      Direct Submission
TITLE      Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL      BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
              - Web : www.genoscope.cns.fr)
COMMENT      1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life Technologies, a
              division of Invitrogen.
FEATURES
              Location/Qualifiers
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               /tissue type="Placenta Cot 25-normalized"
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ORIGIN
Query Match      31.7%; Score 838; DB 6; Length 1655;
Best Local Similarity 99.7%; Pred. NO. 0;
Matches 1078; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1519 AGTGATGCAATCTCTGGCCAGACGATGCTTACCTGGATCCCAAGCTCAACGGTGC 1578
DB 575 AGTGATGCAATCTCTGGCCAGACGATGCTTACCTGGATCCCAAGCTCAACGGTGC 634

QY 1579 TTCTGGGACCTTACCTCTTGGCATCGATCTCTATTGGAGCTTGCTGCCAACCACTTG 1638
DB 635 TTCTGGGACCTTACCTCTTGGCATCGATCTCTATTGGAGCTTGCTGCCAACCACTTG 694

QY 1639 AGCTTCTCAACTCTCTTCAAGATGAAGATGCTCGTCACTCTGGGGTGTGTGACATGGCC 1698
DB 695 AGCTTCTCAACTCTCTTCAAGATGAAGATGCTCGTCACTCTGGGGTGTGTGACATGGCC 754

QY 1699 TTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1758
DB 755 TTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 814

QY 1759 CTGGAGACGCTCGGAGCTCACCTTCTCTGGGGACTCTTCTGGTTACCTCGTGTTCCTA 1818
DB 815 CTGGAGACGCTCGGAGCTCACCTTCTCTGGGGACTCTTCTGGTTACCTCGTGTTCCTA 874

QY 1819 GTCATCTACAAGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1875
DB 875 GTCATCTACAAGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 934

QY 1876 ATCCACTTCAACATGTTCTTCTTCTCCACAGCCCGCAGCAACAGGCTGTCTACCCC 1935
DB 935 ATCCACTTCAACATGTTCTTCTTCTCCACAGCCCGCAGCAACAGGCTGTCTACCCC 994

QY 1936 CGGCAGGAGGTGGTCCAGGCCACGCTGGTGGTCTTGGCCCTTGGCCATGGTGGCCATCCTG 1995
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Db 995 CGCAGGAGGTGGTCCAGGCCACGCTGGTGGTCTTGGCCATGGTGGCCATCCTG 1054
QY 1996 CTGCTTTGGACACACCTCTGCACTGTGTGACACCGCCACCGCCGCTGCGAGGAGGCC 2055
Db 1055 CTGCTTTGGACACACCTCTGCACTGTGTGACACCGCCACCGCCGCTGCGAGGAGGCC 1114
QY 2056 GCTGACCGACAGGAGGAAACAAAGCCGGTGTGTGACCTGCGCTGACGATCTGTGAAT 2115
Db 1115 GCTGACCGACAGGAGGAAACAAAGCCGGTGTGTGACCTGCGCTGACGATCTGTGAAT 1174
QY 2116 GCTGAGCTCCGATGAGGAAAGCAGGGGCCCTGGATGATGAAGAGGAGGCCAGCTC 2175
Db 1175 GCTGAGCTCCGATGAGGAAAGCAGGGGCCCTGGATGATGAAGAGGAGGCCAGCTC 1234
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Db 1235 GTCCCTCGAGGTGCTCATGACACAGGCCATCCACCATCGAGTTCTGCTGGGCTGC 1294
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QY 2296 TCCGAGGTTCCTGCGGCCATGCTGATGCGCATAGGCTGGGCTGGGCCGAGGTTGGC 2355
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QY 2356 GTGGCGGCTGTGGTGTGCTGCTCCCATCTTTGCGGCTTTGCGGTGATGACCTGCTATC 2415
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QY 2416 CTGCTGTGTGATGGAGGACTCTCAGCTTCTGCGACGCCCTGGGCTGACCTGGGTGGA 2475
Db 1475 CTGCTGTGTGATGGAGGACTCTCAGCTTCTGCGACGCCCTGGGCTGACCTGGGTGGA 1534
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Db 1535 TTCCAGAACAACTTCTACTCAGGCACGGCTACAAAGCTGAGTCCCTTACCTTCGCTGC 1594
QY 2536 ACAGATGATAGGGCCCACTGAGTCTGCGACAGCTTCTTCTTCTGACCTCTGAGCAGG 2595
Db 1595 ACAGATGATAGGGCCCACTGAGTCTGCGACAGCTTCTTCTTCTGACCTCTGAGCAGG 1654
QY 2596 A 2596
Db 1655 A 1655

RESULT 4
BX358008      909 bp      mRNA      linear      EST 08-APR-2004
LOCUS      BX358008 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION      clone CS0DI032YN10 5-PRIME, mRNA sequence.
ACCESSION      BX358008
VERSION      BX358008.2 GI:46285730
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE      1 (bases 1 to 909)
AUTHORS      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT      On May 5, 2003 this sequence version replaced gi:30366180.
              Genoscope - Centre National de Sequencage
              2 rue Gaston Crenieux, CP 5706 - 91057 EVRY cedex - FRANCE
              Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
```

was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6186.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1032DG05QPl&c=6186.f.

FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1032YN10"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 27.8%; Score 734; DB 4; Length 909;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 884; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 607 CGCTCTCTGGAGGCGCTCCGCGCTTCTCTATTCAGGCTTCAGGAGCTGGAGCAG 666
DB 9 CGCTCTCTGGAGGCGCTCCGCGCTTCTCTATTCAGGCTTCAGGAGCTGGAGCAG 68
QY 667 CGCTGGAGCACCCTCGTGGGCGAGCCAGCCAGCTGGATGATCTCTCTCTCTCTAC 726
DB 69 CGCTGGAGCACCCTCGTGGGCGAGCCAGCCAGCTGGATGATCTCTCTCTCTAC 128
QY 727 TGGGGTGGAGATCGGACGAGAGATCGGACAGATCAGGAGCTGTCTCACTGCCAGCTC 786
DB 129 TGGGGTGGAGATCGGACGAGAGATCGGACAGATCAGGAGCTGTCTCACTGCCAGCTC 188
QY 787 TTCCCTTTCTGACAGAGAGAGGCGCGCTCGGGGCGCTCGAGAGCTGCAACAGCAG 846
DB 189 TTCCCTTTCTGACAGAGAGAGGCGCGCTCGGGGCGCTCGAGAGCTGCAACAGCAG 248
QY 847 AGCCAGGAGTGCCAGGAGTGCTCGGGGAGACAGAGCGGTCTCTGAGCCAGGTGCTAGGC 906
DB 249 AGCCAGGAGTGCCAGGAGTGCTCGGGGAGACAGAGCGGTCTCTGAGCCAGGTGCTAGGC 308
QY 907 CGGCTGCTGAGTGCTCGGCGCAGGCGAGGTGCGAGTCCAAAGATGAAGCCGTGTAC 966
DB 309 CGGCTGCTGAGTGCTCGGCGCAGGCGAGGTGCGAGTCCAAAGATGAAGCCGTGTAC 368
QY 967 CTGGCCCTGAACAGTGACGCTGACACACGACAGTGCTCTATTCGCGAGGCGCTGG 1026
DB 369 CTGGCCCTGAACAGTGACGCTGACACACGACAGTGCTCTATTCGCGAGGCGCTGG 428
QY 1027 TGCTCTGTGAGACCTGCGCGCTCGAGAGGCGCTCGGGGACAGCTCGATGGAGGAG 1086
DB 429 TGCTCTGTGAGACCTGCGCGCTCGAGAGGCGCTCGGGGACAGCTCGATGGAGGAG 488
QY 1087 GAGTGAAGTCCGCTGCTACCGCATCCCTGCGGGACATGCCCCCACTCATCCGC 1146
DB 489 GAGTGAAGTCCGCTGCTACCGCATCCCTGCGGGACATGCCCCCACTCATCCGC 548
QY 1147 ACCAACCGTTTACGCGCAGCTTCCAGGCGCATCGTGATGCTCTGTTGCTGTGATG 1206
DB 549 ACCAACCGTTTACGCGCAGCTTCCAGGCGCATCGTGATGCTCTGTTGCTGTGATG 608
QY 1207 CAGGAGGTCAACCCCGCTCCATACCATCATCATCTTCCCTTCTGTTGCTGTGATG 1266
DB 609 CAGGAGGTCAACCCCGCTCCATACCATCATCATCTTCCCTTCTGTTGCTGTGATG 668
QY 1267 TTCGGGGATGTGGGCGACCGGCTGCTCATGTTCTCTTGGCCCTGGCCATGTCCTTGG 1326
DB 669 TTCGGGGATGTGGGCGACCGGCTGCTCATGTTCTCTTGGCCCTGGCCATGTCCTTGG 728
QY 1327 GAGAACCGAGCGCTGTGAAGCGCGCAGAGAGATCTGGCAGACTTCTTCAGGGGC 1386

Db 729 GAGAACCGAGCGGCTGTGAAGGCGCGCAGAACGAGATCTGGCAGACTTCTTCAGGGGC 788
QY 1387 CGTACTCTGCTCTGCTTATGGGCGCTTCTTCCATCTACACCGGCTTCATCTACAACGAG 1446
Db 789 CGTACTCTGCTCTGCTTATGGGCGCTTCTTCCATCTACACCGGCTTCATCTACAACGAG 848
QY 1447 TGCTTACGTGCGCGCCACCGACATCTTCCCTCGGCTGGAGTGTGGC 1493
Db 849 TGCTTACGTGCGCGCCACCGACATCTTCCCTCGGCTGGAGTGTGGC 895

RESULT 5

DN996103
LOCUS
DEFINITION
TC110144 Human breast cancer tissue, large insert, pCMV expression
library Homo sapiens cDNA clone TC110144 5', similar to Homo sapiens
T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0
protein a isoform 3 (TCIRG1), transcript variant 2, mRNA sequence.
DN996103 757 bp mRNA linear EST 17-MAY-2005

ACCESSION

VERSION
DN996103.1 GI:6255930
KEYWORDS
EST.

SOURCE

ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE

AUTHORS
1 (bases 1 to 757)
Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
Zhang,X., Jay,G. and He,W.

TITLE

High-throughput cloning of full-length human cDNAs directly from
cDNA libraries optimized for large and rare transcripts

JOURNAL

Unpublished (2005)

COMMENT

Contact: Kovacs, KF
High Throughput cDNA Cloning
Origene Technologies, Inc. (www.origene.com)
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606

Email: cdna@origene.com
This EST submission is part of an on-going human full-length
cloning project at Origene Technologies, Inc.
Please contact Origene for access.
Origene Technologies, Inc.
6 Taft Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
http://www.origene.com

Seq primer: pCMV6 5prime forward vector primer, Origene
Technologies Inc.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC110144"
/tissue_type="Breast cancer"
/clone_lib="Human breast cancer tissue, large insert, pCMV
expression library"
/note="Organ: Mammary gland (cancer tissue); Vector:
pCMV6-XL5; Site_1: EcoRI; Site_2: XhoI/Sall compatible end
ligatio; Oligo-dT primed reverse transcription optimized
for large and GC rich mRNA transcripts, cDNA size
selection, optimized ligation for large inserts into
mammalian expression vector, random clones selected for
end sequence verification of full-length genes"

ORIGIN

Query Match 27.6%; Score 729; DB 9; Length 757;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 377 AGTCGGGAGTGTGGGGCAACCGAGCCCTCGGGGCCAGCTGCACGAGTGTGAGC 436

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Db 29 AGCTGCGGATGTCGGGGCAACACAGAGCCCTCGGGCCCAAGTGCACCACTGCAGC 88
Qy 437 TCACGCGCGCTGTACGCCAGGGCCATGAACCTCAGCTGGCAGCGCCCAACAGATG 496
Db 89 TCACGCGCGCTGTACGCCAGGGCCATGAACCTCAGCTGGCAGCGCCCAACAGATG 148
Qy 497 GGGCTTCAGAGAGGAGCGCCCTGCTCCAGGCCCCCGGGGGCCGACACAGGACCTGAGG 556
Db 149 GGGCTTCAGAGAGGAGCGCCCTGCTCCAGGCCCCCGGGGGCCGACACAGGACCTGAGG 208
Qy 557 TCAACTTTGTGCGAGTGCGGTGAGAGCCCAAGGCCCTTCCCTTAGAGCGCTGCTCT 616
Db 209 TCAACTTTGTGCGAGTGCGGTGAGAGCCCAAGGCCCTTCCCTTAGAGCGCTGCTCT 268
Qy 617 GGAGGCGCTGCGCGGCTTCTCATTTGAGCTTCCAGGAGTGGAGCGCGCTGAGAGC 676
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Qy 677 ACCCGTGTACGGGGGAGGAGCGAGCCAGTGTGATGACCTTCTCATCTTCTACTGSGGTGAGC 736
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Qy 737 AGATCGGACAGAGATCCGCAAGATCAAGACTGCTTCCACTGCCACAGTCTTCCCGTTTC 796
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Db 629 ACCAGTGCAGGTGAGCAGCAGCAGCAGTGCCTCATTTGCCGAGCGCTGCTGCTGTC 688
Qy 1037 GAGACTGCGCCCTGAGGAGGCGCTGCGGGACAGCTCGATGAGGAGGAGTGAAGT 1096
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Db 749 CCGTGGCTC 757
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RESULT 6
BX332189
LOCUS
DEFINITION BX332189 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC008YL06 5-PRIME, mRNA sequence.
ACCESSION BX332189
VERSION BX332189.2 GI:46274586
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1070)
AUTHORS Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:30341122.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
```

Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
6186.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna/s=CS0DC008DF03QPI&c=6186.f.

FEATURES

source

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/clone="CS0DC008YL06"
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/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 26.2%; Score 692; DB 4; Length 1070;
Best Local Similarity 99.6%; Pred. No. 6, 9e-305;
Matches 842; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 838 CAACAGCAGAGCAGGAGCTGCAGAGGTCTTCGGGGAGACAGAGCGGTTCTCTGAGCCAG 897
Db 1 CAACAGCAGAGCAGGAGCTGCAGAGGTCTTCGGGGAGACAGAGCGGTTCTCTGAGCCAG 60
Qy 898 GTGCTAGGCGCGGTGCTCAGCTGTCGCCGACGAGGCGGAGTGCAGGTTCCACAGATGAG 957
Db 61 GTGCTAGGCGCGGTGCTCAGCTGTCGCCGACGAGGCGGAGTGCAGGTTCCACAGATGAG 120
Qy 958 GCCGTGTACCTGGGCCCTGAACACAGTGCAGCTGAGCACCAGCACAAGTGCTCTATTGCC 1017
Db 121 GCCGTGTACCTGGGCCCTGAACACAGTGCAGCTGAGCACCAGCACAAGTGCTCTATTGCC 180
Qy 1018 GAGGCTTGGTGTCTGTGCGAGACCTGCCCGCTTCGAGGAGGCGCTTCGGGACAGCTCG 1077
Db 181 GAGGCTTGGTGTCTGTGCGAGACCTGCCCGCTTCGAGGAGGCGCTTCGGGACAGCTCG 240
Qy 1078 ATGAGGAGGAGGAGTGAAGTGCCTCAGCGCATCCCTCGCGGAGCATGCCCCCAACA 1137
Db 241 ATGAGGAGGAGGAGTGAAGTGCCTCAGCGCATCCCTCGCGGAGCATGCCCCCAACA 300
Qy 1138 CTCATCCGACCAACCCGCTTCACGCGCCAGCTTCCAGGGGATCGTGGATCGCTTACGCGCTG 1197
Db 301 CTCATCCGACCAACCCGCTTCACGCGCCAGCTTCCAGGGGATCGTGGATCGCTTACGCGCTG 360
Qy 1198 GCGCGCTACAGAGAGGTCAACCCGCTCCTTACACCATCATCATCTTCCCTTCTCTGTTT 1257
Db 361 GCGCGCTACAGAGAGGTCAACCCGCTCCTTACACCATCATCATCTTCCCTTCTCTGTTT 420
Qy 1258 GCTGTGATGTTTCGGGATGTGGCCACAGGCTGCTCATGTTCTCTTCGCTCGCTGCGCCATG 1317
Db 421 GCTGTGATGTTTCGGGATGTGGCCACAGGCTGCTCATGTTCTCTTCGCTCGCTGCGCCATG 480
Qy 1318 GTCTTTCGGGAGAACCCGCTGTGAAAGCGCGCAGAACAGATCTTGGCAGACTTTTC 1377
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Qy 1378 TTCAGGCGCGGTACCTGCTCCTGTTATGGGCTGTTTCTCATCTACACCGGCTTCATC 1437
Db 541 TTCAGGCGCGGTACCTGCTCCTGTTATGGGCTGTTTCTCATCTACACCGGCTTCATC 600
Qy 1438 TACACAGAGTGTTCAGTCCGCGCCACAGCATCTTCCCTCGGGCTGGAGTGTGCGCGC 1497
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Db 661 ATGCCCAACAGTCTGGCTGGAGTGATGTCATTCTTGGCCAGCACAGATCTTACCCCTG 720
QY 1558 GATCCCAACAGTACCGGTGCTTCTCTGGGACCCCTACCCCTTGGCATCGATCCCTATTGG 1617
Db 721 GATCCCAACAGTACCGGTGCTTCTCTGGGACCCCTACCCCTTGGCATCGATCCCTATTGG 780
QY 1618 AGCTGCTGCTGCAACCACTTGGAGCTTCTCAACTCTTCAAGATGAAGATGTCGCTCATC 1677
Db 781 AGCTGCTGCTGCAACCACTTGGAGCTTCTCAACTCTTCAAGATGAAGATGTCGCTCATC 840
QY 1678 CTGGG 1682
Db 841 CTGGG 845

CR599870 671 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODI006Y009 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR599870.1 GI:50480677
VERSION HTC; CNSLT cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE 1 (bases 1 to 671)
JOURNAL Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
REMARK Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 671)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoK v sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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/plasmid="pCMVSPORT_6"
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Best Local Similarity 100.0%; Pred. No. 2.9e-295;
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1953 GGCACGCTGGTGGTCTGTCGCTTGGCCATGGTGGCCATCTGCTGGGACACCCCT 2012
Db 1 GGCACGCTGGTGGTCTGTCGCTTGGCCATGGTGGCCATCTGCTGGGACACCCCT 60
QY 2013 GCACCTGCTGCACCGCCGACCGCCCTGCGAGAGGAGCCGCTGACCGACAGAGGA 2072
Db 61 GCACCTGCTGCACCGCCGACCGCCCTGCGAGAGGAGCCGCTGACCGACAGAGGA 120
QY 2073 AACCAAGGCGGGTGTGCTGACCTGCTGACGATCTGTGAATGGCTGGAGCTCCGATGA 2132
Db 121 AACCAAGGCGGGTGTGCTGACCTGCTGACGATCTGTGAATGGCTGGAGCTCCGATGA 180
QY 2133 GGNAAGGCGGGGGCTGGATGATGAGAGGAGGCGGAGCTGCTCCCTCCGAGGTGCT 2192
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Db 181 GGAAGAGGCGAGGGGCGCTGGATGATGAAGAGGAGGCGGAGCTCGTCCCTCCGAGGTGCT 240
QY 2193 CATGCACACAGGCCATCCACACCATCGAGTTCCTGCTGGGCTGCTCTCCACACCGCTC 2252
Db 241 CATGCACACAGGCCATCCACACCATCGAGTTCCTGCTGGGCTGCTCTCCACACCGCTC 300
QY 2253 CTACCTGCGGCTGFGGGCCCTGAGCCTGGGCCACCGCCAGCTGCCAGGTTCTGTGGGC 2312
Db 301 CTACCTGCGGCTGFGGGCCCTGAGCCTGGGCCACCGCCAGCTGCCAGGTTCTGTGGGC 360
QY 2313 CATGCTGATGCGCATAGGCTGGGCTGGGCGGAGGTTGGGCTGGGCTGGGCTGGTGTGCT 2372
Db 361 CATGCTGATGCGCATAGGCTGGGCTGGGCGGAGGTTGGGCTGGGCTGGGCTGGTGTGCT 420
QY 2373 GGTCCCCCATCTTTGGCCGCTTTGGCGGTGATGACCGTGGCTATCTCTGCTGGTGGATGGAGG 2432
Db 421 GGTCCCCCATCTTTGGCCGCTTTGGCGGTGATGACCGTGGCTATCTCTGCTGGTGGAGG 480
QY 2433 ACTCTAGCCTTCTGCAACGCTGGGCTGACCTGGGTTGGAATTCAGAAACAAGTTCTA 2492
Db 481 ACTCTAGCCTTCTGCAACGCTGGGCTGACCTGGGTTGGAATTCAGAAACAAGTTCTA 540
QY 2493 CTCAGGACGCGGTACCAAGCTGAGTCCCTTCACCTTCGCTGCCACAGATGACTAGGCGCC 2552
Db 541 CTCAGGACGCGGTACCAAGCTGAGTCCCTTCACCTTCGCTGCCACAGATGACTAGGCGCC 600
QY 2553 ACTGCAAGTCTTCCAGACCTCTCTCTGCTGACCTTCAGGAGGAGAGGAAATAAGACGGT 2612
Db 601 ACTGCAAGTCTTCCAGACCTCTCTCTGCTGACCTTCAGGAGGAGAGGAAATAAGACGGT 660
QY 2613 CCGCCCTTGGCA 2623
Db 661 CCGCCCTTGGCA 671

RESULT 8
BQ073186 1088 bp mRNA linear EST 02-APR-2002
LOCUS AGENCOURT 6817733 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:575559
DEFINITION 5', mRNA sequence.
ACCESSION BQ073186
VERSION BQ073186.1 GI:19902232
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE 1 (bases 1 to 1088)
JOURNAL NIH-MGC http://mgi.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12799 row: p column: 08
High quality sequence stop: 593.
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/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 25.4%; Score 671; DB 3; Length 1088;
Best Local Similarity 100.0%; Pred. No. 2.8e-295;
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 14 ACAGGCTGCTCTACCCCGGAGGAGGTGTTCAGGCCACGCTGTGTCTGGCCTTGG 73

QY 1979 CATAGTGCCTATCTCTGCTGTGGCACACCTCTGACCTGTGCACCGCCACCGCGCC 2038
DB 74 CATAGTGCCTATCTCTGCTGTGGCACACCTCTGACCTGTGCACCGCCACCGCGCC 133

QY 2039 GCTTCGGAGGAGCCGCTGACCGACAGGAGGAAACAAGCGCGGTGTCTGGACCTGC 2098
DB 134 GCTTCGGAGGAGCCGCTGACCGACAGGAGGAAACAAGCGCGGTGTCTGGACCTGC 193

QY 2099 CTGACGCATCTGTGAATGCTGTGAGTCCGATGAGGAAAGGAGGCGGCTGTGATG 2158
DB 194 CTGACGCATCTGTGAATGCTGTGAGTCCGATGAGGAAAGGAGGCGGCTGTGATG 253

QY 2159 AAGAGGAGCCGAGCTGCTCCCTCGAGGTGCTCATGACAGGCGCATCCACACATCG 2218
DB 254 AAGAGGAGCCGAGCTGCTCCCTCGAGGTGCTCATGACAGGCGCATCCACACATCG 313

QY 2219 AGTTCTGCTGGGCTGCTCTCAACACCGCCTCTTACCTGCGCCTGTGGCGCCTGAGCC 2278
DB 314 AGTTCTGCTGGGCTGCTCTCAACACCGCCTCTTACCTGCGCCTGTGGCGCCTGAGCC 373

QY 2279 TGGCCACGCCAGCTGCTCGAGTCTGTGGCCATGTGTATGCGCATAGGCTGGGCC 2338
DB 374 TGGCCACGCCAGCTGCTCGAGTCTGTGGCCATGTGTATGCGCATAGGCTGGGCC 433

QY 2339 TGGGCGGGAGGTGGCGGTGGCTGTGTGTGTCTCCCATCTTTGCGCCTTTGCGG 2398
DB 434 TGGGCGGGAGGTGGCGGTGGCTGTGTGTGTCTCCCATCTTTGCGCCTTTGCGG 493

QY 2399 TGATGACCGTGTCTATCTCTGTGTGTATGAGGAGCTCTCAGCCTTCTTGACGCGCCTGC 2458
DB 494 TGATGACCGTGTCTATCTCTGTGTGTATGAGGAGCTCTCAGCCTTCTTGACGCGCCTGC 553

QY 2459 GGCTGCACTGGTGGATTCAGACAAAGTTCTACTCAGGACGGGCTACAAGCTGATC 2518
DB 554 GGCTGCACTGGTGGATTCAGACAAAGTTCTACTCAGGACGGGCTACAAGCTGATC 613

QY 2519 CTTTACCTTCGTCGACAGATGACTAGGCGCCACTGAGGTCTGCGCAGACCTCTTC 2578
DB 614 CTTTACCTTCGTCGACAGATGACTAGGCGCCACTGAGGTCTGCGCAGACCTCTTC 673

QY 2579 CTGACCTCTGA 2589
DB 674 CTGACCTCTGA 684

RESULT 9

BU732254/c
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DEFINITION BU732254 664 bp mRNA linear EST 09-OCT-2002
UI-E-COI-afx-k-03-0-UI.81 UI-E-COI Homo sapiens cdna clone
ACCESSION BU732254
VERSION BU732254
KEYWORDS BU732254.1 GI:23657965
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 664)
Bonaldo, M.P., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
8889548
PUBMED

COMMENT

Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue procurement: Dr. Gregg Hageman
cdna Library preparation: Dr. M. Bento Soares, University of Iowa
cdna Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
POLYA=Yes.

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UI-E-COI is a normalized cdna library containing the
following tissue(s): optic nerve. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cdna
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cdna was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cdna contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CCATTAAAGT. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI).
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TAG_LIB=UI-E-COI
TAG_SEQ=CCATTAAAGT"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.2e-272;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 620 TGCACCGCCACCGCCGCTGCGAGGAGGAGCCGCTGACCGACAGGAGGAAACAAGG 561

QY 2081 CCGGGTTGCTGACCTGCTGACGATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGG 2140
DB 560 CCGGGTTGCTGACCTGCTGACGATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGG 501

QY 2141 CAGGGGGCTGTGATGATGAAGAGGAGGCGGAGCTGTCCCTCCGAGGTGCTCATGCACC 2200
DB 500 CAGGGGGCTGTGATGATGAAGAGGAGGCGGAGCTGTCCCTCCGAGGTGCTCATGCACC 441

QY 2201 AGGCCATCCACACCATCGAGTTCTGCTGGGCTGTCTCCAACACCGCCTCTCTACCTGC 2260

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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	Db	361	CCATCGCCACGCTTCCCGTTTTCGACAGAGAGAGAGCCCTCGGGGCCCCCTGAGCA	420
	Hominidae; Homo.	Qy	834	GCTGCAACAGCAGCAGGAGCTGACAGAGCTCTCGGGGAGACAGAGCGGTCTCTGAG	893
REFERENCE	1 (bases 1 to 842)	Db	421	GCTGCAACAGCAGCAGGAGCTGACAGAGCTCTCGGGGAGACAGAGCGGTCTCTGAG	480
AUTHORS	Heil, O., Ebert, L., Hennig, S., Henze, S., Radelof, U., Schneider, D. and Korn, B.	Qy	894	CCAGGTGCTAGGCCCGGCTGCTGACCTGCTGCGCCAGGAGGTGACAGTCCACAAGAT	953
TITLE	Human T-Lymphocytes library	Db	481	CCAGGTGCTAGGCCCGGCTGCTGACCTGCTGCGCCAGGAGGTGACAGTCCACAAGAT	540
JOURNAL	Unpublished (2005)	Qy	954	GAAGGCCGTGACCTGGCCCTGAACAGCTGACAGTGCAGCAGCAGCAGTGCCTCAT	1013
COMMENT	Contact: Inge Airlart	Db	541	GAAGGCCGTGACCTGGCCCTGAACAGCTGACAGTGCAGCAGCAGCAGTGCCTCAT	600
	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH	Qy	1014	TGCCGAGGCGCTGG	1026
	Heubnerweg 6, D-14059 Berlin, Germany	Db	601	TGCCGAGGCGCTGG	613
	Email: www.rzpd.de				
	RZPD; RZPDp901611642.				
	RZPDLIB; (Human T-Lymphocytes) RZPD LIB No. 9016				
	http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact:				
	Inge Airlart				
	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH				
	Heubnerweg 6, D-14059 Berlin, Germany				
	Tel: +49 30 32639 100				
	Fax: +49 30 32639 111				
	www.rzpd.de				
	This clone is available from RZPD;				
	http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPDp901611642				
	contact RZPD (product- support@rzpd.de) for further information.				
	Primer name: q3 4 . Primer sequence: CGGTAACAATTCACAG.				
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	http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml				
	; 1st strand cDNA was prepared from mRNA obtained from				
	human T-Lymphocytes with a NotI - oligo(dT) primer [5,				
	GACTAGTCTAGATCGGAGCGCGCCCTTTTCTTTT 3'].				
	Double-stranded cDNA was ligated to SalI adaptors,				
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Qy	474 GCTGGCAGCGCCGCCACACAGATGGGCGCTCAGAGAGAGCGCCCTGCTCCAGGCGCCCGG	533			
Db	61 GCTGGCAGCGCCGCCACACAGATGGGCGCTCAGAGAGAGCGCCCTGCTCCAGGCGCCCGG	120			
Qy	534 GGGGCGGCAACAGGACCTGAGGCTCAACTTTGTGGCAGTGGCGGTGGAGCCGCCACAAGGC	593			
Db	121 GGGGCGGCAACAGGACCTGAGGCTCAACTTTGTGGCAGTGGCGGTGGAGCCGCCACAAGGC	180			
Qy	594 CCTGCTCCTAGAGCGCTGCTCTGGAGGCGCTGCGCGGCTCTCTATTCAGCTTCAG	653			
Db	181 CCTGCTCCTAGAGCGCTGCTCTGGAGGCGCTGCGCGGCTCTCTATTCAGCTTCAG	240			
Qy	654 GGAGCTGGAGCAGCGCTGGAGCAGCCCGTGCAGCGGCGAGCAGCAGCAGTGCATGACCTT	713			
Db	241 GGAGCTGGAGCAGCGCTGGAGCAGCCCGTGCAGCGGCGAGCAGCAGCAGTGCATGACCTT	300			
Qy	714 CTTCTATCTCTACTGCGGTGAGCAGATCGGACAGAGATCCGCAAGATCACGAGCTGCTT	773			

Db	481	CCTGCCCGCCCTGACGAGGCGCCCTGCGGACAGCTCGATGAGGAGCGAGTGAGTGCCCT	540
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Site_2: Not I; NCI CGAP FL0 is a cDNA library derived from  
a pool of mRNA obtained from 4 cell lines from grade III  
chondrosarcoma tissues. The library was constructed  
according to Bonaldo, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double  
stranded cDNA was ligated to an Ecor I adaptor, digested  
with Not I, and cloned directionally into p77T3-Pac  
vector. The oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is GAGTCTGGTG. The cell line  
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TAG TISSUE=Human Chondrosarcoma Grade 3 cell line mix  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.5e-262;  
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QY 2102 ACGCATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGGACAGGGGGCTTGGATGATGAAG 2161  
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QY 539 ACGCATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGGACAGGGGGCTTGGATGATGAAG 480  
DB |||||||  
QY 2162 AGGAGGCGAGCTGCTCCCTCCGAGGTCTCATGACAGGCCATCCACCATCGAGT 2221  
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QY 479 AGGAGGCGAGCTGCTCCCTCCGAGGTCTCATGACAGGCCATCCACCATCGAGT 420  
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QY 119 TCACCTTCGCTGCCACAGATGACTAGGGGCCACCTGCAGGTCTCTGCCAGACTCTCTCTG 60  
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QY 2582 ACCTCTGAGCGAGGAGGAATAGAGCGTCCGCCCTGGCAAAAAAAAAAAAAA 2640  
DB |||||||  
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 30, 2006, 05:49:39 ; Search time 490 Seconds
(without alignments)
10081.076 Million cell updates/sec

Title: US-10-783-519-1
Perfect score: 2640
Sequence: 1 cggcgctgcggacggcgag.....gcaaaaaaaaaaaaaaaaaa 2640

Scoring table: Oligo NUC
Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2806514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*

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- 10: /EMC_Celerra_SID33/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2640	100.0	2640	3	US-08-684-932A-37
2	2640	100.0	2640	3	US-08-618-304B-1
3	2640	100.0	2655	3	US-09-016-434-1094
4	2640	100.0	2655	3	US-09-023-655-916
5	2640	100.0	2655	4	US-08-880-107-3363
6	2142	81.1	2654	3	US-09-949-016-2404
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23	160	6.1	601	3	US-09-949-016-46215

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41 122 4.6 601 3 US-09-949-016-83495 Sequence 83495, A
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43 122 4.6 601 3 US-09-949-016-107575 Sequence 107575, A
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ALIGNMENTS

RESULT 1
US-08-684-932A-37
; Sequence 37, Application US/08684932A
; Patent No. 6403304
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; APPLICANT: Li, Yi-ping
; APPLICANT: Wuchertfennig, Anne L.
; TITLE OF INVENTION: HUMAN OSTEOCLAST-SPECIFIC AND -RELATED
; TITLE OF INVENTION: DNA SEQUENCES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,932A
; FILING DATE: 19-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC92-02FM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2640 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 58..2523
US-08-684-932A-37


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RESULT 2

US-09-618-304B-1

; Sequence 1, Application US/09618304B

; Patent No. 677537

; GENERAL INFORMATION:

; APPLICANT: Stashenko, Philip

; APPLICANT: Li, Yi-Ping

; TITLE OF INVENTION: Osteoclast Proton Pump Subunit

; FILE REFERENCE: 1564.1006-001

; CURRENT APPLICATION NUMBER: US/09/618,304B

; PRIOR FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: 08/605,378

; PRIOR FILING DATE: 1996-02-22

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2640

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-618-304B-1

Query Match 100.0%; Score 2640; DB 3; Length 2640;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-016-434-1094
; Sequence 1094, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1094:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G1245045
US-09-016-434-1094

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-09-023-655-916
; Sequence 916, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE D
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERSEWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 916:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

QY	61	GGCTCCATGTTTCGGAGCGAGAGGTGGCCCTGGTCCAGCTCTTTCTGCCCCACAGGGCT	120
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QY	61	GGCTCCATGTTTCGGAGCGAGAGGTGGCCCTGGTCCAGCTCTTTCTGCCCCACAGGGCT	120
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QY	121	GCCTACACCTGCGTGAAGTCCGGCTGGCGAGCTGGGCTCGTGGAGTTCAGAGACCTCAAC	180
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QY	121	GCCTACACCTGCGTGAAGTCCGGCTGGCGAGCTGGGCTCGTGGAGTTCAGAGACCTCAAC	180
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QY	181	GCCTCGGTGAGCGCTTCAGAGACGCTTTGTGGTGAATGTTTGGCGCTGTGAGGAGCTG	240
Db			
QY	181	GCCTCGGTGAGCGCTTCAGAGACGCTTTGTGGTGAATGTTTGGCGCTGTGAGGAGCTG	240
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QY	241	GAGAGACCTTCACTTCTGACAGAGAGGTGGCGGGCTGGGCTGGTCTGCCCGG	300
Db			
QY	241	GAGAGACCTTCACTTCTGACAGAGAGGTGGCGGGCTGGGCTGGTCTGCCCGG	300
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QY	301	CCAAAGGGAGGCTGCGGACACCCCAACCCCGGACCTGCTGGCATCCAGGAGGAGAGCG	360
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QY	301	CCAAAGGGAGGCTGCGGACACCCCAACCCCGGACCTGCTGGCATCCAGGAGGAGAGCG	360
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QY	361	GAGCGCTGGCCAGAGCTGGGGATGTGGGGGCAACAGGAGGCCCTGGCGGCCAG	420
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QY	361	GAGCGCTGGCCAGAGCTGGGGATGTGGGGGCAACAGGAGGCCCTGGCGGCCAG	420
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QY	1081	GAGGAGGAGTGAGTGCCTGGCTCACCGCATCCCTGCGGGACATGCCCCCCACATC	1140
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QY	1141	ATCCGACACAAACCGCTTCAACGCGCAGCTTTCAGGGCATCTGTGGATCGCTACGGCGTGGGC	1200
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QY	1441	AACGAGTGTTCAGTCCGCGCACACGAGATCTTCCCTCGGGCTGAGGTGTGGCCGCCATG	1500
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QY	1561	CCCAACGCTCACCGGCTGCTTCTGGGACCTTACCCCTTGGCATCGATCTATTTGGAGC	1620
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QY	1621	CTGGCTGCGCAACCACTTGAGCTTCTCAATCTCTTCAAGATGAAGATGTCGTCACTG	1680
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QY	1621	CTGGCTGCGCAACCACTTGAGCTTCTCAATCTCTTCAAGATGAAGATGTCGTCACTG	1680
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QY	1681	GCGCTGCTGCAATGCGCTTTGGGGTGTCTCGAGTCTTCAACACAGTGCACCTTGGC	1740
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QY	1681	GCGCTGCTGCAATGCGCTTTGGGGTGTCTCGAGTCTTCAACACAGTGCACCTTGGC	1740
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QY	1741	CAGAGGCAACCGCTGCTGCGAGACGCTGCGGAGCTCACTTCTCTGCTGGGACTCTTC	1800
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QY	1741	CAGAGGCAACCGCTGCTGCGAGACGCTGCGGAGCTCACTTCTCTGCTGGGACTCTTC	1800
Db			
QY	1801	GGTTACCTCGTTCCTAGTCACTACAGTGGCTGTGTGTCTGGGCTGCCAGGGCCGCG	1860
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QY	1801	GGTTACCTCGTTCCTAGTCACTACAGTGGCTGTGTGTCTGGGCTGCCAGGGCCGCG	1860
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QY	1861	TGCGCCAGCATCCTCATCACTTCAATCAACATGTTCTCTTCCACAGCCCGCAGCAAC	1920
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QY	1861	TGCGCCAGCATCCTCATCACTTCAATCAACATGTTCTCTTCCACAGCCCGCAGCAAC	1920
Db			
QY	1921	AGGCTGCTTACCCCGCAGAGGTGTTCAGGCAACGCTGGTGGTCTTGGCTTGGCC	1980
Db			
QY	1921	AGGCTGCTTACCCCGCAGAGGTGTTCAGGCAACGCTGGTGGTCTTGGCTTGGCC	1980
Db			
QY	1981	ATGGTCCCATCTGCTGCTTGGCACACCCCTGCACTGCTGTCACCGCCACCGCCGCGC	2040
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QY	1981	ATGGTCCCATCTGCTGCTTGGCACACCCCTGCACTGCTGTCACCGCCACCGCCGCGC	2040
Db			
QY	2041	CTGCGGAGAGGCCCGCTGACCGACAGAGGAAACAAAGGCGGGTGTGAGACCTGCT	2100
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QY	2041	CTGCGGAGAGGCCCGCTGACCGACAGAGGAAACAAAGGCGGGTGTGAGACCTGCT	2100
Db			
QY	2101	GACCATCTGTGAATGGTGGAGTCCGATGAGGAAAGGCAAGGGGCTTGATGATGAA	2160
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QY	2101	GACCATCTGTGAATGGTGGAGTCCGATGAGGAAAGGCAAGGGGCTTGATGATGAA	2160
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QY	2161	GAGGAGGCGAGCTCGTCCCTCGAGGTGTCTATGCAACCGGCCATCCACACCATCGAG	2220
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QY	2161	GAGGAGGCGAGCTCGTCCCTCGAGGTGTCTATGCAACCGGCCATCCACACCATCGAG	2220
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QY	2221	TTCTGCTGGGCTGCTCTCCAAACCCGCTCTACCTGCGCTGTGGGCGCTTGAGGCTG	2280
Db			

2221 TTCTGCTGGCTGCGTCTCAACACCGCTTCTTACCTGGCCCTGTGGGCCCTGAGCTG 2280
2281 GCCACGCCAGCTGTCCGAGGTTCTGTGGGCCATGTGTGATGCGCATAGGCTGGGCTG 2340
2281 GCCACGCCAGCTGTCCGAGGTTCTGTGGGCCATGTGTGATGCGCATAGGCTGGGCTG 2340
2341 GCGCGGAGTGGCGTGGCGTGTGGTGTGCTGCCATCTTTTGGCGCTTTGGCGTG 2400
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2401 ATGACCTGTGCTATCTCTGTGTGATGAGGAGCTCTCAGCCTTCTTGCAGCGCCCTGGG 2460
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2461 CTGCACTGGGTGGAATTCAGAAACAAGTTCTTACTCAGGCACGGGCTACAGCTGAGTCCC 2520
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2521 TTCACTTCTGCTGCACAGATGACTAGGCGCCACTGCAGGTCTTGCAGACCTCTTCTCT 2580
2581 GACCTCTGAGCAGGAGGAGTAACACACGCTCCGCTCGCAAAAAA 2640
2581 GACCTCTGAGCAGGAGGAGTAACACACGCTCCGCTCGCAAAAAA 2640

RESULT 6
US-09-949-016-2404
; Sequence 2404, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2404
; LENGTH: 2654
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2404

Query Match 81.1%; Score 2142; DB 3; Length 2654;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2582; Conservative 0; Mismatches 4; Indels 3; Gaps 1;
38 GCGCAGCACACCGGGGACCATGGGCTCCATGTTCCGAGCGAGAGGTGGCCCTGGTCC 97
66 GCGCAGCACACCGGGGACCATGGGCTCCATGTTCCGAGCGAGGAGGTGGCCCTGGTCC 125
98 AGCTCTTTTCCGACAGCGGCTGCTTACACCTGCTGTGATGCGGCTGGGCGAGTGGGCC 157
126 AGCTCTTTTCCGACAGCGGCTGCTTACACCTGCTGTGATGCGGCTGGGCGAGTGGGCC 185
158 TCGTGGAGTTTCAGAGCTCAACGCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTG 217
186 TCGTGGAGTTTCAGAGCTCAACGCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTG 245
218 ATGTTTGGCGCTGTGAGGAGCTGGAGAAACCTTTCACCTTCTTGCAGGAGGAGTGGCG 277
246 ATGTTTGGCGCTGTGAGGAGCTGGAGAAACCTTTCACCTTCTTGCAGGAGGAGTGGCG 305

278 GGGCTGGCTGGTCTGCTGCCCGCCAAAGGGAGGCTGCGGCAACCCACCCCGGAGCC 337
306 GGGCTGGCTGGTCTGCTGCCCGCCAAAGGGAGGCTGCGGCAACCCACCCCGGAGCC 365
338 TGCTGGCGATTCAGGAGGAGACGAGCGCTTGGCCACAGGAGCTGCGGATGTGCGGGGCA 397
366 TGCTGGCGATTCAGGAGGAGACGAGCGCTTGGCCACAGGAGCTGCGGATGTGCGGGGCA 425
398 ACCAGCAGGCGCTGCTGGGCGCCAGCTGCACAGCTGCAGCTCCACGCGCGCTGTACGCC 457
426 ACCAGCAGGCGCTGCTGGGCGCCAGCTGCACAGCTGCAGCTCCACGCGCGCTGTACGCC 485
458 AGGCGCATGAACCTCAGCTGCGAGCGCCACACAGATGGGGCTTCAGAGAGGAGCGCCC 517
486 AGGCGCATGAACCTCAGCTGCGAGCGCCACACAGATGGGGCTTCAGAGAGGAGCGCCC 545
518 TGCTCCAGGCGCCCGGGGGCGCCGACACAGGAGCTGAGGGTCAACTTTTGGCAGGTGCGG 577
546 TGCTCCAGGCGCCCGGGGGCGCCGACACAGGAGCTGAGGGTCAACTTTTGGCAGGTGCGG 605
578 TGGAGCGCCCAAGGCGCCCTGCGCTAGAGCGCTGTCTTGGAGGGCTGCGCGCGCTTCC 637
606 TGGAGCGCCCAAGGCGCCCTGCGCTAGAGCGCTGTCTTGGAGGGCTGCGCGCGCTTCC 665
638 TCATTGCCAGCTTTCAGGAGCTGAGCAGCGCTGAGGACCCCGTGCACGCGCGCAGCAG 697
666 TCATTGCCAGCTTTCAGGAGCTGAGCAGCGCTGAGGACCCCGTGCACGCGCGCAGCAG 725
698 CCACGTGGATGACCTTCTCTCACTCTCTTCTGGGTGAGCAGATCGGACAGAAATCCGCA 757
726 CCACGTGGATGACCTTCTCTCACTCTCTTCTGGGTGAGCAGATCGGACAGAAATCCGCA 785
758 AGATCAGGAGCTGCTTCTCACTGCGACGCTTCTTCCGCTTCTGCGAGCAGGAGGCGCCGCC 817
786 AGATCAGGAGCTGCTTCTCACTGCGACGCTTCTTCCGCTTCTGCGAGCAGGAGGCGCCGCC 845
818 TCGGGCGCTTGCAGCAGCTGCAACAGCAGCAGCAGGAGCTGAGGAGGCTTCTCGGGGAGA 877
846 TCGGGCGCTTGCAGCAGCTGCAACAGCAGCAGCAGGAGCTGAGGAGGCTTCTCGGGGAGA 905
878 CAGAGCGGTTCTTGCAGCAGCTGAGCGCGGTGCTGAGCTGCTGCCCGCAGGCGAGG 937
906 CAGAGCGGTTCTTGCAGCAGCTGAGCGCGGTGCTGAGCTGCTGCCCGCAGGCGAGG 965
938 TGCAGGTCCACAAAGATGAAGCGCTGTACTGCGCCCTGAAACCAAGTGCGAGCTGAGACCA 997
966 TGCAGGTCCACAAAGATGAAGCGCTGTACTGCGCCCTGAAACCAAGTGCGAGCTGAGACCA 1025
998 CGCACAAAGTGCTTCAATTGCGGAGCGCTGTGCTGTGCGAGACCTGCGCGCCCTGAGG 1057
1026 CGCACAAAGTGCTTCAATTGCGGAGCGCTGTGCTGTGCGAGACCTGCGCGCCCTGAGG 1085
1058 AGGCGCTTGGGGGACAGCTCGATGAGGAGGAGTGTGCTGCTGCGAGACCTGCGCGCCCTGAGG 1117
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1118 GCGGGGACATGCCCCCACAATCATCCGACCAACCGCTTTCAGGCGCAGCTTCCAGGGCA 1177
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1178 TCGTGGATCGCTAGGCGGTGGGCGCTACACAGAGGTCAACCCCGCTTCCCTACACCATCA 1237
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1266 TCACCTTCCCTTCTTGTGCTGTGATGTTTGGGGATGTGGGCGACGCGCTGCTCATGT 1325
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1326 TCCTTCTTGGCGCTTGGCGATGGTCTTTCGCGAGAACCGACCGGCTGTGAAAGCGCGCAGA 1385
1358 ACGAGATCTGGCAGACTTTTCTTTCAGGGGCGCGCTACCTGCTCTGCTTATGGGCGCTGTCT 1417

1386 ACAGATCTGGCAGACTTTCTTTCAGGGCGCTACCTGCTCTGCTTATGGGCTGTCT 1445
1418 CCATCTACACCGGCTTCTATCAACAGAGTGCTTCAAGTCGGCCACACAGATCTTCCCT 1477
1446 CCATCTACACCGGCTTCTATCAACAGAGTGCTTCAAGTCGGCCACACAGATCTTCCCT 1505
1478 CGGGCTGGAGTGTCGGCCGATGGCCAAACAGTCTGGCTGGAGTATGATCTTCTGGCCC 1537
1506 CGGGCTGGAGTGTCGGCCGATGGCCAAACAGTCTGGCTGGAGTATGATCTTCTGGCCC 1565
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1566 AGCACACGATGCTTACCTTGGATCCCAAGGTCAACGGTGTCTTCTGGGACCTTACCT 1625
1598 TTGGATCATCTCTATTGGAGCTGGCTGGCCAAACACATGAGCTTCTCAATCTTCA 1657
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1658 AGATGAAGATGTCGCTCATCTGGGCGTGTGCACATGGCTTTGGGGTGTCTCTGGAG 1717
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1718 TCTTCAACACGTCGACTTTGGCCAGAGGACCGGCTGCTGTGGAGACGCTGCCGAGC 1777
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1778 TCACCTCTCTGCTGGAGCTTCTCGGTACTCTGTGTCTTCTAGTATCTCAAGTGCTGT 1837
1806 TCACCTCTCTGCTGGAGCTTCTCGGTACTCTGTGTCTTCTAGTATCTCAAGTGCTGT 1865
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1926 TCTCTTCTCCACAGCCCGCAGCAACAGGCTGCTTACCCCGGCGAGGAGTGCTCCAG 1985
1955 CCAGCTGTGTGCTTGGGCTTGGCCATGCTGGTCCCATCTGCTGTGGCACACCCCTGC 2014
1986 CCAGCTGTGTGCTTGGGCTTGGCCATGCTGGTCCCATCTGCTGTGGCACACCCCTGC 2045
2015 ACTGTGTGACCCGACCGCCGCTGCGAGAGGCGGCTGACCGACAGGAGGAAA 2074
2046 ACTGTGTGACCGCCACCGCCGCTGCGAGAGGCGGCTGACCGACAGGAGGAAA 2105
2075 ACAAGCCGGGTTGCTGGACCTGCTGACCGCATCTGTGAATGGCTGGAGCTCCGATGAG 2134
2106 ACAAGCCGGGTTGCTGGACCTGCTGACCGCATCTGTGAATGGCTGGAGCTCCGATGAG 2165
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2255 ACTGCGCTGTGGGCTTGAAGCTGGCCACGCGCAGCTGTCCGAGGTCTGTGGGCA 2314
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2346 TGGTGAATGGCATAGGCTTGGGCTGGGCGGAGGTGGGCTGGGCTGTGGTCTGG 2405
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2406 TCCCATCTTTGGGCTTGGGCTGATGACCGTGGCTATCTGCTGGTGGAGGGGAC 2465
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2555 TGCAGTCTCTGCGACAGCTTCTTCTGACCTCTGAGGCGAGGAGGAATAAAGACGGTCC 2614
2586 TGCAGTCTCTGCGACAGCTTCTTCTGACCTCTGAGGCGAGGAGGAATAAAGACGGTCC 2645
2615 GCCCTGGCA 2623
2646 GCCCTGGCA 2654

RESULT 7
US-09-949-016-2405
; Sequence 2405, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2405
; LENGTH: 2654
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2405

Query Match 81.1%; Score 2142; DB 3; Length 2654;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2582; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

38 GCGAGCACACCGGGGACCATGGGCTCCATCTTCCGAGCGAGAGGTGGCCCTGGTCC 97
66 GCGAGCACACCGGGGACCATGGGCTCCATCTTCCGAGCGAGAGGTGGCCCTGGTCC 125
98 AGCTCTTTCTGCCACACGCGCTGCTACACCTGCTGAGTCCGCTGGCGAGCTGGGCC 157
126 AGCTCTTTCTGCCACACGCGCTGCTACACCTGCTGAGTCCGCTGGCGAGCTGGGCC 185
158 TGTGCGAGTTTACAGACCTCAACCGCTCGGTGAGCGCTTCCAGAGACGCTTTGTGTTG 217
186 TGTGCGAGTTTACAGACCTCAACCGCTCGGTGAGCGCTTCCAGAGACGCTTTGTGTTG 245
218 ATGTTTGGGCTGTGAGAGCTGGAGAGACCTTCACTCTCTGTCAGGAGGAGTGGCG 277
246 ATGTTTGGGCTGTGAGAGCTGGAGAGACCTTCACTCTCTGTCAGGAGGAGTGGCG 305
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306 GGGCTGGGCTGTGCTTCTGCCCGCCGCAAGGGGAGGCTGCGGACACCCCGGGGACC 365
338 TGTCTCGCATTCAGAGAGAGAGCGAGCGCTGCGCCACAGAGCTGCGGAGATGTGCGGGCA 397
366 TGTCTCGCATTCAGAGAGAGAGCGAGCGCTGCGCCACAGAGCTGCGGAGATGTGCGGGCA 425
398 ACCACAGGCGCTTGGGCGCCAGCTGACCGCTGACCTCCAGCCCGCTGTACGCGC 457
426 ACCACAGGCGCTTGGGCGCCAGCTGACCGCTGACCTCCAGCCCGCTGTACGCGC 485
458 AGGGCCATGAACCTCAGCTGGCAGCGCCGCCACACAGATGGGGCTCTCAGAGAGACGCC 517

RESULT 8

US-09-949-016-2975

US-03-243-010-2373
; Sequence 2975, Application US/09949016

; Sequence 2373, App
; Patent No. 6812339

; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

; AFFILIANT: VENER, O. CLARY et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

1. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

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; PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

;
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: Fast

; SEQ ID NO 2975

; LENGTH: 27

TYPE: DNA

; ORGANISM: Human

Query Match 80.6%; Score 2127; DB 3; Length 2706;

Query Match 80.8%; Score 2127;
Best Local Similarity 99.7%; Pred No. 0;

2000 Local Similarity 33.74; Area: 0;
Matches 2567; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

Qy	53	GGACCATGGGCTCCATGTTTCGGAGCGAGAGAGTGGCCCTGGTTCAGCTCTTTCTGCCCCA	112
Db	133	GGACCATGGGCTCCATGTTTCGGAGCGAGAGAGTGGCCCTGGTTCAGCTCTTTCTGCCCCA	192
Qy	113	CAGCGGCTTGCTTACACCTGCGTAGTCCGCTGGGCGAGCTGGGCGCTCGTGGAGTTTCAGAG	172
Db	193	CAGCGGCTTGCTTACACCTGCGTAGTCCGCTGGGCGAGCTGGGCGCTCGTGGAGTTTCAGAG	252
Qy	173	ACCTCAAACGCGCTCGGTGAGCGCCCTTCAGAGACGCTTTGTTGGTTGATGTTTGGCGCTGTG	232
Db	253	ACCTCAAACGCGCTCGGTGAGCGCCCTTCAGAGACGCTTTGTTGGTTGATGTTTGGCGCTGTG	312
Qy	233	AGGAGCTGGAGAAAGACCTTCAACCTTCCTGACAGGAGGAGTGGCGGGCGCTGGGCTGGTGCC	292
Db	313	AGGAGCTGGAGAAAGACCTTCAACCTTCCTGACAGGAGGAGTGGCGGGCGCTGGGCTGGTGCC	372
Qy	293	TGCCCCCGCCAAAGGGGAGGCTGCCGGCACCCGCCAACCTGCTGGCGATCCACGG	352
Db	373	TGCCCCCGCCAAAGGGGAGGCTGCCGGCACCCGCCAACCTGCTGGCGATCCACGG	432
Qy	353	AGGAGACGGAGCGCTGCGCCACAGAGAGCTGCGGAGTGTGCGGGGCAACAGCAGGCGCCCTGC	412
Db	433	AGGAGACGGAGCGCTGCGCCACAGAGAGCTGCGGAGTGTGCGGGGCAACAGCAGGCGCCCTGC	492
Qy	413	GGGCCCCAGCTGCACAGCTGCAGCTCCACGCGCGCGTGTCTACGCCAGGCGCCATGAACCTTC	472
Db	493	GGGCCCCAGCTGCACAGCTGCAGCTCCACGCGCGCGTGTCTACGCCAGGCGCCATGAACCTTC	552
Qy	473	AGCTGGAGCGCGCCCAACACAGATGGGCGCTCAGAGAGGACGCCCGTGTCTCAGGCGCCCGG	532
Db	553	AGCTGGAGCGCGCCCAACACAGATGGGCGCTCAGAGAGGACGCCCGTGTCTCAGGCGCCCGG	612
Qy	533	GGGGCGCGCAACAGGACTGAGGGGTCAAATTTTGTGGCAGGTGCCGTGGAGGCCCAACAAGG	592
Db	613	GGGGCGCGCAACAGGACTGAGGGGTCAAATTTTGTGGCAGGTGCCGTGGAGGCCCAACAAGG	672
Qy	593	CCCTCGCCCTAGAGCGCTGCTTGAGGGGCTGCCCGGCTTCTCATTCGACGCTTCA	652
Db	673	CCCTCGCCCTAGAGCGCTGCTTGAGGGGCTGCCCGGCTTCTCATTCGACGCTTCA	732
Qy	653	GGGAGCTGGAGACGACCGCTGGAGACACCCCGTGAACGGGCGAGCAGCCACAGTGGATGACCT	712


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QY 953 TGAAGGCGCTGTACCTGGCCCTGAACACAGTGCAGCGTGAGCACCACGACCAAGTGCTCA 1012
Db 1033 TGAAGGCGCTGTACCTGGCCCTGAACACAGTGCAGCGTGAGCACCACGACCAAGTGCTCA 1092
QY 1013 TTGCCAGGCGCTGTGCTCTGTGCGAGACCTGCGCCCTCTGCAGGAGCGCCTGCGGGA 1072
Db 1093 TTGCCAGGCGCTGTGCTCTGTGCGAGACCTGCGCCCTCTGCAGGAGCGCCTGCGGGA 1152
QY 1073 GCTCGATGAGAGGAGGTGAGTGCCTGCTCAACCGATCCCTGCGCGGAGCATGCCGCC 1132
Db 1153 GCTCGATGAGAGGAGGTGAGTGCCTGCTCAACCGATCCCTGCGCGGAGCATGCCGCC 1212
QY 1133 CCACACTCATCGCACCAACCGCTTCAACGCGCAGCTTCCAGGSCATCGTGATCGTACG 1192
Db 1213 CCACACTCATCGCACCAACCGCTTCAACGCGCAGCTTCCAGGSCATCGTGATCGTACG 1272
QY 1193 GGTGGGCGCGTACACGAGGAGTCAACCCCGCTCCCTACACCATCATCATCTTCCCTTCC 1252
Db 1273 GGTGGGCGCGTACACGAGGAGTCAACCCCGCTCCCTACACCATCATCATCTTCCCTTCC 1332
QY 1253 TGTTTGTCTGTATGTTGCGGAGATGCGGCGACCGGCTGCTCATGTTCTTCTTCTGCGCTGG 1312
Db 1333 TGTTTGTCTGTATGTTGCGGAGATGCGGCGACCGGCTGCTCATGTTCTTCTTCTGCGCTGG 1392
QY 1313 CCATGCTCTTGGGAGAACCGACCGGCTGTGAAGCGCGGAGAACGAGATCTGGCAGA 1372
Db 1393 CCATGCTCTTGGGAGAACCGACCGGCTGTGAAGCGCGGAGAACGAGATCTGGCAGA 1452
QY 1373 CTTTCTTCAAGGCGCGCTACCTGCTCTGCTTATGGGCTGTTCTTCACTACACCGGCT 1432
Db 1453 CTTTCTTCAAGGCGCGCTACCTGCTCTGCTTATGGGCTGTTCTTCACTACACCGGCT 1512
QY 1433 TCATCTAACAGATGCTTCACTGCGGCGCACGAGCATCTTCCCTCGGGCTGGAAGTGG 1492
Db 1513 TCATCTAACAGATGCTTCACTGCGGCGCACGAGCATCTTCCCTCGGGCTGGAAGTGG 1572
QY 1493 CGGCATGSCCAACAGCTCTGCTGGAGTGATGATTCCTGCGCAGACACGATGCTTA 1552
Db 1573 CGGCATGSCCAACAGCTCTGCTGGAGTGATGATTCCTGCGCAGACACGATGCTTA 1632
QY 1553 CCTCGATCCCAAGCTACCGGTGCTTCTCGGACCCCTACCCCTTTGGCATCGATCTTA 1612
Db 1633 CCTCGATCCCAAGCTACCGGTGCTTCTCGGACCCCTACCCCTTTGGCATCGATCTTA 1692
QY 1613 TTTGGAGCTGCTGCGCAACCACTTGAAGTCTTCACTCTTCAAGATGAAGATGCTCG 1672
Db 1693 TTTGGAGCTGCTGCGCAACCACTTGAAGTCTTCACTCTTCAAGATGAAGATGCTCG 1752
QY 1673 TCATCTGGGCGCTGCTGACATGGCTTTGGGCTGCTCGAGTCTTCAACCAAGTGC 1732
Db 1753 TCATCTGGGCGCTGCTGACATGGCTTTGGGCTGCTCGAGTCTTCAACCAAGTGC 1812
QY 1733 ACTTTGGCAGAGGCAACCGGCTGCTGCTGAGACGCTGCGGAGTCACTTCTGCTGG 1792
Db 1813 ACTTTGGCAGAGGCAACCGGCTGCTGCTGAGACGCTGCGGAGTCACTTCTGCTGG 1872
QY 1793 GACTCTTGGTTACTCTGTTCTTAGTCACTCAAGTGGCTGTGTGTTGCTGGGTGCCA 1852
Db 1873 GACTCTTGGTTACTCTGTTCTTAGTCACTCAAGTGGCTGTGTGTTGCTGGGTGCCA 1932
QY 1853 GGGCGCGCTCG--CCACAGCTCTCATCTTCAATCAACATGTTCTTCTTCTCCACA 1909
Db 1933 GGGCGCGCTCGGGCCCGACATCTCTCATCTTCAATCAACATGTTCTTCTTCTCCACA 1992
QY 1910 GCGCCAGCAACAGGCTGCTTACCCCGGAGAGGTGTCAGGCGACGCTGGTGGTCC 1969
Db 1993 GCGCCAGCAACAGGCTGCTTACCCCGGAGAGGTGTCAGGCGACGCTGGTGGTCC 2052
QY 1970 TGGCCTTGGCATGTTGGCCATCTGCTGTTGGCACACCCCTGCACTGCTGCAACCGC 2029
Db 2053 TGGCCTTGGCCATGTTGGCCATCTGCTGTTGGCACACCCCTGCACTGCTGCAACCGC 2112
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QY 2030 ACCGCGCGCGCTGCGGAGGAGCGCGCTGACCGACAGAGGAAACAAAGCGCGGTTGC 2089
Db 2113 ACCGCGCGCGCTGCGGAGGAGCGCGCTGACCGACAGAGGAAACAAAGCGCGGTTGC 2172
QY 2090 TGGACCTGCTGACGACATCTGTGAATGGCTGGAGTCCGATGAGGAAAGGAGGCGGC 2149
Db 2173 TGGACCTGCTGACGACATCTGTGAATGGCTGGAGTCCGATGAGGAAAGGAGGCGGC 2232
QY 2150 TGGATGATGAAGAGAGGCGGAGCTGCTCCCTCCGAGGTGCTCATGCAACAGGCGCATCC 2209
Db 2233 TGGATGATGAAGAGAGGCGGAGCTGCTCCCTCCGAGGTGCTCATGCAACAGGCGCATCC 2292
QY 2210 ACACCATCGAGTTCCTGCTGGCTGCTCACAACCGCCTCTACCTGCGCCTGTGG 2269
Db 2293 ACACCATCGAGTTCCTGCTGGCTGCTCACAACCGCCTCTACCTGCGCCTGTGG 2352
QY 2270 CCTTGAGCCTGSCCCACGCGGCTGCTCGAGGTTCTTGGGCCATGCTGATGCGCATAG 2329
Db 2353 CCTTGAGCCTGSCCCACGCGGCTGCTCGAGGTTCTTGGGCCATGCTGATGCGCATAG 2412
QY 2330 GCTTGGGCTTGGGCGGAGGTGGGCGTGGCGGCTGTGTGTTGTTCCCATCTTTTGGCG 2389
Db 2413 GCTTGGGCTTGGGCGGAGGTGGGCGTGGCGGCTGTGTGTTGTTCCCATCTTTTGGCG 2472
QY 2390 CCTTTGGCGTGAATGACCGTGGCTATCCTGCTGCTGATGAGAGGACTCTCAGCCTTCTCTGC 2449
Db 2473 CCTTTGGCGTGAATGACCGTGGCTATCCTGCTGCTGATGAGAGGACTCTCAGCCTTCTCTGC 2532
QY 2450 AGCGCCTTGGCTGCACTGGGTGGAAATCCAGAAACAAGTTCTACTCAGGCAAGGCTACA 2509
Db 2533 AGCGCCTTGGCTGCACTGGGTGGAAATCCAGAAACAAGTTCTACTCAGGCAAGGCTACA 2592
QY 2510 AGCTGAGTCCCTTCACTTCCCTGCTGCCACAGATGACTAGGCGGCACTGAGGCTTCTGCGCAG 2569
Db 2593 AGCTGAGTCCCTTCACTTCCCTGCTGCCACAGATGACTAGGCGGCACTGAGGCTTCTGCGCAG 2652
QY 2570 ACTCTCTTCTGACCTCTGAGCAGGAGGAAATAAGACGCTCGCCCTGGCA 2623
Db 2653 ACTCTCTTCTGACCTCTGAGCAGGAGGAAATAAGACGCTCGCCCTGGCA 2706
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RESULT 10

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US-09-949-016-1330
; Sequence 1330, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1330
; LENGTH: 2457
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1330
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Query Match 63.3%; Score 1670; DB 3; Length 2457;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2060; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 561 CTTTGTGAGAGTGCCTGGAGCGCCCAAGGCGCCTGCGCTTAGAGCGGCTCTCTGGAG 620

Db 392 CTTTGTGAGAGTGCCTGGAGCGCCCAAGGCGCCTGCGCTTAGAGCGGCTCTCTGGAG 451


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/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1331
/ LENGTH: 2457
/ TYPE: DNA
/ ORGANISM: Human
/ US-09-949-016-1331

Query Match      63.3%; Score 1670; DB 3; Length 2457;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 561 CTTTGTGGAGGTGCGGTGGAGGCCCAAGGCCCTTGCCCTAGAGCGCTGCTGGAG 620
DB 392 CTTTGTGGAGGTGCGGTGGAGGCCCAAGGCCCTTGCCCTAGAGCGCTGCTGGAG 451
QY 621 GGCCTGCGCGGCTTCTCATTTGCCAGCTTCAGGGAGCTGGAGCGCGCTGGAGCACCC 680
DB 452 GGCCTGCGCGGCTTCTCATTTGCCAGCTTCAGGGAGCTGGAGCGCGCTGGAGCACCC 511
QY 681 CGTGACGGGCGAGCCAGCCAGCTGGATGACCTTCTCATCTCCTACTCGGGGTGAGCAGAT 740
DB 512 CGTGACGGGCGAGCCAGCCAGCTGGATGACCTTCTCATCTCCTACTCGGGGTGAGCAGAT 571
QY 741 CGGACAGAGAGATCCGCAAGATCAACGACTGCTTTCACCTGCTGCACTGCGGTTCGCA 800
DB 572 CGGACAGAGAGATCCGCAAGATCAACGACTGCTTTCACCTGCTGCACTGCGGTTCGCA 631
QY 801 GCAGGAGGAGGCGCGCTCGGGCCCTGCGAGCTGCAAGCTGCAACGACGAGCGAGTGCA 860
DB 632 GCAGGAGGAGGCGCGCTCGGGCCCTGCGAGCTGCAAGCTGCAACGACGAGCGAGTGCA 691
QY 861 GGAGGTCTCTCGGGGAGACAGAGCGGTTCCTGAGCCAGGTGCTAGGCGCGGTGCTGAGCT 920
DB 692 GGAGGTCTCTCGGGGAGACAGAGCGGTTCCTGAGCCAGGTGCTAGGCGCGGTGCTGAGCT 751
QY 921 GCTGCGCCAGAGGAGGTGAGTCCAGAGTCAAGATGAAGGCGGTGTAAGTCCGCTGAAACA 980
DB 752 GCTGCGCCAGAGGAGGTGAGTCCAGAGTCAAGATGAAGGCGGTGTAAGTCCGCTGAAACA 811
QY 981 GTGACGCTGAGCACCAACGACCAAGTGCCTCATTTGCCGAGGCTGCTGCTGCGAGA 1040
DB 812 GTGACGCTGAGCACCAACGACCAAGTGCCTCATTTGCCGAGGCTGCTGCTGCGAGA 871
QY 1041 CTTGCCCGCCCTGACGAGGCGCTGCGGACAGCTCGATGGAGGAGGTGAGTGCCGT 1100
DB 872 CTTGCCCGCCCTGACGAGGCGCTGCGGACAGCTCGATGGAGGAGGTGAGTGCCGT 931
QY 1101 GGTCTACCGGATCCCTGCGGGACATGCGCCGCCACACTCATTCGACCAACCGCTTAC 1160
DB 932 GGTCTACCGGATCCCTGCGGGACATGCGCCGCCACACTCATTCGACCAACCGCTTAC 991
QY 1161 GGCACGCTTCCAGGGCATCGTGGATCGCTAGGCGGTGGCGCTACACGAGGTCAACCC 1220
DB 992 GGCACGCTTCCAGGGCATCGTGGATCGCTAGGCGGTGGCGCTACACGAGGTCAACCC 1051
QY 1221 CGTCCCTTACACCATCATCACTTCCCTTCTGTTTGTGTTGCTGATGTTTCGGGATGAGG 1280
DB 1052 CGTCCCTTACACCATCATCACTTCCCTTCTGTTTGTGTTGCTGATGTTTCGGGATGAGG 1111
QY 1281 CCACGGGCTGCTCATGTTCTTCTGCGCTTGGCCATGTTCTTGGGAGAACCGACCGGC 1340
DB 1112 CCACGGGCTGCTCATGTTCTTCTGCGCTTGGCCATGTTCTTGGGAGAACCGACCGGC 1171
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QY 1341 TGTGAAGCGCGCAGAACGAGATCTGGCAGACTTTCTTCAGGGCGCGCTACTGCTCCT 1400
DB 1172 TGTGAAGCGCGCAGAACGAGATCTGGCAGACTTTCTTCAGGGCGCGCTACTGCTCCT 1231
QY 1401 GCTTATGGGCGCTGTTCTCCATCTACACGGGCTTCTACTACACGAGTGTCTCAGTGC 1460
DB 1232 GCTTATGGGCGCTGTTCTCCATCTACACGGGCTTCTACTACACGAGTGTCTCAGTGC 1291
QY 1461 CACACGATCTTTCCTCTCGGGCTGAGTGTGGCGCCATGGCCAAACAGTCTGGCTGGAG 1520
DB 1292 CACACGATCTTTCCTCTCGGGCTGAGTGTGGCGCCATGGCCAAACAGTCTGGCTGGAG 1351
QY 1521 TGATGATCTTTCCTGCGCCAGCACACCATGCTTACCTGGATCCCAAGTCAACGCTGCTT 1580
DB 1352 TGATGATCTTTCCTGCGCCAGCACACCATGCTTACCTGGATCCCAAGTCAACGCTGCTT 1411
QY 1581 CTTGGGACCTTACCTCTTGGCATCGATCTTATTTGGAGCCTTGGCTGCCAAACACCTTGAG 1640
DB 1412 CTTGGGACCTTACCTCTTGGCATCGATCTTATTTGGAGCCTTGGCTGCCAAACACCTTGAG 1471
QY 1641 CTTTCTCAACTCTCTTCAAGATGAAGTGTCTGTCATCTCTGGGCTGCTGCAATGGCTT 1700
DB 1472 CTTTCTCAACTCTCTTCAAGATGAAGTGTCTGTCATCTCTGGGCTGCTGCAATGGCTT 1531
QY 1701 TGGGGTGTCTCGGAGTCTTCAACACGTCACATTTGGCCAGAGGACCCGCTGCTGCT 1760
DB 1532 TGGGGTGTCTCGGAGTCTTCAACACGTCATCTTGGCCAGAGGACCCGCTGCTGCT 1591
QY 1761 GGAGAGCTGCTGCGGAGCTCACCTTCTGCTGGAGCTTCTTGGTTTACCTCGTGTCTCAT 1820
DB 1592 GGAGAGCTGCTGCGGAGCTCACCTTCTGCTGGAGCTTCTTGGTTTACCTCGTGTCTCAT 1651
QY 1821 CATCTAAGAGTGTGTGTGCTGGGCTGCGAGGCGCGCTCG---CCACGATCCTCAT 1877
DB 1652 CATCTAAGAGTGTGTGTGCTGGGCTGCGAGGCGCGCTCGCGGCCCGCAGCATCTCAT 1711
QY 1878 CCACCTTCAACAATGTTCTCTTCTCCACAGCCCGCAGCAACAGCTGCTTACCCCCG 1937
DB 1712 CCACCTTCAACAATGTTCTCTTCTCCACAGCCCGCAGCAACAGCTGCTTACCCCCG 1771
QY 1938 GCAGGAGTGTGTCCAGGCGCACGCTGTGTCTTGGCTTGGCCATGTGTGCCATCTGCT 1997
DB 1772 GCAGGAGTGTGTCCAGGCGCACGCTGTGTCTTGGCTTGGCCATGTGTGCCATCTGCT 1831
QY 1998 GCTTGGCACACCTCTGCACTGCTGCAACGCGCCACGCGCGCTGCGAGAGGCGCCG 2057
DB 1832 GCTTGGCACACCTCTGCACTGCTGCAACGCGCCACGCGCGCTGCGAGAGGCGCCG 1891
QY 2058 TGACCGACAGAGGAGAAACAAGGCGCGGTGTGTCACCTGTCGACGATCTGTGAATGG 2117
DB 1892 TGACCGACAGAGGAGAAACAAGGCGCGGTGTGTCGACCTGTCGACGATCTGTGAATGG 1951
QY 2118 TTGGAGCTCCGATGAGGAGAAAGGACAGGCGCTGTGATGATGAAGAGGCGCGAGCTGCT 2177
DB 1952 TTGGAGCTCCGATGAGGAGAAAGGACAGGCGCTGTGATGATGAAGAGGCGCGAGCTGCT 2011
QY 2178 CCGCTCCGAGGTGCTCATGCAACGCGCATTCACACCATTCGAGTTCGCTGGGCTGCT 2237
DB 2012 CCGCTCCGAGGTGCTCATGCAACGCGCATTCACACCATTCGAGTTCGCTGGGCTGCT 2071
QY 2238 CTTCCAAACCGGCTCTTACCTGCGCTGTGGGCGCTGAGCCTTGGCCCGCAGCGCTGCT 2297
DB 2072 CTTCCAAACCGGCTCTTACCTGCGCTGTGGGCGCTTGAAGCTTGGCCCGCAGCGCTGCT 2131
QY 2298 CGAGGTCTTGTGGGCAATGGTGTATGCGCATAGGCTTGGGCTTGGGCGGGAAGTGGGCGT 2357
DB 2132 CGAGGTCTTGTGGGCAATGGTGTATGCGCATAGGCTTGGGCTTGGGCGGGAAGTGGGCGT 2191
QY 2358 GCGGCTGTGTGCTGCTGCTTTCGCGCTTTCGCGGTGATGACGCTGCTGCTATCCT 2417
DB 2192 GCGGCTGTGTGCTGCTGCTTTCGCGCTTTCGCGGTGATGACGCTGCTGCTATCCT 2251
QY 2418 GCTGTGATGGAGGAGCTCTCAGCCTTCTGTCACGCGCTTCTGCGGCTGCACTGGGTGGAAT 2477
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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-83505

Job time : 492 secs

Query Match 8.4%; Score 221; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.4e-69;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 254 CTTTCTGCAGGAGGAGGTGCGCGGGCTGGGTGCTCTGCCCCCGCCAAAGGGGAGGC 313
Db |||||||
70 CTTTCTGCAGGAGGAGGTGCGCGGGCTGGGTGCTCTGCCCCCGCCAAAGGGGAGGC 129
QY 314 TGC CGGACACCCACCCCGGACCTGCTGGCATCCAGGAGGAGCGGCGCTGGCCC 373
Db |||||||
130 TGC CGGACACCCACCCCGGACCTGCTGGCATCCAGGAGGAGCGGCGCTGGCCC 189
QY 374 AGGAGCTGGGGATGTGCGGGCAACACGAGGCCCTGCGGGCCAGCTGCACCACTGC 433
Db |||||||
190 AGGAGCTGGGGATGTGCGGGCAACACGAGGCCCTGCGGGCCAGCTGCACCACTGC 249
QY 434 AGCTCCACGCGCGGTGCTACGCCAGGGCCATGAACCTCAG 474
Db |||||||
250 AGCTCCACGCGCGGTGCTACGCCAGGGCCATGAACCTCAG 290

RESULT 15

US-09-949-016-107576
; Sequence 107576, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107576
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-107576

Query Match 8.4%; Score 221; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.4e-69;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 254 CTTTCTGCAGGAGGAGGTGCGCGGGCTGGGTGCTCTGCCCCCGCCAAAGGGGAGGC 313
Db |||||||
70 CTTTCTGCAGGAGGAGGTGCGCGGGCTGGGTGCTCTGCCCCCGCCAAAGGGGAGGC 129
QY 314 TGC CGGACACCCACCCCGGACCTGCTGGCATCCAGGAGGAGCGGCGCTGGCCC 373
Db |||||||
130 TGC CGGACACCCACCCCGGACCTGCTGGCATCCAGGAGGAGCGGCGCTGGCCC 189
QY 374 AGGAGCTGGGGATGTGCGGGCAACACGAGGCCCTGCGGGCCAGCTGCACCACTGC 433
Db |||||||
190 AGGAGCTGGGGATGTGCGGGCAACACGAGGCCCTGCGGGCCAGCTGCACCACTGC 249
QY 434 AGCTCCACGCGCGGTGCTACGCCAGGGCCATGAACCTCAG 474
Db |||||||
250 AGCTCCACGCGCGGTGCTACGCCAGGGCCATGAACCTCAG 290

Search completed: June 30, 2006, 09:22:32

181 GCTTCGGTGAAGCCCTTCAGAGACGCTTTGTGGTTGATGTTTGGCGCTGTGAGGAGCTG 240
241 GAGAGACCTTCACTTCCTGAGAGAGAGGTGCGCGGGCTGGGTGCTTCGCCCCCG 300
241 GAGAGACCTTCACTTCCTGAGAGAGAGGTGCGCGGGCTGGGTGCTTCGCCCCCG 300
301 CCAAGGGGAGGCTGCGGCAACCCCAACCCCGGACCTGCTGGCATCCAGAGAGAGAGCG 360
301 CCAAGGGGAGGCTGCGGCAACCCCAACCCCGGACCTGCTGGCATCCAGAGAGAGAGCG 360
361 GAGCGCTTGGCCAGAGAGCTGCGGAGTGTGCGGGCAACAGCAGGACCTTGGCGGCCAG 420
361 GAGCGCTTGGCCAGAGAGCTGCGGAGTGTGCGGGCAACAGCAGGACCTTGGCGGCCAG 420
421 CTGACACAGTGTGAGCTCAACGCGCGGTCTACGCGAGGCGCATGAACTCAGCTGGCA 480
421 CTGACACAGTGTGAGCTCAACGCGCGGTCTACGCGAGGCGCATGAACTCAGCTGGCA 480
481 GCGGCCACACAGATGGGGCTCAGAGAGAGCGCCCTGCTCCAGGCGCCCGGGGGCG 540
481 GCGGCCACACAGATGGGGCTCAGAGAGAGCGCCCTGCTCCAGGCGCCCGGGGGCG 540
541 CACAGGACCTGAGGGTCAACTTTGTGGAGGTGCGGTGGAGCCCAAGGCGCCCTGCC 600
541 CACAGGACCTGAGGGTCAACTTTGTGGAGGTGCGGTGGAGCCCAAGGCGCCCTGCC 600
601 CTAGAGCGCTGCTCTGAGAGGGCTGCGCGGGCTTCTCATTTGCCAGCTTCAGGGAGCTG 660
601 CTAGAGCGCTGCTCTGAGAGGGCTGCGCGGGCTTCTCATTTGCCAGCTTCAGGGAGCTG 660
661 GAGCAGCGCTGAGACCCGCTGACGGGCGAGCCAGCCAGCTGGATGACCTTCCTCATC 720
661 GAGCAGCGCTGAGACCCGCTGACGGGCGAGCCAGCCAGCTGGATGACCTTCCTCATC 720
721 TCTACTGCGGTGAGCAGATCGGACAGAGATCCGCAAGATCACGAGCTGCTTCCACTGC 780
721 TCTACTGCGGTGAGCAGATCGGACAGAGATCCGCAAGATCACGAGCTGCTTCCACTGC 780
781 CACGTCTTCGCTTCTGAGAGAGAGGCGCGCTCGGGGCTTGCAGAGCTGCAAA 840
781 CACGTCTTCGCTTCTGAGAGAGAGGCGCGCTCGGGGCTTGCAGAGCTGCAAA 840
841 CAGCAGAGCAGGAGCTGAGAGGTCCTCGGGGAGACAGAGCGGTTCCTGAGCCAGGTG 900
841 CAGCAGAGCAGGAGCTGAGAGGTCCTCGGGGAGACAGAGCGGTTCCTGAGCCAGGTG 900
901 CTAGGCGGGTGTGAGCTGTGCGCCAGGCGAGGTGCAAGTCCACAAGATGAAGGCC 960
901 CTAGGCGGGTGTGAGCTGTGCGCCAGGCGAGGTGCAAGTCCACAAGATGAAGGCC 960
961 GTGTACTGGCCTGAAACAGTGTGAGCTGAGCAACAAGTGCCTCATTTGCCGAG 1020
961 GTGTACTGGCCTGAAACAGTGTGAGCTGAGCAACAAGTGCCTCATTTGCCGAG 1020
1021 GCTGTGTCTGTGCGAGACTGCGCGCCCTGCAAGGAGCGCTGCGGACAGCTCGATG 1080
1021 GCTGTGTCTGTGCGAGACTGCGCGCCCTGCAAGGAGCGCTGCGGACAGCTCGATG 1080
1081 GAGGAGGAGTGAAGTCCGCTGCTCAACCGCATCCCTGCGGGAATATGCCCCCACATC 1140
1081 GAGGAGGAGTGAAGTCCGCTGCTCAACCGCATCCCTGCGGGAATATGCCCCCACATC 1140
1141 ATCCGCAACAAACGCTTCAACGCGAGCTTCAAGGCAATCGTGGATCGCTACGCGGTGGC 1200
1141 ATCCGCAACAAACGCTTCAACGCGAGCTTCAAGGCAATCGTGGATCGCTACGCGGTGGC 1200
1201 CGTACAGAGGTCAACCCGCTCCCTACACATCATCATCTCCCTTCCTGTTGCT 1260
1201 CGTACAGAGGTCAACCCGCTCCCTACACATCATCATCTCCCTTCCTGTTGCT 1260
1261 GTGATGTTCCGGGATGTGGGCCACAGGCTGCTCATGTTCTTCCGCTTGGCCATGCTC 1320

1261 GTGATGTTCCGGGATGTGGGCCACAGGCTGCTCATGTTCTTTCGCCCTTGCCATGGTC 1320
1321 CTTGCGGAGAACCGACCGGCTGTGAAAGCCGCGCAAGACGAGATCTGGCAGACTTTCTTC 1380
1321 CTTGCGGAGAACCGACCGGCTGTGAAAGCCGCGCAAGACGAGATCTGGCAGACTTTCTTC 1380
1381 AGGGGCGCTACCTGCTCTGCTTATGGGCTGTCTCCATCTACACGGCTTCTCAT 1440
1381 AGGGGCGCTACCTGCTCTGCTTATGGGCTGTCTCCATCTACACGGGCTTCTCAT 1440
1441 AACAGTGTCTCAGTCTGGGCCACACAGCATCTTCCCTCGGGCTGAGTGTGGCGCCATG 1500
1441 AACAGTGTCTCAGTCTGGGCCACACAGCATCTTCCCTCGGGCTGAGTGTGGCGCCATG 1500
1501 GCCAACAGTCTGGCTGAGTATGCAATTCCTGGGCCAGCAACAGATGCTTACCTGGAT 1560
1501 GCCAACAGTCTGGCTGAGTATGCAATTCCTGGGCCAGCAACAGATGCTTACCTGGAT 1560
1561 CCCAACGTCACCGGTGCTTCTGCGGACCCCTACCCCTTTGGCATCGATCTTATTTGGAGC 1620
1561 CCCAACGTCACCGGTGCTTCTGCGGACCCCTACCCCTTTGGCATCGATCTTATTTGGAGC 1620
1621 CTGGCTGGCCAACTGAGCTTCTCAACTCTTCAAGATGAAGATGTCCGTCATCTCTG 1680
1621 CTGGCTGGCCAACTGAGCTTCTCAACTCTTCAAGATGAAGATGTCCGTCATCTCTG 1680
1681 GCGCTGTGCAATGCGCTTTGGGGTGTCTCGAGTCTTCAACACAGTGCATTTGGC 1740
1681 GCGCTGTGCAATGCGCTTTGGGGTGTCTCGAGTCTTCAACACAGTGCATTTGGC 1740
1741 CAGAGCACCGGCTGCTGCGGAGACGCTGCGGAGCTCACCTTCTGCTGGGACTCTTC 1800
1741 CAGAGCACCGGCTGCTGCGGAGACGCTGCGGAGCTCACCTTCTGCTGGGACTCTTC 1800
1801 GGTTACCTCGTGTCTCTAGTCACTACAAAGTGGCTGTGTCTGCGGCTGCCAGGCGCGC 1860
1801 GGTTACCTCGTGTCTCTAGTCACTACAAAGTGGCTGTGTCTGCGGCTGCCAGGCGCGC 1860
1861 TCGCCAGGATCTCATCACTTCAATCAATGTTCTTCTTCTCCACAGCCCCAGCAAC 1920
1861 TCGCCAGGATCTCATCACTTCAATCAATGTTCTTCTTCTCCACAGCCCCAGCAAC 1920
1921 AGGCTGTCTACCCCGGAGAGTGTCCAGGCAACCTGCACTGCTGCAACCGCGCGC 1980
1921 AGGCTGTCTACCCCGGAGAGTGTCCAGGCAACCTGCACTGCTGCAACCGCGCGC 1980
1981 ATGTGCCCCATCTGCTGCTGGCACACCCCTGCACTGCTGCAACCGCGCGC 2040
1981 ATGTGCCCCATCTGCTGCTGGCACACCCCTGCACTGCTGCAACCGCGCGC 2040
2041 CTGCGGAGAGGCGCGCTGACCGAGAGGAGAAACAGGCGGGTGTGCTGACCTGCT 2100
2041 CTGCGGAGAGGCGCGCTGACCGAGAGGAGAAACAGGCGGGTGTGCTGACCTGCT 2100
2101 GACCATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGAGGAGGGGCTGATGATGA 2160
2101 GACCATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGAGGAGGGGCTGATGATGA 2160
2161 GAGGAGGCGGAGCTGCTCCCTTCCAGGCTGCTCATGCAACCGGCTTCCACCATCGAG 2220
2161 GAGGAGGCGGAGCTGCTCCCTTCCAGGCTGCTCATGCAACCGGCTTCCACCATCGAG 2220
2221 TTTGCTGCTGGGCTGCTTCCAAACCGGCTCTCACTGCGGCTGTGGGCTTGGGCTG 2280
2221 TTTGCTGCTGGGCTGCTTCCAAACCGGCTCTCACTGCGGCTGTGGGCTTGGGCTG 2280
2281 GCGCACGCGCAGCTCTCCAGGCTTCTGCGGCTATGTTGATGCGCATAGGCTTGGGCTG 2340
2281 GCGCACGCGCAGCTCTCCAGGCTTCTGCGGCTATGTTGATGCGCATAGGCTTGGGCTG 2340
2341 GCGCGGAGGTGGGCTGCGGCTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2400
2341 GCGCGGAGGTGGGCTGCGGCTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2400

QY 2401 ATGACCGTGGCTATCTCTGCTGGTATGAGAGGACTCTCAGCCTTCTCTGACGCGCCTCGGG 2460
DB 2401 ATGACCGTGGCTATCTCTGCTGGTATGAGAGGACTCTCAGCCTTCTCTGACGCGCCTCGGG 2460
QY 2461 CTGCACTGGGTGGAATTCACAGAACAGTCTTACTCAGGACGGGCTACAAGCTGAGTCCC 2520
DB 2461 CTGCACTGGGTGGAATTCACAGAACAGTCTTACTCAGGACGGGCTACAAGCTGAGTCCC 2520
QY 2521 TTCACTTCTGCTGACACAGATGACTAGGGCCCACTGCAAGGTCTCTGCGACAGCTCTTCTCT 2580
DB 2521 TTCACTTCTGCTGACACAGATGACTAGGGCCCACTGCAAGGTCTCTGCGACAGCTCTTCTCT 2580
QY 2581 GACCTCTGAGGACGAGAGGAATAAAGACGGTCCGCCCTGCAAAAAA 2640
DB 2581 GACCTCTGAGGACGAGAGGAATAAAGACGGTCCGCCCTGCAAAAAA 2640

RESULT 2
US-09-962-436-278
; Sequence 278, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR FILING DATE: 2000-09-25
; PRIOR FILING DATE: 2000-09-25
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 278
; LENGTH: 2655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-278

Query Match 100.0%; Score 2640; DB 3; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCTGCGGACGGGACGACGAGCGAGGCGCGGCGGACGACACACCGGGGACCATG 60
DB 1 CGCGCTGCGGACGGGACGACGAGCGAGGCGCGGCGGACGACACACCGGGGACCATG 60
QY 61 GGCTCCATGTTCCGGAGCGAGGAGGTGGCCCTGGTCCAGCTCTTTCTGCGCCACAGCGGCT 120
DB 61 GGCTCCATGTTCCGGAGCGAGGAGGTGGCCCTGGTCCAGCTCTTTCTGCGCCACAGCGGCT 120
QY 121 GCCTACACCTGCTGAGTCCGGCTGGGCGAGCTGGGCTCGTGAGTTTCAGAGACCTCAAC 180
DB 121 GCCTACACCTGCTGAGTCCGGCTGGGCGAGCTGGGCTCGTGAGTTTCAGAGACCTCAAC 180
QY 181 GCCTCGGTGAGCGCTTTCAGAGACGCTTTGTGTGATGTTTGGCGCTGTGAGGAGCTG 240
DB 181 GCCTCGGTGAGCGCTTTCAGAGACGCTTTGTGTGATGTTTGGCGCTGTGAGGAGCTG 240
QY 241 GAGAAGACTTCACTTCTGACAGGAGAGGTGCGGCGGCTGGGTGCTGCTGCGCCCG 300
DB 241 GAGAAGACTTCACTTCTGACAGGAGAGGTGCGGCGGCTGGGTGCTGCTGCGCCCG 300
QY 301 CCAAGGGAGGCTGCGGACCCCGGAGCTGGGCTCGTGCGCATCCAGAGGAGAGG 360
DB 301 CCAAGGGAGGCTGCGGACCCCGGAGCTGGGCTCGTGCGCATCCAGAGGAGAGG 360
QY 361 GAGCGCTGCGCCAGGAGCTGCGGAGTGTGCGGGGCAACACAGAGGCGCTGCGGGCCAG 420
DB 361 GAGCGCTGCGCCAGGAGCTGCGGAGTGTGCGGGGCAACACAGAGGCGCTGCGGGCCAG 420

QY 421 CTGCAACAGCTGCAAGTCTCAGCGCGCGCTGCTAGCCAGGGCCATGAACCTCAGCTGGCA 480
DB 421 CTGCAACAGCTGCAAGTCTCAGCGCGCGCTGCTAGCCAGGGCCATGAACCTCAGCTGGCA 480
QY 481 GCGCCACACAGATGGGGCTCAGAGAGAGCGCCCTGCTCCAGGCCCCCGGGGGCGG 540
DB 481 GCGCCACACAGATGGGGCTCAGAGAGAGCGCCCTGCTCCAGGCCCCCGGGGGCGG 540
QY 541 CACAGAGACTGAGGGTCAAATTTGTGGCAGGTGCGGTGGAGCCCCCAAGGCCCTTGC 600
DB 541 CACAGAGACTGAGGGTCAAATTTGTGGCAGGTGCGGTGGAGCCCCCAAGGCCCTTGC 600
QY 601 CTAGAGCGCTGCTCTGAGAGGGCTGCGCGGGCTTCTCATTTGCCAGCTTTCAGGAGCTG 660
DB 601 CTAGAGCGCTGCTCTGAGAGGGCTGCGCGGGCTTCTCATTTGCCAGCTTTCAGGAGCTG 660
QY 661 GAGCAGCGCTGAGACACCCCGTGAACGGGCGAGCAGCAGCTGGATGACCTTCTCATC 720
DB 661 GAGCAGCGCTGAGACACCCCGTGAACGGGCGAGCAGCAGCTGGATGACCTTCTCATC 720
QY 721 TCCTACTGGGGTGAACAGATCGACAGAAATCGGCAAGATCAACGACTGCTTCCATGTC 780
DB 721 TCCTACTGGGGTGAACAGATCGACAGAAATCGGCAAGATCAACGACTGCTTCCATGTC 780
QY 781 CACGTCTTCCCGTCTGAGAGAGGAGGCGCGCTCGGGGCGCTGCAAGACTGCA 840
DB 781 CACGTCTTCCCGTCTGAGAGAGGAGGCGCGCTCGGGGCGCTGCAAGACTGCA 840
QY 841 CAGCAGAGCAGGAGCTGAGGAGGTCTCGGGGAGACAGAGGCTTCTGAGCAGGTG 900
DB 841 CAGCAGAGCAGGAGCTGAGGAGGTCTCGGGGAGACAGAGGCTTCTGAGCAGGTG 900
QY 901 CTAGGCGGGTGTCTGAGCTGCTGCGCCAGGGCAGGTGCAAGTCCAAAGATGAAGGCC 960
DB 901 CTAGGCGGGTGTCTGAGCTGCTGCGCCAGGGCAGGTGCAAGTCCAAAGATGAAGGCC 960
QY 961 GTGTACTGSCCTCTGAACAGAGTGAACAGCAGCAGCAAGTGCCTCATTTGCCGAG 1020
DB 961 GTGTACTGSCCTCTGAACAGAGTGAACAGCAGCAGCAAGTGCCTCATTTGCCGAG 1020
QY 1021 GCCTGTGTCTCTGCGAGACCTGCGCGCTCGAGGAGGCGCTGCGGGACAGCTCGATG 1080
DB 1021 GCCTGTGTCTCTGCGAGACCTGCGCGCTCGAGGAGGCGCTGCGGGACAGCTCGATG 1080
QY 1081 GAGGAGGAGTGAAGTGCCTGCTCAACCGATCCCTGCGGGACATGCCCCCACACTC 1140
DB 1081 GAGGAGGAGTGAAGTGCCTGCTCAACCGATCCCTGCGGGACATGCCCCCACACTC 1140
QY 1141 ATCCGACCAACCGCTTTCAGCGGCTTCCAGGGCATCGTGGATCGCTAGCGGCTGGGC 1200
DB 1141 ATCCGACCAACCGCTTTCAGCGGCTTTCAGCGGCTTCCAGGGCATCGTGGATCGCTAGCGGCTGGGC 1200
QY 1201 CGCTACAGGAGTCAACCGCGCTCCCTACACATCATCACTTCCCTTCTGTTTGTCT 1260
DB 1201 CGCTACAGGAGTCAACCGCGCTCCCTACACATCATCACTTCCCTTCTGTTTGTCT 1260
QY 1261 GTGATGTTGGGGATGTGGGCTCAAGGCGCGGAGAACAGATCTGGGAGACTTCTTTC 1320
DB 1261 GTGATGTTGGGGATGTGGGCTCAAGGCGCGGAGAACAGATCTGGGAGACTTCTTTC 1320
QY 1321 CTTTGGGAGAACCGAGCGGCTGTGAAGCGCGGAGAACAGATCTGGGAGACTTCTTTC 1380
DB 1321 CTTTGGGAGAACCGAGCGGCTGTGAAGCGCGGAGAACAGATCTGGGAGACTTCTTTC 1380
QY 1381 AGGGGCGCTTACCTGCTTCTGCTTATGGGCTGTTCCTACATCACACGCGCTCATCTAC 1440
DB 1381 AGGGGCGCTTACCTGCTTCTGCTTATGGGCTGTTCCTACATCACACGCGCTCATCTAC 1440
QY 1441 AACAGTGTCTTCACTGCGGCGCAGCATCTTCCCTCGGGCTGGAGTGTGGCGCCATG 1500
DB 1441 AACAGTGTCTTCACTGCGGCGCAGCATCTTCCCTCGGGCTGGAGTGTGGCGCCATG 1500
QY 1501 GCCAACAGCTCTGGCTGGAGTGAATTCCTGGGCCAGCAGCATGCTTACCCTGGAT 1560

[illegible]

Db 2581 GACCTCTGAGCGCAGGAGAGGAATAAAGACGGTCCGCTCGCCCTGGCAAAAAAAAAAAAAAAAA 264

RESULT 3

US-09-880-107-3363

; Sequence 3363, Application US/09880107

; Patent No. US20020142981A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Darci T.

; APPLICANT: Vockley, Joseph G.

; APPLICANT: Scherf, Uwe

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

; FILE REFERENCE: 44921-5028-WO

; CURRENT APPLICATION NUMBER: US/09/880,107

; CURRENT FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: US 60/211,379

; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: US 60/237,054

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 3950

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3363

; LENGTH: 2655

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U45285

US-09-880-107-3363

	Query Match	100.0%;	Score 2640;	DB 3;	Length 2655;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2640;	Conservative	0;	Mismatches	0; Indels
					Gaps
Qy	1	CGCGGTGCGCGGACCGCGGACGCCAGCAGCGGAGCGCGCGCAGCACA	CACCGCGGAGACCATG	60	
Db	1	CGCGGTGCGCGGACCGCGGACGCCAGCAGCGGAGCGCGCGCAGCACA	CACCGCGGAGACCATG	60	
Qy	61	GGCTCCATGTTCCGGAGCGAGGAGGTGGCCCTGGTCCAGCTCTTTCTG	CCCCACAGCGGCT	120	
Db	61	GGCTCCATGTTCCGGAGCGAGGAGGTGGCCCTGGTCCAGCTCTTTCTG	CCCCACAGCGGCT	120	
Qy	121	GCCTACACCTGCGTGAGTCCGGCTGGCGGCGAGCTGGGCTCTGTGGAG	TTTCAGAGACCTCAAC	180	
Db	121	GCCTACACCTGCGTGAGTCCGGCTGGCGGAGCTGGGCTCTGTGGAG	TTTCAGAGACCTCAAC	180	
Qy	181	GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTGATGTTTGGCGCTG	TGAGGAGCTG	240	
Db	181	GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTGATGTTTGGCGCTG	TGAGGAGCTG	240	
Qy	241	GAGAGACCTTCACCTTCCTGCGAGGAGGAGTGCGCGGGCTGGGCTGGT	CTGCTGCCCCG	300	
Db	241	GAGAGACCTTCACCTTCCTGCGAGGAGGAGTGCGCGGGCTGGGCTGGT	CTGCTGCCCCG	300	
Qy	301	CCAAAGGGGAGGCTGCGGCACCCCAACCCCGGGA	CTGTGCGCATCCAGGAGGAGACG	360	
Db	301	CCAAAGGGGAGGCTGCGGCACCCCAACCCCGGGA	CTGTGCGCATCCAGGAGGAGACG	360	
Qy	361	GAGCGCTGCGCCAGGAGCTGCGGATGTGCGGGGCAACAGCAGGCGCTG	CGGGGCCAG	420	
Db	361	GAGCGCTGCGCCAGGAGCTGCGGATGTGCGGGGCAACAGCAGGCGCTG	CGGGGCCAG	420	
Qy	421	CTGCACCACTGTCAGCTCCACGCGCGCGTGTACGCCAGGGCCATGAA	CTCAGCTGGCA	480	
Db	421	CTGCACCACTGTCAGCTCCACGCGCGCGTGTACGCCAGGGCCATGAA	CTCAGCTGGCA	480	
Qy	481	GCGGCCACACAGATGGGGCTCAGAGAGACGCCCTCTGTCCAGGCCCC	CGGGGGGCGG	540	
Db	481	GCGGCCACACAGATGGGGCTCAGAGAGACGCCCTCTGTCCAGGCCCC	CGGGGGGCGG	540	
Qy	541	CACAGGACCTGAGGGTCAACTTTGTGGCAGGTGCGGTGAGCCCAAGG	CCCCCTTGCC	600	
Db	541	CACAGGACCTGAGGGTCAACTTTGTGGCAGGTGCGGTGAGCCCAAGG	CCCCCTTGCC	600	

Qy	601	CTAGAGCGCTGCTCTGAGAGGCGCTGCGCGGCTTCTCATTTGCCAGCTTCAGGAGCTG	660
Db	601	CTAGAGCGCTGCTCTGAGAGGCGCTGCGCGGCTTCTCATTTGCCAGCTTCAGGAGCTG	660
Qy	661	GAGCAGCCGCTGGAGCACCCGCTGACGGGCGAGCCAGCCAGTGGATGACCTTCCTCATC	720
Db	661	GAGCAGCCGCTGGAGCACCCGCTGACGGGCGAGCCAGCCAGTGGATGACCTTCCTCATC	720
Qy	721	TCCTACTGGGGTGAGCAGATCGGACAGAAGATCCGCAAGATPCACGGACTGCTTCCACTGC	780
Db	721	TCCTACTGGGGTGAGCAGATCGGACAGAAGATCCGCAAGATPCACGGACTGCTTCCACTGC	780
Qy	781	CACGCTTCCCGTTTCTGACAGGAGGAGCGCCCTCGGGGCCCTGACAGCAGCTGCAA	840
Db	781	CACGCTTCCCGTTTCTGACAGGAGGAGCGCCCTCGGGGCCCTGACAGCAGCTGCAA	840
Qy	841	CAGCAGAGCCAGGAGCTGACGAGGTCCTCGGGGAGACAGAGCGGTTCTTGAGCCAGGTG	900
Db	841	CAGCAGAGCCAGGAGCTGACGAGGTCCTCGGGGAGACAGAGCGGTTCTTGAGCCAGGTG	900
Qy	901	CTAGGCGGGTGTCGAGCTGCTGCGGACAGGTCGCGGACAGGTCGAGTCCAAAGATGAAGGCC	960
Db	901	CTAGGCGGGTGTCGAGCTGCTGCGGACAGGTCGCGGACAGGTCGAGTCCAAAGATGAAGGCC	960
Qy	961	GTGTACCTGGCCCTGAAACCAAGTCAGGTCGAGCACCACGACAGTGCCTCATTTGCCGAG	1020
Db	961	GTGTACCTGGCCCTGAAACCAAGTCAGGTCGAGCACCACGACAGTGCCTCATTTGCCGAG	1020
Qy	1021	GCCTGGTGCTCTGTGCGAGACCTTCCCGCCCTGACGAGGCGCTTCGCGGACAGCTCGATG	1080
Db	1021	GCCTGGTGCTCTGTGCGAGACCTTCCCGCCCTGACGAGGCGCTTCGCGGACAGCTCGATG	1080
Qy	1081	GAGAGGGAGTGAGTGCCTGGCTCAACGATCCCTGCGCGGACATGCCCCCACAATC	1140
Db	1081	GAGAGGGAGTGAGTGCCTGGCTCAACGATCCCTGCGCGGACATGCCCCCACAATC	1140
Qy	1141	ATCCGACCAACCGCTTACAGGCGAGCTTCCAGGCGCATCGTGATCGTACGGGTGGGC	1200
Db	1141	ATCCGACCAACCGCTTACAGGCGAGCTTCCAGGCGCATCGTGATCGTACGGGTGGGC	1200
Qy	1201	CGCTACAGGAGGTCAACCCCGCTCCCTACACCATCATCACTTCCCTTCTGTTTGTCT	1260
Db	1201	CGCTACAGGAGGTCAACCCCGCTCCCTACACCATCATCACTTCCCTTCTGTTTGTCT	1260
Qy	1261	GTGATGTTGGGGATGTGGGCAAGGGTGCTCATGTTCTCTTTCGCCCTGGGCCATGGTC	1320
Db	1261	GTGATGTTGGGGATGTGGGCAAGGGTGCTCATGTTCTCTTTCGCCCTGGGCCATGGTC	1320
Qy	1321	CTTTCGGAGAACCCAGCCGGCTGTAAAGCCGCGCAGAACGAGATCTCGCAGACTTCTTC	1380
Db	1321	CTTTCGGAGAACCCAGCCGGCTGTAAAGCCGCGCAGAACGAGATCTCGCAGACTTCTTC	1380
Qy	1381	AGGGGCGCTACCTGCTCCTGCTTATGGGCGCTGTTCTTCCATCTACACCGGCTTCATCTAC	1440
Db	1381	AGGGGCGCTACCTGCTCCTGCTTATGGGCGCTGTTCTTCCATCTACACCGGCTTCATCTAC	1440
Qy	1441	AACAGATGCTTCAGTTCGGGCCACAGCATCTTCCCTTCGGGCTGGAGTGTGGCCCATG	1500
Db	1441	AACAGATGCTTCAGTTCGGGCCACAGCATCTTCCCTTCGGGCTGGAGTGTGGCCCATG	1500
Qy	1501	GCCAAACAGTCTGGCTGGAGTGATGATCTCTGSCCCAGACACAGATGCTTACCTGGAT	1560
Db	1501	GCCAAACAGTCTGGCTGGAGTGATGATCTCTGSCCCAGACACAGATGCTTACCTGGAT	1560
Qy	1561	CCCAACGTCAACCGTGTCTTCTGGGACCCCTACCCCTTTGGCATCGATCTTATTTGGAGC	1620
Db	1561	CCCAACGTCAACCGTGTCTTCTGGGACCCCTACCCCTTTGGCATCGATCTTATTTGGAGC	1620
Qy	1621	CTGGCTGCCAACCACTTGAGCTTCTCAATCTTCAAGATGAAGATGTCGGTCATCCTG	1680
Db	1621	CTGGCTGCCAACCACTTGAGCTTCTCAATCTTCAAGATGAAGATGTCGGTCATCCTG	1680

Qy	1681	GGCGTCGTGCACATGGCGCTTTGGGGTGGTGCTCCTCGAGATCTTTCAACACAGCTGCACCTTGGC	1740
Db	1681	GGCGTCGTGCACATGGCGCTTTGGGGTGGTGCTCCTCGAGATCTTTCAACACAGCTGCACCTTGGC	1740
Qy	1741	CAGAGGCACCGGCTGCTGCTGGAGAGCGTCCGCGAGCTCACCTTCTGCTGGGACCTTTC	1800
Db	1741	CAGAGGCACCGGCTGCTGCTGGAGAGCGTCCGCGAGCTCACCTTCTGCTGGGACCTTTC	1800
Qy	1801	GGTTACCTCGTGTTCTTAGTCATCTACAAGTGGCTGTGTCTGGGCTGCGAGGGCGCGC	1860
Db	1801	GGTTACCTCGTGTTCTTAGTCATCTACAAGTGGCTGTGTCTGGGCTGCGAGGGCGCGC	1860
Qy	1861	TCGCCGAGCATCTCATCTCACTTCAACAATGTTCTCTTCTCCACAGCCCGCCAGCAAC	1920
Db	1861	TCGCCGAGCATCTCATCTCACTTCAACAATGTTCTCTTCTCCACAGCCCGCCAGCAAC	1920
Qy	1921	AGGCTGCTTACCCCGGACAGGAGTGGTCCAGGCCACGCTGTGTGTCTCTGGGCTTTGGCC	1980
Db	1921	AGGCTGCTTACCCCGGACAGGAGTGGTCCAGGCCACGCTGTGTGTCTCTGGGCTTTGGCC	1980
Qy	1981	ATGGTGCCCATCTGCTGTCTTGGCACACCCCTGCACCTGTGTCACGCCACCGCCCGCCCGC	2040
Db	1981	ATGGTGCCCATCTGCTGTCTTGGCACACCCCTGCACCTGTGTCACGCCACCGCCCGCCCGC	2040
Qy	2041	CTGCGGAGGAGGCGCGCTGACCGACAGGAGGAAAAAAGGCCGGGTGCTGACCTTGCCT	2100
Db	2041	CTGCGGAGGAGGCGCGCTGACCGACAGGAGGAAAAAAGGCCGGGTGCTGACCTTGCCT	2100
Qy	2101	GACGCATCTGTAATGCTGGAGCTCCGATGAGGAAAGCGAGGGGCTCGATGATGAA	2160
Db	2101	GACGCATCTGTAATGCTGGAGCTCCGATGAGGAAAGCGAGGGGCTCGATGATGAA	2160
Qy	2161	GAGGAGCCGAGCTCGTCCCTCCGAGGTGCTCATGCAACAGGCCATCCACACCATCGAG	2220
Db	2161	GAGGAGCCGAGCTCGTCCCTCCGAGGTGCTCATGCAACAGGCCATCCACACCATCGAG	2220
Qy	2221	TTCTGCTGGGCTGCGTCTCAACACGCGCTCTACTCTGGCGCTGTGGGCGCTTGAGCCTG	2280
Db	2221	TTCTGCTGGGCTGCGTCTCAACACGCGCTCTACTCTGGCGCTGTGGGCGCTTGAGCCTG	2280
Qy	2281	GCCACGCCAGCTGTCCGAGGTTCTGTGGGCCATGATGCGCATAGGCGCTTGCGCCTG	2340
Db	2281	GCCACGCCAGCTGTCCGAGGTTCTGTGGGCCATGATGCGCATAGGCGCTTGCGCCTG	2340
Qy	2341	GGCCGGAGGTGGGCGTGGCGGCTGTGTGCTGGTCCCATCTTTTCCGCGCTTTGCGCTG	2400
Db	2341	GGCCGGAGGTGGGCGTGGCGGCTGTGTGCTGGTCCCATCTTTTCCGCGCTTTGCGCTG	2400
Qy	2401	ATGACCGTGGCTATCTCTGCTGTGATGGAGGACCTCTCAGCCTTCTCTGACGCCCTGCGG	2460
Db	2401	ATGACCGTGGCTATCTCTGCTGTGATGGAGGACCTCTCAGCCTTCTCTGACGCCCTGCGG	2460
Qy	2461	CTGCACCTGGTGGAATTCAGAACAGATTCTACTCAGGCACGGGCTTACAGCTGATGCC	2520
Db	2461	CTGCACCTGGTGGAATTCAGAACAGATTCTACTCAGGCACGGGCTTACAGCTGATGCC	2520
Qy	2521	TTCACTTCTCGCTGCCACAGATGACTAGGGCCCACTGCAGTCTCTGCAGACCTCTTCTCT	2580
Db	2521	TTCACTTCTCGCTGCCACAGATGACTAGGGCCCACTGCAGTCTCTGCAGACCTCTTCTCT	2580
Qy	2581	GACCTCTGAGGCGAGGAGGAAATAAGACGGTCCGCGCTTGGCAAAAAAATAAAAAA	2640
Db	2581	GACCTCTGAGGCGAGGAGGAAATAAGACGGTCCGCGCTTGGCAAAAAAATAAAAAA	2640

RESULT 4

RESOL 4
US-09-968-007A-212

US 03 008 007A-212
; Sequence 212, Application US/09968007A

; Publication No. US20040115625A1

GENERAL INFORMATION:

; APPLICANT: Ebner, Reinhard

TITLE OF INVENTION: Cancer Gen

;	TITLE OF INVENTION:	Gene Sets
;	TITLE OF INVENTION:	Gene Sets


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/ FILE REFERENCE: 689290-71
/ CURRENT APPLICATION NUMBER: US/09/968,007A
/ CURRENT FILING DATE: 2001-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,172
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,173
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,278
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,294
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,295
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: US/60/237,316
/ PRIOR FILING DATE: 2000-10-02
/ NUMBER OF SEQ ID NOS: 1001
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 212
/ TYPE: DNA
/ LENGTH: 2655
/ ORGANISM: Homo sapiens
/ US-09-968-007A-212

Query Match      100.0%; Score 2640; DB 3; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 GCCTGGTGAGCGCTTCCAGAGACGCTTTGTGGTGTGATGTTGGCGCTGAGAGCTG 240
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DB 481 GCGCGCCACACAGATGGGCGCTCAGAGAGGACGCGCCCTGCTCCAGGCGCGCGGGCGG 540

QY 541 CACAGAGACCTGAGGCTCAACTTTGTGGCAGGTGCGGTGGAGCCCAACAGGCGCCCTGCC 600
DB 541 CACAGAGACCTGAGGCTCAACTTTGTGGCAGGTGCGGTGGAGCCCAACAGGCGCCCTGCC 600

QY 601 CTAGAGCGCTGCTCTGAGAGGCGCTGCGCGGCTTCTCATTTGCCAGCTTCAAGGAGCTG 660
DB 601 CTAGAGCGCTGCTCTGAGAGGCGCTGCGCGGCTTCTCATTTGCCAGCTTCAAGGAGCTG 660

QY 661 GAGCAGCGCTGAGGACACCCCTGAGCGGCGAGGACCAACCGTGAATGAACCTTCTCATC 720
DB 661 GAGCAGCGCTGAGGACACCCCTGAGCGGCGAGGACCAACCGTGAATGAACCTTCTCATC 720
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1021 GCCTGGTCTCTGTCGAGAGCTGCGGCCCTGCAAGAGGCGCTCGGGACAGCTCGATG 1080

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Db 901 CTAGGCGGGTGTCTGAGCTGCTGCCCGCAGGCGAGTGCAGTCCACAGATGAAGGCC 960
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Qy 1081 GAGGAGGAGTGTAGTGTGCTGTACCGCATCCCTGCGGACATGCCCCCACAATC 1140
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Qy 1141 ATCCGACCAACCGCTTTCAGGCGAGCTTTCAGGCGATGTGTGATCGCTACGCGGTGGG 1200
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Qy 1201 CGCTACGAGAGTCAACCGCGCTTACACCATCATCACTTCCCTTCCCTTCTGTTTGT 1260
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Qy 1261 GTGATGTTGCGGATGTGGCCACGCGCTGCTCATGTTCCTTTCGCGCTTGGCCATGTC 1320
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Qy 1321 CTTGCGGAGAACCGACCGGTGTGAAGCGCGCGAGAACGAGATCTGGGAGACTTCTTC 1380
Db 1321 CTTGCGGAGAACCGACCGGTGTGAAGCGCGCGAGAACGAGATCTGGGAGACTTCTTC 1380
Qy 1381 AGGGGCGCTTACCTGTCTGCTTATGGGCGCTTCTCCATCTACACCGGCTTCACTAC 1440
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Qy 1501 GCCAACAGTGTGGCTGGAGTGTGATTCCTGGGCGCGAGCACAGTGTACCTTGGAT 1560
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Qy 1681 GGGCTGTGCACATGGCCCTTGGGCTGTCTCGAGTGTTCACACAGTGTGACTTTGGC 1740
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Qy 1741 CAGAGCACCGCTGTCTGTGAGAGCTGCGGAGCTCACCTTCTGTGGGACTCTTC 1800
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Qy 1801 GGTACCTGTGTCTGTAGTGTCTCAAGTGTGTGTCTGGGCTGCGAGGCGCGC 1860
Db 1801 GGTACCTGTGTCTGTAGTGTCTCAAGTGTGTGTCTGGGCTGCGAGGCGCGC 1860
Qy 1861 TGGCCAGCATCTCATCACTTCAATCAATGTTCTCTTCCACAGGCGCGAGCAAC 1920
Db 1861 TGGCCAGCATCTCATCACTTCAATCAATGTTCTCTTCCACAGGCGCGAGCAAC 1920
Qy 1921 AGGCTGTCTTACCCCGGAGAGGTGTTCAGGCGCACGCTGTGTCTGTGGCTTGGC 1980
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Db 1981 ATGTGTGCCATCTGTCTGTGGCACACCCCTGTGACCTGTGACACCGCACCGCGCGC 2040
Qy 2041 CTGCGGAGAGGCGCGCTGTGACCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100
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Qy 2101 GAGCGATCTGTAAATGGCTGTGAGCTCCGATGAGGAGGAGGAGGAGGAGGAGGAG 2160
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RESULT 6

US-10-641-643-916

; Sequence 916, Application US/10641643

; Publication No. US20040077003A1

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; Suan G. Stuart

; Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL

; GENE EXPRESSION

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/641,643

; FILING DATE: 14-Aug-2003

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: <Unknown>

; FILING DATE: <Unknown>


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RESULT 7

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US-10-843-641A-2737
; Sequence 2737, Application US/10843641A
; Publication No. US2005006454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843, 641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
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; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2737
; LENGTH: 2655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-2737
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Query Match 100.0%; Score 2640; DB 10; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CGGCGTGGCGGACCGGAGCGGAGCGGAGCGGCGGCGGAGCACACCGGGGACCATG 60
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QY 361 GAGCGCTGGCCACGAGCTGGGATGTGGGGGCAACCCAGAGGAGCTGCGGGCCAG 420
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Db 361 GAGCGCTGGCCACGAGCTGGGATGTGGGGGCAACCCAGAGGAGCTGCGGGCCAG 420
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QY 421 CTGCAACAGCTGAGCTCCACGCGCGCTGTCTACGCGGCGCATGAACTCAGCTGGCA 480
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Db 421 CTGCAACAGCTGAGCTCCACGCGCGCTGTCTACGCGGCGCATGAACTCAGCTGGCA 480
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QY 481 GCGGCGCACAGATGGGCGCTCAGAGGAGCGCCCTGCTCCAGGCGCCCGGGGGCGG 540
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Db 481 GCGGCGCACAGATGGGCGCTCAGAGGAGCGCCCTGCTCCAGGCGCCCGGGGGCGG 540
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Db 541 CACCAAGGAGCTGAGGCTCAACTTTGTGGCAGGTGGCGGAGCCCAAGGCGCCCTGCC 600
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DB 721 TCCTACTGGGTGAGCAGATCGGACAGAGATCCGCAAGATCAAGGACTGCTTCCACTGC 780
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DB 781 CAGCTCTCCGCTTCTGACAGCAGAGAGAGAGCCCGCCTCGGGGCCCTGACAGCAGCTGCAA 840
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DB 841 CAGCAGAGCCAGGAGCTGACAGAGTCTCGGGAGACAGAGCGGTTCCTGAGCCAGGTG 900
QY 901 CTAGGCGGGGTGCTGACAGTCTGCTCCGCGCAGGAGAGTGCAGTCCCAAGATCAAGGCC 960
DB 901 CTAGGCGGGGTGCTGACAGTCTGCTCCGCGCAGGAGAGTGCAGTCCCAAGATCAAGGCC 960
QY 961 GTGTACTGCTGCTGACAGTCCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1020
DB 961 GTGTACTGCTGCTGACAGTCCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 1020
QY 1021 GCCTGTGCTGCTGTCGAGACCTGCGCGCCTGACAGAGCCCTGCGGAGCAGCTCGATG 1080
DB 1021 GCCTGTGCTGCTGTCGAGACCTGCGCGCCTGACAGAGCCCTGCGGAGCAGCTCGATG 1080
QY 1081 GAGGAGGAGTGTGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1081 GAGGAGGAGTGTGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
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DB 1141 ATCCGACCAACCGCTTTCAGCGGCAGCTTCCAGGAGCAGTGCAGTGCAGTGCAGTGCAG 1200
QY 1201 CGCTACAGAGGTCAACCGCGCTTCCATACAGTATCATCTTCCCTTCTGTTTGTCT 1260
DB 1201 CGCTACAGAGGTCAACCGCGCTTCCATACAGTATCATCTTCCCTTCTGTTTGTCT 1260
QY 1261 GTGATGTTCCGGGATGTGGGCGCAGCGGCTGCTCATGTTCTTCTTCCGCTGCGCATGCTC 1320
DB 1261 GTGATGTTCCGGGATGTGGGCGCAGCGGCTGCTCATGTTCTTCTTCCGCTGCGCATGCTC 1320
QY 1321 CTTGCGGAGAACCGACCGCTGTGAAAGCGCGCAGAGAGATCTGCGAGACTTCTTCTTC 1380
DB 1321 CTTGCGGAGAACCGACCGCTGTGAAAGCGCGCAGAGAGATCTGCGAGACTTCTTCTTC 1380
QY 1381 AGGGCGCGCTACCTGCTCTGCTTATGGGCTGTTCTTCAATCTACACCGGCTCATCTAC 1440
DB 1381 AGGGCGCGCTACCTGCTCTGCTTATGGGCTGTTCTTCAATCTACACCGGCTCATCTAC 1440
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DB 1441 AACGAGTGTTCAGTTCGCGCCACAGCATCTTCCCTCGGGCTGGAGTGGCGCCCATG 1500
QY 1501 GCCAACAGTCTGGCTGGAGTGTGATCTTCTGCGCCAGCAGCATGCTTACCTTGGAT 1560
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DB 1741 CAGAGGACCGGTGCTGTGGAGACGCTGCGGAGCTCACTTCTTCTGCTGGAGCTTTC 1800
QY 1801 GGTTACTCGTGTCTTCTAGTCACTACAGTGGCTGTGTGCTGGGCTGCCAGGGCGGCC 1860

DB 1801 GGTTACTCGTGTCTTCTAGTCACTACAGTGGCTGTGTGTCTGGGCTGCCAGGGCGGCC 1860
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QY 1921 AGGCTGCTTACCCCGGCGAGGAGTGTTCAGGCGACGCTGTGTGTCTTGGCTTGGCC 1980
DB 1921 AGGCTGCTTACCCCGGCGAGGAGTGTTCAGGCGACGCTGTGTGTCTTGGCTTGGCC 1980
QY 1981 ATGTGTGCCCATCTCTGCTTGTGGCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
DB 1981 ATGTGTGCCCATCTCTGCTTGTGGCACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
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DB 2401 ATGACGCTGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
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DB 2461 CTGACCTGGTGAAATTCAGAAACAAGTTTCTACAGGACGCGGCTACAAGCTGAGTCCC 2520
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DB 2521 TTCACCTTCTGCTGCCACAGATGACTAGGCGCCACTGAGGCTGCTGCTGCTGCTGCTGCTGCT 2580
QY 2581 GACCTCTGAGGACGAGAGGAAATAAGACCGCTCGGCTCGGCTGCGCAAAAAA 2640
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RESULT 8

US-10-843-641A-6682

; Sequence 6682, Application US/10843641A

; Publication No. US2005006454A1

; GENERAL INFORMATION:

; APPLICANT: Avalon Pharmaceuticals, Inc.

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using

; FILE REFERENCE: Signature Gene Sets

; CURRENT APPLICATION NUMBER: US/10/843,641A

; CURRENT FILING DATE: 2004-05-12

; PRIOR APPLICATION NUMBER: US/09/873,367

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US/09/954,531

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: US/09/954,456

; PRIOR FILING DATE: 2001-09-25

	PRIOR APPLICATION NUMBER:	US/09/962,436	
	PRIOR FILING DATE:	2001-09-25	
	PRIOR APPLICATION NUMBER:	US/09/962,832	
	PRIOR FILING DATE:	2001-09-25	
	PRIOR APPLICATION NUMBER:	US/09/964,824	
	PRIOR FILING DATE:	2001-09-27	
	PRIOR APPLICATION NUMBER:	US/09/967,768	
	PRIOR FILING DATE:	2001-09-28	
	PRIOR APPLICATION NUMBER:	US/09/968,007	
	PRIOR FILING DATE:	2001-10-02	
	PRIOR APPLICATION NUMBER:	US/09/969,347	
	PRIOR FILING DATE:	2001-10-02	
	PRIOR APPLICATION NUMBER:	US/09/969,708	
	PRIOR FILING DATE:	2001-10-03	
	Remaining Prior Application data removed - See File Wrapper or PALM.		
	NUMBER OF SEQ ID NOS:	8447	
	SOFTWARE:	Patentin version 3.0	
	SEQ ID NO	6682	
	LENGTH:	2655	
	TYPE:	DNA	
	ORGANISM:	Homo sapiens	
	FEATURE:		
	NAME/KEY:	misc.feature	
	LOCATION:	(1)..(2655)	
	OTHER INFORMATION:	n=a,t,g or c	
	US-10-843-641A-6682		
	Query Match	100.0%; Score 2640; DB 10; Length 2655;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 2640; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
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Qy	61	GGCTCCCATGTTCGGAGCGAGAGTGCCCTGGTCCAGCTCTTTCTGCCACACGGCGT	120
Db	61	GGCTCCCATGTTCGGAGCGAGAGTGCCCTGGTCCAGCTCTTTCTGCCACACGGCGT	120
Qy	121	GCCTACACCTCGGTGAGTCGGCTGGCGGAGCTGGGGCTCGTAGGTTCAAGACTCAAC	180
Db	121	GCCTACACCTCGGTGAGTCGGCTGGCGGAGCTGGGGCTCGTAGGTTCAAGACTCAAC	180
Qy	181	GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTGATGTTTGGCGCTGTGAGGAGCTG	240
Db	181	GCCTCGGTGAGCGCTTCCAGAGACGCTTTGTGGTTGATGTTTGGCGCTGTGAGGAGCTG	240
Qy	241	GAGAAGACCTTCACTTCTCGAGAGAGGTGCGCGCGGGCTGGGCTGGTCTGCCCCCG	300
Db	241	GAGAAGACCTTCACTTCTCGAGAGAGGTGCGCGCGGGCTGGGCTGGTCTGCCCCCG	300
Qy	301	CCAAGGGGAGGCTCGCGGACCCCCAACCCCGGAGCTGCTGCGCATCCAGGAGGAGCG	360
Db	301	CCAAGGGGAGGCTCGCGGACCCCCAACCCCGGAGCTGCTGCGCATCCAGGAGGAGCG	360
Qy	361	GAGCGCTGGGCCCAGGAGCTGCGGATGTGCGGGGCAACACAGAGCCCTGCGGGCCCG	420
Db	361	GAGCGCTGGGCCCAGGAGCTGCGGATGTGCGGGGCAACACAGAGCCCTGCGGGCCCG	420
Qy	421	CTGCAACAAGCTGCACTCCACGCGCCCGTGTCTACGCCAGGGCCATGAACCTCAGCTGGCA	480
Db	421	CTGCAACAAGCTGCACTCCACGCGCCCGTGTCTACGCCAGGGCCATGAACCTCAGCTGGCA	480
Qy	481	GCCGCCCAACAAGATGGGGCTCAGAGAGGACGCCCTCTCTCAGGGCCCCGGGGGGCG	540
Db	481	GCCGCCCAACAAGATGGGGCTCAGAGAGGACGCCCTCTCTCAGGGCCCCGGGGGGCG	540
Qy	541	CACCAGGACCTGAGGGTCAAATTTCGTGACGTGCGGTGGAGCCCAACAAGSCCCTGCC	600
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Qy	601	CTAGAGCGCTGCTCTGGAGGGCTCGCGCGGCTCTCTCATTTGCCAGCTTCAAGGAGCTG	660


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DB 961 GTGTACTCTGGCCTGAACAGGTGACGGTGAGCACCAACGCAAGTGCTCATTTGCCGAG 1020
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DB 1021 GCCTGTGTCTGTGCGAGACCTGCCCCGCTCGACGAGGCGCTCGCGGACAGCTCGATG 1080
QY 1081 GAGGAGGAGTGTGAGTGTGCTGACCGGATCCCGGAGCATGCCCCCGCCACATCTC 1140
DB 1081 GAGGAGGAGTGTGAGTGTGCTGACCGGATCCCGGAGCATGCCCCCGCCACATCTC 1140
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DB 1741 CAGAGCACCGGTGTCTGGAGCGCTGCGGAGCTCACCTTCTGCTGGGACTCTTTC 1800
QY 1801 GGTGTCTGTCTGTAGTTCATCTAACAGTGGCTGTGTGTGGGCTGCCAGGGCGGC 1860
DB 1801 GGTGTCTGTCTGTAGTTCATCTAACAGTGGCTGTGTGTGGGCTGCCAGGGCGGC 1860
QY 1861 TCGCCGAGCATCTCATCACTTTCATCAACATGTTCTCTCTCCACAGCCCCCAGCAAC 1920
DB 1861 TCGCCGAGCATCTCATCACTTTCATCAACATGTTCTCTCTCCACAGCCCCCAGCAAC 1920
QY 1921 AGGCTGCTCTACCCCCGCGAGGAGTGGTCCAGGCCACGCTGGTGGTCTCTGGCCTTGGCC 1980
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QY 2041 CTGCGGAGGCGCCGCTGACCGACAGGAGGAAACAGGCGGGTGTGTGACCTTGCCT 2100
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QY 2221 TTCTGCTGGGCTGTGCTCCAAACACCGCTTCTACCTGGGCTGTGGGCTTGGGCTG 2280
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DB 2521 TTCACTTGTGTGCGACAGATGATAGGGCCACCTGAGGCTCTGCCAGACCTCTCTCT 2580
QY 2581 GACCTCTCAGGCGAGGAGGAATAAGACGGTTCGCGCTGGCAAAAAA 2640
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RESULT 10

US-10-145-012-1

; Sequence 1, Application US/10145012

; Publication No. US20030124614A1

; GENERAL INFORMATION:

; APPLICANT: UTUK et al.

; TITLE OF INVENTION: T-CELL MEMBRANE PROTEIN (TIRC7), PEPTIDES AND ANTIBODIES DERIVED

; FILE REFERENCE: 4400-0105P

; CURRENT APPLICATION NUMBER: US/10/145,012

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2488

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (537)..(2378)

US-10-145-012-1

Query Match 63.9%; Score 1687; DB 7; Length 2488;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2077; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 561 CTTTGTGGCAGGTGCGGTGGAGCCCCACAAAGGCCCTTGCCCTAGAGCGCCTGCTCTGGAG 620
Db 392 CTTTGTGGCAGGTGCGGTGGAGCCCCACAAAGGCCCTTGCCCTAGAGCGCCTGCTCTGGAG 451
QY 621 GGCCTGCGCGGCTTCTCATTTGCCAGCTTTCAGGGAGCTGGAGCAGCGCTGGAGCACCC 680
Db 452 GGCCTGCGCGGCTTCTCATTTGCCAGCTTTCAGGGAGCTGGAGCAGCGCTGGAGCACCC 511
QY 681 CGTGA CGGGCGAGCCAGCCACGCTGGATGACCTTCTCATCTCTCTACTCTGGGGTGGAGCAGAT 740
Db 512 CGTGACGGCGAGCCAGCCAGCTGGATGACCTTCTCATCTCTCTACTCTGGGGTGGAGCAGAT 571
QY 741 CGGACAGAGATCGGACAGATCAGGAGCTGCTTCCACTGCGACAGCTCTTCCGTTTCTGCA 800
Db 572 CGGACAGAGATCGGACAGATCAGGAGCTGCTTCCACTGCGACAGCTCTTCCGTTTCTGCA 631
QY 801 GCAGGAGAGGCCCGCCCTCGGGGCCCTGCGAGCAGCTGCAACAGCAGAGCCAGGAGCTGCA 860
Db 632 GCAGGAGAGGCCCGCCCTCGGGGCCCTGCGAGCAGCTGCAACAGCAGAGCCAGGAGCTGCA 691
QY 861 GGAAGTCTCGGGGAGACAGAGCGGTTCTTGAAGCAGGTGCTAGGCGGGTGTGTCAGCT 920
Db 692 GGAAGTCTCGGGGAGACAGAGCGGTTCTTGAAGCAGGTGCTAGGCGGGTGTGTCAGCT 751
QY 921 GCTGCCGCCAGGGCAGGTGAGGTGCAAAAGATGAAGCCGTGACCTGGCCCTGGAACCA 980
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QY 1878 CCATCTCATCAACATGTTCCTTCTCCACAGCCCCAGCAACAGGCTGTCTACCCCG 1937
Db 1712 CCATCTCATCAACATGTTCCTTCTCCACAGCCCCAGCAACAGGCTGTCTACCCCG 1771
QY 1938 GCAGGAGGTGGTCCAGGCCACGCTGTGTGCTTGGCTTGGCCATGGTGGCCCATCTGCT 1997
Db 1772 GCAGGAGGTGGTCCAGGCCACGCTGTGTGCTTGGCTTGGCCATGGTGGCCCATCTGCT 1831
QY 1998 GCTTGGCACAACCTTGCACCTGTGTGACCCGCAACCGCCGCGCTGCGAGGAGCGCCG 2057
Db 1832 GCTTGGCACAACCTTGCACCTGTGTGACCCGCAACCGCCGCGCTGCGAGGAGCGCCG 1891
QY 2058 TGACCGACAGGAGGAAACAAAGCCGGTGTGCTGACCTGCTGACGATCTGTGAATGG 2117
Db 1892 TGACCGACAGGAGGAAACAAAGCCGGTGTGCTGACCTGCTGACGATCTGTGAATGG 1951
QY 2118 CTGGAGTCTCGATGAGGAAAGGACGGGCGCTTGGATGATGAAGAGGAGGCGAGCTCGT 2177
Db 1952 CTGGAGTCTCGATGAGGAAAGGACGGGCGCTTGGATGATGAAGAGGAGGCGAGCTCGT 2011
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Db 2012 CCCCTCGAGGTGCTCATGCAACAGGCCATTCACCATCGAGTTCCTGCGCTGGCTGGCT 2071
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QY 2298 CGAGGTCTGTGGGCCATGGTGTGATGCGCATAGGCTTGGGCTGCGGCGGAGGCTGGCGT 2357
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Db 2372 AGATGACTAGGCGCCCATGTGAGTCTTGCAGACCTCTTTCCTGACCTCTTGAGGACAGAG 2431
QY 2598 AGGAATAAGACCGCTCGCCCTCGGCAAAAAAAAAAAAAA 2640
Db 2432 AGGAATAAGACCGCTCGCCCTCGGCAAAAAAAAAAAAAA 2474

RESULT 11
US-11-126-866-1
; Sequence 1, Application US/11126866
; Publication No. US20050220789A1

GENERAL INFORMATION:
APPLICANT: UTKU, et al., NALAN
TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS TO
TITLE OF INVENTION: AN EXTRACELLULAR DOMAIN OF A TIR7 MEMBRANE PROTEIN
FILE REFERENCE: 1472/71099-ZA/JPM/AG
CURRENT APPLICATION NUMBER: US/11/126,866
CURRENT FILING DATE: 2005-05-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1

LENGTH: 2488
TYPE: DNA
ORGANISM: human
FEATURE:
NAME/KEY: CDS
LOCATION: (537)...(2378)
US-11-126-866-1

Query Match 63.9%; Score 1687; DB 13; Length 2488;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2077; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY	561	CTTTGTGGCAGTGGCGTGGAGCCCAAGGCCCTGCTAGAGCGCTGCTGGAG	620
DB	392	CTTTGTGGCAGTGGCGTGGAGCCCAAGGCCCTGCTAGAGCGCTGCTGGAG	451
QY	621	GGCGTGGCGGCTTCTCATTTGCCAGCTTCAGGGAGCTGGAGCGCGCTGAGCACCC	680
DB	452	GGCGTGGCGGCTTCTCATTTGCCAGCTTCAGGGAGCTGGAGCGCGCTGAGCACCC	511
QY	681	CGTGACGGCGGAGCCAGCCAGCTGGATGACCTTCTCATCTCTACTGGGGTGGAGCAT	740
DB	512	CGTGACGGCGGAGCCAGCCAGCTGGATGACCTTCTCATCTCTACTGGGGTGGAGCAT	571
QY	741	CGGACAGAAAGATCCGCAAGATCAAGGACTGCTTCCATCCCACTTCCCGTTCTGCA	800
DB	572	CGGACAGAAAGATCCGCAAGATCAAGGACTGCTTCCATCCCACTTCCCGTTCTGCA	631
QY	801	GAGGAGGAGGCGCGCTCGGGCCCTGAGCCAGCTGCTAGCCAGGCTGCTGAGCT	860
DB	632	GAGGAGGAGGCGCGCTCGGGCCCTGAGCCAGCTGCTAGCCAGGCTGCTGAGCT	691
QY	861	GGAGTCTCTCGGGAGACAGAGCGGTTCTGAGCCAGCTGCTAGCCAGGCTGCTGAGCT	920
DB	692	GGAGTCTCTCGGGAGACAGAGCGGTTCTGAGCCAGCTGCTAGCCAGGCTGCTGAGCT	751
QY	921	GCTGCCCGCAGGCGAGTGCAGGTCACAAAGATGAAGCCGCTGTACCTGGCCCTGAACCA	980
DB	752	GCTGCCCGCAGGCGAGTGCAGGTCACAAAGATGAAGCCGCTGTACCTGGCCCTGAACCA	811
QY	981	GTGCAAGGTGAGCACACACAGTGCCCTCATTTGCCAGGCGCTGGTCTCTGTGGAGA	1040
DB	812	GTGCAAGGTGAGCACACACAGTGCCCTCATTTGCCAGGCGCTGGTCTCTGTGGAGA	871
QY	1041	CTGCGCCGCTGCGAGGAGCCCTGCGGACAGCTCGATGAGGAGGAGTGAAGTGGCGT	1100
DB	872	CTGCGCCGCTGCGAGGAGCCCTGCGGACAGCTCGATGAGGAGGAGTGAAGTGGCGT	931
QY	1101	GGCTACCGCATCCCTGCGGACATGCCCCCACTCATCCGACCAACCGCTTAC	1160
DB	932	GGCTACCGCATCCCTGCGGACATGCCCCCACTCATCCGACCAACCGCTTAC	991
QY	1161	GGCGAGCTTCAGGGATCGTGATGCTACCGCGTGGCGCTACCAAGGATCAACC	1220
DB	992	GGCGAGCTTCAGGGATCGTGATGCTACCGCGTGGCGCTACCAAGGATCAACC	1051
QY	1221	CGCTCCCTACACCATCATCACTTCCCTTCTGTTGCTGTGATGTTTGGGGATGTGG	1280
DB	1052	CGCTCCCTACACCATCATCACTTCCCTTCTGTTGCTGTGATGTTTGGGGATGTGG	1111
QY	1281	CCACGGGCTGCTCATGTTCTCTTGGCCCTGGCCATGCTTGGGAGAACCGACCGGC	1340
DB	1112	CCACGGGCTGCTCATGTTCTCTTGGCCCTGGCCATGCTTGGGAGAACCGACCGGC	1171

QY	1341	TGTGAAGCGCGCAGAGATCTGGCAGACTTCTTTCAGGGCCGCTACCTGCTCCT	1400
DB	1172	TGTGAAGCGCGCAGAGATCTGGCAGACTTCTTTCAGGGCCGCTACCTGCTCCT	1231
QY	1401	GCTTATGGGCGCTGTTCTCATCTACACGGGCTTCTATCTACACAGAGTGTCTCAGTGGCGC	1460
DB	1232	GCTTATGGGCGCTGTTCTCATCTACACGGGCTTCTATCTACACAGAGTGTCTCAGTGGCGC	1291
QY	1461	CACAGCATCTTCCCTCGGGCTGAGTGTGGCCCATGGCCAAACAGTCTTGGCTGGAG	1520
DB	1292	CACAGCATCTTCCCTCGGGCTGAGTGTGGCCCATGGCCAAACAGTCTTGGCTGGAG	1351
QY	1521	TGATGATCTTCTGGGCGCCAGCACCATGCTTACCTGGATCCCAACAGTCAACGGTGTCTT	1580
DB	1352	TGATGATCTTCTGGGCGCCAGCACCATGCTTACCTGGATCCCAACAGTCAACGGTGTCTT	1411
QY	1581	CCTGGAGCCCTACCCCTTTGGCATCGATCTTATTTGGAGCCCTGGCTGCCAACCATTTGAG	1640
DB	1412	CCTGGAGCCCTACCCCTTTGGCATCGATCTTATTTGGAGCCCTGGCTGCCAACCATTTGAG	1471
QY	1641	CTTCTCTAACTCTTTCAAGATGAAGATGTCTGCTCATCTTGGGCGTCTGTGCAATGGCTTT	1700
DB	1472	CTTCTCTAACTCTTTCAAGATGAAGATGTCTGCTCATCTTGGGCGTCTGTGCAATGGCTTT	1531
QY	1701	TGGGGTGGTCTCGGAGTCTTCAACACAGTGCACCTTTGGCCAGAGGCAACGGCTGCTGT	1760
DB	1532	TGGGGTGGTCTCGGAGTCTTCAACACAGTGCACCTTTGGCCAGAGGCAACGGCTGCTGT	1591
QY	1761	GGAGACGCTGCGGAGCTCACCTTCTGCTGGGACCTTTCGGTTTACCTGCTGTTCTAGT	1820
DB	1592	GGAGACGCTGCGGAGCTCACCTTCTGCTGGGACCTTTCGGTTTACCTGCTGTTCTAGT	1651
QY	1821	CATCTAACAGTGGCTGTGTCTGGCTGCGAGGCGCGCTCG---CCAGCATCTCTCAT	1877
DB	1652	CATCTAACAGTGGCTGTGTCTGGCTGCGAGGCGCGCTCG---CCAGCATCTCTCAT	1711
QY	1878	CCACTTCATCAACATGTTCTCTTCTCCACAGCCCAAGAGGCTGCTTACCCCG	1937
DB	1712	CCACTTCATCAACATGTTCTCTTCTCCACAGCCCAAGAGGCTGCTTACCCCG	1771
QY	1938	GAGGAGTGGTCCAGGCGCACGCTGTGTCTGCTGCTTGGCCATGCTGCTGCTGCT	1997
DB	1772	GAGGAGTGGTCCAGGCGCACGCTGTGTCTGCTGCTTGGCCATGCTGCTGCTGCT	1831
QY	1998	GCTTGGCACACCCCTGCGACCTGTGCGACCGCCACCGCCCGCCCTGCGGAGAGGCGCGC	2057
DB	1832	GCTTGGCACACCCCTGCGACCTGTGCGACCGCCACCGCCCGCCCTGCGGAGAGGCGCGC	1891
QY	2058	TGACCGACAGAGGAGAAACAGGCGCGGTTGCTGGAACCTGCTGACGATCTGTGAATGG	2117
DB	1892	TGACCGACAGAGGAGAAACAGGCGCGGTTGCTGGAACCTGCTGACGATCTGTGAATGG	1951
QY	2118	CTGGAGCTCCGATGAGGAGAAAGAGGAGGCGCTGATGATGAAGAGGAGGCGGAGCTGT	2177
DB	1952	CTGGAGCTCCGATGAGGAGAAAGAGGAGGCGCTGATGATGAAGAGGAGGCGGAGCTGT	2011
QY	2178	CCCTTCCGAGGTGCTCATGCGACCGCCATTCACACATCGAGTTCTGCTGGGCTGCGT	2237
DB	2012	CCCTTCCGAGGTGCTCATGCGACCGCCATTCACACATCGAGTTCTGCTGGGCTGCGT	2071
QY	2238	CTCCAAACCGCTCTTACCTGCGCTGTGGGCGCTGAGGCTGCGCCACCGCCAGCTGTC	2297
DB	2072	CTCCAAACCGCTCTTACCTGCGCTGTGGGCGCTGAGGCTGCGCCACCGCCAGCTGTC	2131
QY	2298	CGAGGTCTTGTGGGCGCATGTTGATCGCATAGGCTTGGGCGCTTGGGCGGAGGTGGCGT	2357
DB	2132	CGAGGTCTTGTGGGCGCATGTTGATCGCATAGGCTTGGGCGCTTGGGCGGAGGTGGCGT	2191
QY	2358	GGCGGCTGTGTGCTGGTCCCATCTTTGCGCGCTTGTGGCGGTGATGACCGTGGCTATCT	2417
DB	2192	GGCGGCTGTGTGCTGGTCCCATCTTTGCGCGCTTGTGGCGGTGATGACCGTGGCTATCT	2251

QY 2418 GCTGGTATGAGGAGCTCTCAGCTTCTGTCAGCGCCCTCGGCTGCACTGGTGGAAATT 2477
Db 2452 GCTGGTATGAGGAGCTCTCAGCTTCTGTCAGCGCCCTCGGCTGCACTGGTGGAAATT 2311
QY 2478 CCAGAACAAAGTTTACTCAGGACGCGGCTACAAGCTGAGTCCCTTTCACCTTCGCTGCCAC 2537
Db 2312 CCAGAACAAAGTTTACTCAGGACGCGGCTACAAGCTGAGTCCCTTTCACCTTCGCTGCCAC 2371
QY 2538 AGATGACTAGGGCCCACTGACGAGTCTGCGGACCTCTTCTGACCTCTGAGGAGGAG 2597
Db 2372 AGATGACTAGGGCCCACTGACGAGTCTGCGGACCTCTTCTGACCTCTGAGGAGGAG 2431
QY 2598 AGGAATAAGACGCTCGCCCTGCGCAAAAAAAAAAAAAA 2640
Db 2432 AGGAATAAGACGCTCGCCCTGCGCAAAAAAAAAAAAAA 2474

RESULT 12

US-11-126-841A-1

; Sequence 1, Application US/11126841A

; Publication No. US20050271659A1

; GENERAL INFORMATION:

; APPLICANT: UTU, et al., NALAN

; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS TO

; TITLE OF INVENTION: AN EXTRACELLULAR DOMAIN OF A TIRC7 MEMBRANE PROTEIN

; FILE REFERENCE: 1472/1099-ZB/JPW/AG

; CURRENT APPLICATION NUMBER: US/11/126,841A

; CURRENT FILING DATE: 2005-05-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1

; LENGTH: 2488

; TYPE: DNA

; ORGANISM: human

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (537) ..(2378)

US-11-126-841A-1

Query Match 63.9%; Score 1687; DB 15; Length 2488;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2077; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 561 CTTTGTGGCAGGTGCGGTGAGCCCAAGGCCCTTGCCTAGAGCGCTGCTCTGGAG 620
Db 392 CTTTGTGGCAGGTGCGGTGAGCCCAAGGCCCTTGCCTAGAGCGCTGCTCTGGAG 451
QY 621 GGCTGCGCGGCTTCTCTATTCAGCTTCAGGAGCTGAGCAGCGGCTGGAGCACC 680
Db 452 GGCTGCGCGGCTTCTCTATTCAGCTTCAGGAGCTGAGCAGCGGCTGGAGCACC 511
QY 681 CGTGACGGGCGAGCAGCCAGCTGGATGACCTTCTCATCTCTTACCTGGGGTGGAGCAGAT 740
Db 512 CGTGACGGGCGAGCAGCCAGCTGGATGACCTTCTCATCTCTTACCTGGGGTGGAGCAGAT 571
QY 741 CGGACAGAGATCGGAAAGTACAGGACTGCTTCACTGCACTGCGCTTCCGTTTGTGCA 800
Db 572 CGGACAGAGATCGGAAAGTACAGGACTGCTTCACTGCACTGCGCTTCCGTTTGTGCA 631
QY 801 GCAGGAGGAGCGCGCTCGGGCCCTGACAGCTGCAAGCAGGAGCTGCAAGGAGCTGCA 860
Db 632 GCAGGAGGAGCGCGCTCGGGCCCTGACAGCTGCAAGCAGGAGCTGCAAGGAGCTGCA 691
QY 861 GGAGGTCTCTGGGGAGACAGAGCGGTTCTTGAGCAGGTGCTAGGCGGGTGTGTCAGCT 920
Db 692 GGAGGTCTCTGGGGAGACAGAGCGGTTCTTGAGCAGGTGCTAGGCGGGTGTGTCAGCT 751
QY 921 GCTGCGCCACAGGAGGTGAGGTGCAAGAGTGAAGCGGCTGTA CTTGGCCCTGAAACCA 980
Db 752 GCTGCGCCACAGGAGGTGAGGTGCAAGAGTGAAGCGGCTGTA CTTGGCCCTGAAACCA 811
QY 981 GTGACGGTACACCAAGTGCCTTATTCAGGCGCTGCTGTGCGAGA 1040

Db 812 GTGACGGTACACCAAGTGCCTCATTCGCGAGCCCTGCTGTGTCGAGA 871
QY 1041 CTTGCCCGCCCTGACGAGGCGCTGCGGACAGCTCGATCGAGGAGGAGTGTAGTCCGT 1100
Db 872 CTTGCCCGCCCTGACGAGGCGCTGCGGACAGCTCGATCGAGGAGGAGTGTAGTCCGT 931
QY 1101 GGCTACCGCATCCCTGCGGGACATGCCCCCACA CTA CTATCCGACCAACCGCTTCA 1160
Db 932 GGCTACCGCATCCCTGCGGGACATGCCCCCACA CTA CTATCCGACCAACCGCTTCA 991
QY 1161 GGCCAGCTTCCAGGSCATCGTGGATCGCTACGGGTGGCGCTACCAAGGAGGTCAA 1220
Db 992 GGCCAGCTTCCAGGSCATCGTGGATCGCTACGGGTGGCGCTACCAAGGAGGTCAA 1051
QY 1221 CGCTCCCTACACCATCATCACTTCCCTTCTCTGTTGCTGTGATGTTGCGGGATGTGG 1280
Db 1052 CGCTCCCTACACCATCATCACTTCCCTTCTCTGTTGCTGTGATGTTGCGGGATGTGG 1111
QY 1281 CCAGGGGTGCTCATGTTCTCTTTCGCGCTGCGCATGCTCTTGGGAGAAACCGACCGC 1340
Db 1112 CCAGGGGTGCTCATGTTCTCTTTCGCGCTGCGCATGCTCTTGGGAGAAACCGACCGC 1171
QY 1341 TGTGAAAGCGCGCAGAACGAGATCTGCGAGACTTCTTCAAGGGCGCGCTACCTGCTCT 1400
Db 1172 TGTGAAAGCGCGCAGAACGAGATCTGCGAGACTTCTTCAAGGGCGCGCTACCTGCTCT 1231
QY 1401 GCTTATGGGCTGTTTCTCCATCTACACCGGCTTCTATCTACAAAGAGTCTTCACTCGCGC 1460
Db 1232 GCTTATGGGCTGTTTCTCCATCTACACCGGCTTCTATCTACAAAGAGTCTTCACTCGCGC 1291
QY 1461 CACAGCATCTTCCCTCGGGCTGGAGTGGCGCGCATGCGCAACCAAGTCTGGCTGGAG 1520
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QY 1521 TGATGCAATCTTGGCGCGCAGACGATGCTTACCTGATCCCAAGCTCACCGGTGCTT 1580
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Db 1412 CTTGGGACCTTACCCCTTTCGCTGCTGATCTTATTTGGAGCTGCTGCAACCACTTGGAG 1471
QY 1641 CTTCTCAACTCTTCAAGATGAGATGCTCGCTCATCTGCGGCTGCTGTCACATGGCCTT 1700
Db 1472 CTTCTCAACTCTTCAAGATGAGATGCTCGCTCATCTGCGGCTGCTGTCACATGGCCTT 1531
QY 1701 TGGGCTGCTTGGAGTCTTCAACCAAGTGTGCTTGGCGCAGGAGCAGCGGCTGCTGCT 1760
Db 1532 TGGGCTGCTTGGAGTCTTCAACCAAGTGTGCTTGGCGCAGGAGCAGCGGCTGCTGCT 1591
QY 1761 GGAGACGCTGCGGAGCTCACCTTCTGCTGGGACTCTTGGGTACCTCTGTTTCTTAGT 1820
Db 1592 GGAGACGCTGCGGAGCTCACCTTCTGCTGGGACTCTTGGGTACCTCTGTTTCTTAGT 1651
QY 1821 CATCTCAAGTGGTGTGTCTGCGGCTGCAAGGCGGCTCTG --- CCCAGCATCTCTCAT 1877
Db 1652 CATCTCAAGTGGTGTGTCTGCGGCTGCAAGGCGGCTCTGCGGCGGCTCTGCACTCTCAT 1711
QY 1878 CCACTTCAACATGTTTCTTCTTCCACAGCCCGCAGCAACAGGCTGTCTTACCCCG 1937
Db 1712 CCACTTCAACATGTTTCTTCTTCCACAGCCCGCAGCAACAGGCTGTCTTACCCCG 1771
QY 1938 GCAGGAGGTGGTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1997
Db 1772 GCAGGAGGTGGTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1831
QY 1998 GCTTGGACACCCCTGCACTGCTGCAACCGCGCAGCGCGCTGCTGCGAGGAGGCGCGC 2057
Db 1832 GCTTGGACACCCCTGCACTGCTGCAACCGCGCAGCGCGCTGCTGCGAGGAGGCGCGC 1891
QY 2058 TGACCGACAGGAGGAGAAAGCGCGGTTGCTGGAACCTGCTGCAACCTGCTGGAATGG 2117
Db 1892 TGACCGACAGGAGGAGAAAGCGCGGTTGCTGGAACCTGCTGGAACCTGCTGGAATGG 1951

1592	GGAGACGCTGCGGAGCTCACCTTCTGCTGGGACTCTTTCGGTTACCTCGTGTTCCTAGT	1651
1821	CATCTACAAGTGGCTGTGTGTCTGGGCTGCCAGGCGCGCTCG---CCCAGCATCTCTCAT	1877
1652	CATCTACAAGTGGCTGTGTGTCTGGGCTGCCAGGCGCGCTCGGCGCCCAAGCATCTCTCAT	1711
1878	CCACTTCATCAAACTGTTCTCTTCTCCACAGCCCCAGCAACAGGCTGCTCTACACCCCG	1937
1712	CCACTTCATCAAACTGTTCTCTTCTCCACAGCCCCAGCAACAGGCTGCTCTACACCCCG	1771
1938	GCAGGAGTGGTCCAGGCCACGCTGGTGGTCTTGCGCTTGCGCCATGGTGCCCATCTCTGCT	1997
1772	GCAGGAGTGGTCCAGGCCACGCTGGTGGTCTTGCGCTTGCGCCATGGTGCCCATCTCTGCT	1831
1998	GCTTGGGACACCCCTGCACCTGCTGCACCGGCACCGCGCGCGCTCGGAGAGGAGCCCGC	2057
1832	GCTTGGGACACCCCTGCACCTGCTGCACCGGCACCGCGCGCGCTCGGAGAGGAGCCCGC	1891
2058	TGACCGACAGGAGGAAAAAAGGCGGGTGTCTGGACCTGCTGCAGCGCATCTGTGAATGG	2117
1892	TGACCGACAGGAGGAAAAAAGGCGGGTGTCTGGACCTGCTGCAGCGCATCTGTGAATGG	1951
2118	CTGGAGCTCCGATGAGGAAAAAGGCGGGGCTTGATGATGAAGAGGAGGCCGAGCTCGT	2177
1952	CTGGAGCTCCGATGAGGAAAAAGGCGGGGCTTGATGATGAAGAGGAGGCCGAGCTCGT	2011
2178	CCCTTCGAGGTGCTCATGACACAGGCCATCCACACCATCAGATTCTGCGCTGGGCTCGT	2237
2012	CCCTTCGAGGTGCTCATGACACAGGCCATCCACACCATCAGATTCTGCGCTGGGCTCGT	2071
2238	CTCCAACACCGCTCTTACCTTGGCGCTGTGGGCGCTCGAGCTGCGCCACAGCCGAGCTGTC	2297
2072	CTCCAACACCGCTCTTACCTTGGCGCTGTGGGCGCTGAGCTGGCCACAGCCGAGCTGTC	2131
2298	CGAGGTCTGTGGGCCATGTGTATGCGCATAGGCTGGGCGCTGGGCGGAGGTGGGCGT	2357
2132	CGAGGTCTGTGGGCCATGTGTATGCGCATAGGCTGGGCGCTGGGCGGAGGTGGGCGT	2191
2358	GCGCGCTGTGGTGTGCTGCCATCTTTTGGCGCTTTTGGCGTGATGACCGTGGCTATCCT	2417
2192	GCGCGCTGTGGTGTGCTGCCATCTTTTGGCGCTTTTGGCGTGATGACCGTGGCTATCCT	2251
2418	GCTGGTGATGAGGAGGACTCTCAGCCTTCTTCGACGCCCTCGCGGCTGCACCTGGGTGGAAAT	2477
2252	GCTGGTGATGAGGAGGACTCTCAGCCTTCTTCGACGCCCTCGCGGCTGCACCTGGGTGGAAAT	2311
2478	CCAGAACAAAGTTCTACTCAGGCACGGGCTACAGCTGAGTCCCTTACCTTCGCTGCCAC	2537
2312	CCAGAACAAAGTTCTACTCAGGCACGGGCTACAGCTGAGTCCCTTACCTTCGCTGCCAC	2371
2538	AGATGACTAGGCGCCACTGCAAGTCCCTGCGACAGCCTCTTCTCTGACCTCTGAGGCAAGG	2597
2372	AGATGACTAGGCGCCACTGCAAGTCCCTGCGACAGCCTCTTCTCTGACCTCTGAGGCAAGG	2431
2598	AGGAATAAGACGGTCCGCGCTCGCAAAAAAAAAAAAAAAAAAAAAA	2640
2432	AGGAATAAGACGGTCCGCGCTCGCAAAAAAAAAAAAAAAAAAAAAA	2474

RESULT 14
 US-11-126-866-12
 ; Sequence 12, Application US/11126866
 ; Publication No. US20050220789A1
 ; GENERAL INFORMATION:
 ; APPLICANT: UTKU, et al., NALAN
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS TO
 ; TITLE OF INVENTION: AN EXTRACELLULAR DOMAIN OF A TIRC7 MEMBRANE PROTEIN
 ; FILE REFERENCE: 1472/71099-2A/3PW/AG
 ; CURRENT APPLICATION NUMBER: US/11/126,866
 ; CURRENT FILING DATE: 2005-05-10
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 12

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QY 1521 TGATGCAATTCCTGGCCAGCACACGATGCTTACCTTGGATCCCAAGTCACCGGTGCTTT 1580
Db 1352 TGATGCAATTCCTGGCCAGCACACGATGCTTACCTTGGATCCCAAGTCACCGGTGCTTT 1411
QY 1581 CTTGGACCTTACCCCTTTGGGCAATCGAATCTATTTGGAGCTTGGCTGCCAACACATTGAG 1640
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QY 1641 CTTCTCAACTCTTCAAGATGAAGATGTCGGTCATCTGGGGCTGTCGACATGACATGACCTT 1700
Db 1472 CTTCTCAACTCTTCAAGATGAAGATGTCGGTCATCTGGGGCTGTCGACATGACATGACCTT 1531
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Db 1532 TGGGGTGGTCTCTGGAGTCTTCAACACAGCTGCACTTTGGCCAGAGGACCGGCTGCTGT 1591
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Db 1592 GGAGAGCTGCGGGAGCTCACCTTCTGCTGGGACTCTTGGGTTACTCTGTTTCTAGT 1651
QY 1821 CATCTAAGTGGCTGTGTGCTGGGCTGCGAGGGCGGCTCG---CCAGCATCTCAT 1877
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QY 1878 CCACTTTCATCAATGTTCTCTTCTCCACAGCCCCAGCAACAGGCTGCTTACCCCCG 1937
Db 1712 CCACTTTCATCAATGTTCTCTTCTCCACAGCCCCAGCAACAGGCTGCTTACCCCCG 1771
QY 1938 GCAGAGGTGTCAGGCCACGCTGTGTGTCCTGGGCTTGGCCATGGTCCCATCTGCT 1997
Db 1772 GCAGAGGTGTCAGGCCACGCTGTGTGTCCTGGGCTTGGCCATGGTCCCATCTGCT 1831
QY 1998 GCTTGGCACACCCCTGCACCTGTCACCGCCATCCACCGCCGCGCTGGGAGGAGGCCCG 2057
Db 1832 GCTTGGCACACCCCTGCACCTGTCACCGCCATCCACCGCCGCGCTGGGAGGAGGCCCG 1891
QY 2058 TGACCGACAGGAGGAAAAAAGCCCGGGTGTGTGGACCTGCTGACGCACTCTGTGAATGG 2117
Db 1892 TGACCGACAGGAGGAAAAAAGCCCGGGTGTGTGGACCTGCTGACGCACTCTGTGAATGG 1951
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Db 1952 CTGGAGCTCCGATGAGGAAAAAGCAGGGGCTTGGATGATGAAGAGAGGCCAGCTCGT 2011
QY 2178 CCCCTCCGAGGTGCTCATGCACAGGCCATCCACACCATCGAGTTCTGGCTGGGCTGCGT 2237
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QY 2238 CTTCCAACACCGCTCTTACCTGCGCTGTGGGCCCTGAGCCTGGCCAGCCCGAGGTGTC 2297
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QY 2298 CGAGGTTCTGTGGGCCATGGTGAATGGGATAGGCCCTGGGCCCTGGGGCCGGAGGTGGCGT 2357
Db 2132 CGAGGTTCTGTGGGCCATGGTGAATGGGATAGGCCCTGGGCCCTGGGGCCGGAGGTGGCGT 2191
QY 2358 GGGCGCTGTGGTGGTCCCATCTTTGCGCGCTTTGCGGCTGATGACCGTGGCTATCCT 2417
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QY 2418 GCTGTGATGAGGAGGACTCTCAGCCTTCTGACAGCCCTGCGGCTGCACTGGGTGGAATT 2477
Db 2252 GCTGTGATGAGGAGGACTCTCAGCCTTCTGACAGCCCTGCGGCTGCACTGGGTGGAATT 2311
QY 2478 CCAGAACAAATTCTACTAGGCACGGGCTTACAAGCTGAGTCCCTTCACTTCTGCTGCCAC 2537
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Db 2372 AGATGACTAGGGCCCACTGACGCTCTGCAGACCTCTTCTTGACCTCTGAGGCAAGG 2431
QY 2598 AGGAATAAAGACGGTCCGCCCTGGCAAAAAAAGGAAAAA 2640
Db 2432 AGGAATAAAGACGGTCCGCCCTGGCAAAAAAAGGAAAAA 2474

RESULT 15
US-11-126-841A-12
; Sequence 12, Application US/11126841A
; Publication No. US20050271659A1
; GENERAL INFORMATION:
; APPLICANT: UTNU, et al., NALAN
; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS 1
; FILE REFERENCE: AN EXTRACELLULAR DOMAIN OF A TIRC7 MEMBRANE PROTEIN
; FILE REFERENCE: 1472/71099-ZB/JPW/AG
; CURRENT APPLICATION NUMBER: US/11/126,841A
; CURRENT FILING DATE: 2005-05-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 2488
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (537)..(2378)
US-11-126-841A-12
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Query Match 62.0%; Score 1636; DB 15; Length 2488;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2076; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

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QY 561 CTTTGTGGCAGTGTGCGTGGAGCCCAACAGGCCCTGCCCCTAGAGCGCTGCTCTGGAG 620
Db 392 CTTTGTGGCAGTGTGCGTGGAGCCCAACAGGCCCTGCCCCTAGAGCGCTGCTCTGGAG 451
QY 621 GGCCTGCCCGCGCTTCTCATTTGCCAGCTTTCAGGGAGCTGGAGCAGCCGCTGGAGCACCC 680
Db 452 GGCCTGCCCGCGCTTCTCATTTGCCAGCTTTCAGGGAGCTGGAGCAGCCGCTGGAGCACCC 511
QY 681 CTTGACGGCGGAGCCAGCCACCGTGGATGACCTTCTCATCTCTACTGCGGTGAGCAGAT 740
Db 512 CTTGACGGCGGAGCCAGCCACCGTGGATGACCTTCTCATCTCTACTGCGGTGAGCAGAT 571
QY 741 CGGACAGAGATCCGCGAGATCAACGAGCTGCTTCCACTGCCAGCTTCCCGTTCTGCA 800
Db 572 CGGACAGAGATCCGCGAGATCAACGAGCTGCTTCCACTGCCAGCTTCCCGTTCTGCA 631
QY 801 GCAGAGAGAGGCCCGCTCGGGCCCTGCGAGCAGCTGCAACAGCAGAGCCAGAGCTGCA 860
Db 632 GCAGAGAGAGGCCCGCTCGGGCCCTGCGAGCAGCTGCAACAGCAGAGCCAGAGCTGCA 691
QY 861 GGAGGTCTCTCGGGAGACAGAGCGTTCCTGAGCCAGGTGCTAGGCCGGGTGCTGAGCT 920
Db 692 GGAGGTCTCTCGGGAGACAGAGCGTTCCTGAGCCAGGTGCTAGGCCGGGTGCTGAGCT 751
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QY 981 GTGACGCTGTAGCACACACCAAGTGCCTCATTTGCCAGGCTGTGTGCTCTGTGCGAGA 1040
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QY 1041 CTTGCCCGCCCTTGCAGGAGGCCCTTGCAGGACAGCTCGATGAGAGGAGGAGTGAAGTCCCGT 1100
Db 872 CTTGCCCGCCCTTGCAGGAGGCCCTTGCAGGACAGCTCGATGAGAGGAGGAGTGAAGTCCCGT 931
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QY 1101 GGCTCAGCGATCCCTGCCGGGACATGCCCCCACACTCATCGCACCAACCGGTTCCAC 1160
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QY 1221 CGCTCCCTACACATCATCACTTCCCTTCCCTGCTGCTGCTGATGTTGCGGGATGTGGG 1280
Db 1052 CGCTCCCTACACATCATCACTTCCCTTCCCTGCTGCTGCTGATGTTGCGGGATGTGGG 1111
QY 1281 CCAGGGCTGCTCATGTTCTTCTTCCCTGCGCCATGCTTGGGAGAACCCAGCGGC 1340
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QY 1341 TGTGAAGCCGCGAGAACAGATCTGGCAGACTTCTTCAAGGGCGCGCTACCTGCTCCT 1400
Db 1172 TGTGAAGCCGCGAGAACAGATCTGGCAGACTTCTTCAAGGGCGCGCTACCTGCTCCT 1231
QY 1401 GCTTATGGGCTGTTCTCCATCTACACGGCTTCACTTACAAACAGTGTCTCACTGCGC 1460
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QY 1461 CACCAGCATCTTCCCTCGGGCTGGAGTGTGGCGCCATGGCCAAACAGTCTGGCTGGAG 1520
Db 1292 CACCAGCATCTTCCCTCGGGCTGGAGTGTGGCGCCATGGCCAAACAGTCTGGCTGGAG 1351
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Db 1352 TGATGCATCTTGGCCCGACACAGATGCTTACCTCGATCCCAACGTACCGGTGCTT 1411
QY 1581 CTTGGGACCTTACCCCTTTGGCATCGATCTTATTTGGAGCTGTGCTGCCAACCACTTGAG 1640
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QY 1701 TGGGGTGGTCTCTCGAGTCTTCAACACGTGCACTTTGGCCAGAGGACACGGCTGTGCT 1760
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QY 1761 GAGAGCGCTGCGGAGTCACTTCTGCTGGGACTCTTGGTTTACCTGCTGTTCTTGTAGT 1820
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QY 1821 CATCTACAAGTGGCTGTGCTGGGCTGCGAGGCGCGCTCG ---CCAGCATCTCAT 1877
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Db 1772 GCAGGAGTGGTCCAGGCCACGCTGTGGTCTTGGCCCTTGGCCATGGTCCCATCTGCT 1831
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Db 1832 GCTTGGGACACCCCTGCACTGTGACCGCCACCGCGCGCTGGGAGGAGGCGCGC 1891
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QY 2118 CTGGAGCTCCGATCAGGAGAAAGGAGGCGCTTGGATGATGAAGAGGAGGCGGAGCTCGT 2177
Db 1952 CTGGAGCTCCGATCAGGAGAAAGGAGGCGCTTGGATGATGAAGAGGAGGCGGAGCTCGT 2011
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Db 2012 CCCCTCCGAGGTGCTCATGACACGAGGCATCCACACCATCGAGTTCTGCTGGGCTGCGT 2071
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Db 2192 GCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2251
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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Title: US-10-783-519-1

Perfect score: 2640

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Searched: 809770 seqs, 591248006 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1619416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Published Applications NA New:

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- 3: /EMC Celerra_SID33/ptodata/2/pubpna/US07_NEW_PUB.seq:
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- 7: /EMC Celerra_SID33/ptodata/2/pubpna/US11_NEW_PUB.seq:
- 8: /EMC Celerra_SID33/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2142	81.1	2700	6	US-10-511-937-410
2	775	29.4	1696	7	US-11-266-748A-76629
3	775	29.4	1696	7	US-11-266-748A-109489
4	775	29.4	1696	7	US-11-266-748A-129440
5	760	28.8	1000	7	US-11-266-748A-221798
6	760	28.8	1000	7	US-11-266-748A-287153
7	760	28.8	1000	7	US-11-266-748A-338582
8	760	28.8	1000	7	US-11-266-748A-397768
9	760	28.8	1000	7	US-11-266-748A-468814
10	581	22.0	1042	7	US-11-266-748A-76627
11	581	22.0	1042	7	US-11-266-748A-109487
12	581	22.0	1042	7	US-11-266-748A-129438
13	532	20.2	671	7	US-11-266-748A-54130
14	500	18.9	738	7	US-11-266-748A-76628
15	500	18.9	738	7	US-11-266-748A-109488
16	500	18.9	738	7	US-11-266-748A-129439
17	489	18.5	831	7	US-11-266-748A-8067
18	454	17.2	561	7	US-11-266-748A-362824
19	454	17.2	561	7	US-11-266-748A-446203
20	423	16.0	1839	7	US-11-266-748A-361154
21	423	16.0	1839	7	US-11-266-748A-444533
22	391	14.8	1469	7	US-11-266-748A-98830
23	391	14.8	1469	7	US-11-266-748A-151641
24	340	12.9	1127	7	US-11-266-748A-76630
25	340	12.9	1127	7	US-11-266-748A-109490

ALIGNMENTS

RESULT 1

US-10-511-937-410
; Sequence 410, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 410
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-410

Query Match 81.1%; Score 2142; DB 6; Length 2700;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2582; Conservative 0; Mismatches 4; Indels 3; Gaps 1;
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DB 89 GCGCAGCACACCGGGGACCATGGCTCCATGTTCCGAGCGAGAGGTGGCCCTGGTCC 148
QY 98 AGCTCTTCTGCGCCACAGCGGCTGCTACACCTGCGTGGAGTCCGCTCGGAGCTGGGCC 157
DB 149 AGCTCTTCTGCGCCACAGCGGCTGCTACACCTGCGTGGAGTCCGCTCGGAGCTGGGCC 208
QY 158 TCGTGGAGTTTCAGAGACCTCAACGCTTCGCTGAGCGCTTCCAGAGACGCTTTTGTGTTG 217
DB 209 TCGTGGAGTTTCAGAGACCTCAACGCTTCGCTGAGCGCTTCCAGAGACGCTTTTGTGTTG 268

QY	218	ATGTTTGGCGCTGTGAGAGCTGGAGAAAGACTTCACTTCTGCAGGAGGAGTGC	277
DB	269	ATGTTTCGGCGCTGTGAGAGCTGGAGAAAGACTTCACTTCTGCAGGAGGAGTGC	328
QY	278	GGGCTTGGGCTGGTCTGTGCCCCCGCCAAAGGGGAGGCTTGC	337
DB	329	GGGCTTGGGCTGGTCTGTGCCCCCGCCAAAGGGGAGGCTTGC	388
QY	338	TGCTGCGCATTCAGAGAGAGACGAGCGCCTTGGCCAGAGAGCTGCGGATGTGCGGGACA	397
DB	389	TGCTGCGCATTCAGAGAGAGAGACGAGCGCCTTGGCCAGAGAGCTGCGGATGTGCGGGACA	448
QY	398	ACCAGAGGCCCTTCGGGCCCAAGCTGCACAGCTGCAGCTCCACGCCCGCTGTACGCC	457
DB	449	ACCAGAGGCCCTTCGGGCCCAAGCTGCACAGCTGCAGCTCCACGCCCGCTGTACGCC	508
QY	458	AGGGCCATGAACCTCAGCTTGGCAGCGCCCAACAGATGGGGCCTCAGAGAGAGCGCCC	517
DB	509	AGGGCCATGAACCTCAGCTTGGCAGCGCCCAACAGATGGGGCCTCAGAGAGAGCGCCC	568
QY	518	TGCTCCAGGCCCCCGGGGGCCGACACAGAGACTTGAGGGTCAACTTTGTGTCAGGTCCG	577
DB	569	TGCTCCAGGCCCCCGGGGGCCGACACAGAGACTTGAGGGTCAACTTTGTGTCAGGTCCG	628
QY	578	TGGAGCCCCACAAGGCCCTTGCCTTAGAGCGCTGTCTTGAGAGGCCCTGCGCGGCTTCC	637
DB	629	TGGAGCCCCACAAGGCCCTTGCCTTAGAGCGCTGTCTTGAGAGGCCCTGCGCGGCTTCC	688
QY	638	TCATTGCCAGCTTCAGGGAGCTTGAGCAGCGCTTGGAGCACCCCGTGA	697
DB	689	TCATTGCCAGCTTCAGGGAGCTTGAGCAGCGCTTGGAGCACCCCGTGA	748
QY	698	CCAGTGTGATGACCTTCCTCATCTCCTACTGSGGTGAGCAGATCGGACAGAGATCCGCA	757
DB	749	CCAGTGTGATGACCTTCCTCATCTCCTACTGSGGTGAGCAGATCGGACAGAGATCCGCA	808
QY	758	AGATCACGGACTGTCTTCCACTGCCACAGCTTTCCCGTTTCTGCACGAGGAGAGCGCCGCC	817
DB	809	AGATCACGGACTGTCTTCCACTGCCACAGCTTTCCCGTTTCTGCACGAGGAGAGCGCCGCC	868
QY	818	TGGGGGCCCTGCAGAGCTGTCAAACAGCAGAGCCAGAGCTGCAGGAGGTCTTCGGGAGA	877
DB	869	TGGGGGCCCTGCAGAGCTGTCAAACAGCAGAGCCAGAGCTGCAGGAGGTCTTCGGGAGA	928
QY	878	CAGAGCGGTTCCTGAGCCAGGTGTAGCCGGGTGCTGACGTCTGCCGCCAGGGCAGG	937
DB	929	CAGAGCGGTTCCTGAGCCAGGTGTAGCCGGGTGCTGACGTCTGCCGCCAGGGCAGG	988
QY	938	TGCAGGTCCAAGAATGAAGCCCGTGTACTTGGCCCTTGAAACAGTCAGCGGTGAGCACCA	997
DB	989	TGCAGGTCCAAGAATGAAGCCCGTGTACTTGGCCCTTGAAACAGTCAGCGGTGAGCACCA	1048
QY	998	CGCACAGTGCCTCATTTGCCAGCGCTGTGTCTGTGCGAGACCTGCCCGCCTTGAGG	1057
DB	1049	CGCACAGTGCCTCATTTGCCAGCGCTGTGTCTGTGCGAGACCTGCCCGCCTTGAGG	1108
QY	1058	AGGCCCTTCCGGGACAGCTTCGATGAGAGGGAGGTAGTGGCGTGGCTCACGGCATCCCTT	1117
DB	1109	AGGCCCTTCCGGGACAGCTTCGATGAGAGGGAGGTAGTGGCGTGGCTCACGGCATCCCTT	1168
QY	1118	GCCGGGACATGCCCCCCACACTCATTCGGCACAAACCGCTTTCAGCGGCAGGTTC	1177
DB	1169	GCCGGGACATGCCCCCCACACTCATTCGGCACAAACCGCTTTCAGCGGCAGGTTC	1228
QY	1178	TCGTGATTCGCTACGGCGTGGGCGCTTACAGAGAGGTCAACCCCGCTTCCCTTACACATCA	1237
DB	1229	TCGTGATTCGCTACGGCGTGGGCGCTTACAGAGAGGTCAACCCCGCTTCCCTTACACATCA	1288
QY	1238	TCACCTTCCCTTCTCTGTTTCTGTGATGTTTGGGGATGTGGGCCACGGGCTGCTCATGT	1297
DB	1289	TCACCTTCCCTTCTCTGTTTCTGTGATGTTTGGGGATGTGGGCCACGGGCTGCTCATGT	1348
QY	1298	TCCTTTTGGCCCTTGGCCATGGTCTCTTGGGAGAACCGACCGGCTTGTGAAGACCGCGCAGA	1357

Db	1349	TCCTTTTCGGCCCTGGCCATGGTCTCTTTCGGAGAAACGACCGGTGTGAAGGCGCGCAGA	1408
Qy	1358	ACGAGATCTTGGCAGACTTTCTTTCAGGGGCGCTACCTGTCTCTGCTTATGGGCGCTGTTC	1417
Db	1409	ACGAGATCTTGGCAGACTTTCTTTCAGGGGCGCTACCTGTCTCTGCTTATGGGCGCTGTTC	1468
Qy	1418	CCATCTACACGGGCTTCATCTACAAAGAGTGTTCAGTTCGGCGCACACAGCATCTTCCCT	1477
Db	1469	CCATCTTACACGGGCTTCATCTTACAAAGAGTGTTCAGTTCGGCGCACACAGCATCTTCCCT	1528
Qy	1478	CGGGCTGGAGTGTGGCGCCGATGCCAACACAGTCTGGCTGGAGTGATGCAATTCCTGGCCC	1537
Db	1529	CGGGCTGGAGTGTGGCGCGCATGGCCAAACAGTCTGGCTGGAGTGATGCAATTCCTGGCCC	1588
Qy	1538	AGCACACGATGCTTACCTCGATGCCMAACGTCAACGGGTGTCTCTGGAGACCTACCCCT	1597
Db	1589	AGCACACGATGCTTACCTCGATGCCMAACGTCAACGGGTGTCTCTGGAGACCTACCCCT	1648
Qy	1598	TTGGCATCGATCTTATTTTGGAGCTTGGCTGCCAAACACTTGGAGCTTCTCAACTCTCTTCA	1657
Db	1649	TTGGCATCGATCTTATTTTGGAGCTTGGCTGCCAAACACTTGGAGCTTCTCAACTCTCTTCA	1708
Qy	1658	AGATGAAGATGTCCGTTCATCTCTGGCGGTCTGCACATGGCTTTTGGGGTGGTCTCTCGAG	1717
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Qy	1718	TCCTTCAACACGATGCACTTTTGGCGAGAGGCAACGGGTGTCTGTGGAGACGCTGCCGGAGC	1777
Db	1769	TCCTTCAACACGATGCACTTTTGGCGAGAGGCAACGGGTGTCTGTGGAGACGCTGCCGGAGC	1828
Qy	1778	TCACCTTCTCTGTGGGACTCTTGGGTACCTCTGGTTCCTAGTCACTACAGTGACTGT	1837
Db	1829	TCACCTTCTCTGTGGGACTCTTGGGTACCTCTGGTTCCTAGTCACTACAGTGACTGT	1888
Qy	1838	GTGTCTGGGCTGCCAGGGCGCGCTCG --- CCCAGCATCTCTCATCCACTTCATCAACATGT	1894
Db	1889	GTGTCTGGGCTGCCAGGGCGCGCTCGGGCCCCAGCATCTCTATCCACTTCATCAACATGT	1948
Qy	1895	TCCTCTTCTCCACAGCCCCAGCAACAGGTGTCTTACCCCGGGCAGAGGTGGTCCAGG	1954
Db	1949	TCCTCTTCTCCACAGCCCCAGCAACAGGTGTCTTACCCCGGGCAGAGGTGGTCCAGG	2008
Qy	1955	CCAGCTGTGTCTGGGCTTGGCATGGTGCCCATCTGTCTGTGGCAGACACCCCTGC	2014
Db	2009	CCAGCTGTGTGTCTGGGCTTGGCATGGTGCCCATCTGTCTGTGGCAGACACCCCTGC	2068
Qy	2015	ACCTGTGTGCAACCGCACACCGCGCGCTTGGGAGGAGGCCGTGACCGACAGGAGGAAA	2074
Db	2069	ACCTGTGTGCAACCGCACACCGCGCGCTTGGGAGGAGGCCGTGACCGACAGGAGGAAA	2128
Qy	2075	ACAAGGCGGGTGTCTGGACCTGCTGACCGCATCTGTGAAATGGCTGGAGCTCCGATGAGG	2134
Db	2129	ACAAGGCGGGTGTCTGGACCTGCTGACCGCATCTGTGAAATGGCTGGAGCTCCGATGAGG	2188
Qy	2135	AAAAGGCAGGGGCTTGGATGATGAAGAGAGGCGGAGCTCTGTCCCTCCGAGGTGCTCA	2194
Db	2189	AAAAGGCAGGGGCTTGGATGATGAAGAGAGGCGGAGCTCTGTCCCTCCGAGGTGCTCA	2248
Qy	2195	TGCAACAGGGCATCCACACCATTCAGTTCCTGGCTGGGCTGCGTCTCTCAACACCGCTCTCT	2254
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Qy	2255	ACTTGGGCTTGTGGGCGCTGAGCTGGCCCAACGCCACAGTGTCCGAGGTTCGTGGGCGCA	2314
Db	2309	ACTTGGGCTTGTGGGCGCTGAGCTGGCCCAACGCCACAGTGTCCGAGGTTCGTGGGCGCA	2368
Qy	2315	TGTGTATGCCATAGGCTGGGCTGGGCGGAGGTGGGCGTGGGCGTGTGGTCTCTGG	2374
Db	2369	TGTGTATGCCATAGGCTGGGCTGGGCGGAGGTGGGCGTGGGCGTGTGGTCTCTGG	2428
Qy	2375	TCGCCATCTTTGGCGGCTTTGGCGTATGACCGTGGCTATCTCTGTCTGTGTATGGAGGGAC	2434

Db	2429	TCCCATCTTTGGCGCCTTTGGCGGTGATGACCGGTGGCTATCTCTCGTGGTGTGAGGGAC	2488
Qy	2435	TCTCAGCCTTTCTCTGCAGCCCTGGCGGTGCACTGGGTGGAATTCAGAACAAAGTTCTTACT	2494
Db	2489	 TCTCAGCCTTTCTCTGCAGCCCTGGCGGTGCACTGGGTGGAATTCAGAACAAAGTTCTTACT	2548
Qy	2495	CAGGCACGGGGCTACAAGCTGAGTCCCTTCACCTTCGCTGCCACAGATGACTAGGGGCCAC	2554
Db	2549	 CAGGCACGGGGCTACAAGCTGAGTCCCTTCACCTTCGCTGCCACAGATGACTAGGGGCCAC	2608
Qy	2555	TGCAGGTCTCTGCCACAGACTCTCTTCCTGCACCTCTCAGGCAGGAGAGGAATAAAGACGGTCC	2614
Db	2609	 TGCAGGTCTCTGCCACAGACTCTCTTCCTGCACCTCTCAGGCAGGAGAGGAATAAAGACGGTCC	2668
Qy	2615	GCCTCTGGCA	2623
Db	2669	 GCCTCTGGCA	2677

RESULT 2

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US-11-266-748A-76629
; Sequence 76629, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76629
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-76629

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	Best Local Similarity	99.3%;	Pred. No. 1.2e-212;		
	Matches 1505;	Conservative 0;	Mismatches 5;	Indels 5;	Gaps 3;
QY	781	CAGCTCTTCCCGTTTCTGCAGCAGGAGGAGGCCGCTCGGGGCCCTGCAGCAGCTGCAA	840		
DB	28	CAGCTCTTCCCGTTTCTGCAGGAGGAGGCCGCTCGGGGCCCTGCAGCAGCTGCAA	87		
QY	841	CAGCAGAGCCAGGAGCTGCAGGAGGTCTCTCGGGGAGACAGAGCGGTTTCTTGAGCCAGGTG	900		
DB	88	CAGCAGAGCCAGGAGCTGCAGGAGGTCTCTCGGGGAGACAGAGCGGTTTCTTGAGCCAGGTG	147		
QY	901	CTAGGCCGGGTGTGTCAGCTGCTGCCCGCAGGCGCAGTGTCCACAGATGTAAGGCC	960		
DB	148	CTAGGCCGGGTGTGTCAGCTGCTGCCCGCAGGCGCAGTGTCCACAGATGTAAGGCC	207		
QY	961	GTGTACTCTGCCCTGTGAACCAAGTCAGCGTGAGCAGCACCAAGTCACCTCATTTGCCGAG	1020		

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Qy 2096 TGCTCAGCCATCTGTGAATGGCTGGAGCTCCGATGAGGAAGAGGAGGGGCTGGATG 2155
Db 1348 TGCTCAGCCATCTGTGAATGGCTGGAGCTCCGATGAGGAAGAGGAGGGGCTGGATG 1407
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Qy 2216 TGAGTTCTGCTGGGCTGGCTTCCAAACACCGCTCTCTACCTGCGGCTGTGGGCGCTGA 2275
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Qy 2276 GCGTGGCCCAAGGCC 2290
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RESULT 3

US-11-266-748A-109489
; Sequence 109489, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
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; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 109489
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-109489

Query Match 29.4%; Score 775; DB 7; Length 1696;
Best Local Similarity 99.3%; Pred. No. 1.2e-212;
Matches 1505; Conservative 0; Mismatches 5; Indels 5; Gaps 3;
Qy 781 CACGTCTCCCGTTTCTGCAGCAGGAGGAGGCGCGCTCGGGGCGCTGCAGCAGCTGCAC 840
Db 28 CACGTCTCCCGTTTCTGCAGCAGGAGGAGGCGCGCTCGGGGCGCTGCAGCAGCTGCAC 87
Qy 841 CAGCAGGAGCAGGAGCTGCAGAGGTCTCGGGGAGACAGAGCGGTTCCTGAGCCAGGTG 900
Db 88 CAGCAGGAGCAGGAGCTGCAGAGGTCTCGGGGAGACAGAGCGGTTCCTGAGCCAGGTG 147
Qy 901 CTAGGCCGGGTGCTGCAGCTGCTGCCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
Db 148 CTAGGCCGGGTGCTGCAGCTGCTGCCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 207
Qy 961 GTGTACCTGGCCCTGAACCAAGTGCAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAG 1020

Db 208 GTGTACTGCGCCCTGAAACCAAGTGCAGCTGAGCACAACGCAAGAGTGCCTCATTTGCCGAG 267
Qy 1021 GCCTGGTGTCTGTGCGAGACCTGCGCGCCCTGCGAGGAGGCGCTGCGGAGACAGTCTGATG 1080
Db 268 GCCTGGTGTCTGTGCGAGACCTGCGCGCCCTGCGAGGAGGCGCTGCGGAGACAGTCTGATG 327
Qy 1081 GAGGAGGAGTGAAGTGGCTGCGCTCAACGCAATCCCTGCGGAGACATGCGCCCAACATC 1140
Db 328 GAGGAGGAGTGAAGTGGCTGCGCTCAACGCAATCCCTGCGGAGACATGCGCCCAACATC 387
Qy 1141 ATCCGCAACCAACCGCTTCAACGCGCAGCTTCAACGCGCATCGTGGATCGCTACGCGTGGGC 1200
Db 388 ATCCGCAACCAACCGCTTCAACGCGCAGCTTCAACGCGCATCGTGGATCGCTACGCGTGGGC 447
Qy 1201 CGCTACAGGAGGTCAACCCCGCTCCCTACACCATCATCCTTCCCTTCCCTTCTGTTTGTCT 1260
Db 448 CGCTACAGGAGGTCAACCCCGCTCCCTACACCATCATCCTTCCCTTCCCTTCTGTTTGTCT 507
Qy 1261 GTGATGTTGGGGATGTGGGCGCACGGGCTGCTCATGTTCTCTTCCGCTTGGCCATGCTC 1320
Db 508 GTGATGTTGGGGATGTGGGCGCACGGGCTGCTCATGTTCTCTTCCGCTTGGCCATGCTC 567
Qy 1321 CTTTGGGAGAACCGGCTGTGAAAGCGCGCAGAAAGAGATCTGGCAGACTTTTCTTC 1380
Db 568 CTTTGGGAGAACCGGCTGTGAAAGCGCGCAGAAAGAGATCTGGCAGACTTTTCTTC 627
Qy 1381 AGGGGCGCTACCTGCTCTGCTTATGCGCTTCTCATCTACACCGGCTTATCTATC 1440
Db 628 AGGGGCGCTACCTGCTCTGCTTATGCGCTTCTCATCTACACCGGCTTATCTATC 687
Qy 1441 AACGAGTCTTCAGTGGGCGCACAGCATCTTCCCTCGGGCTGGAGTGTGGCGGCTG 1500
Db 688 AACGAGTCTTCAGTGGGCGCACAGCATCTTCCCTCGGGCTGGAGTGTGGCGGCTG 747
Qy 1501 GCCAACCAAGTCTGGGCTGAGTGCATGCAATTCCTGGGCGCAGCACACATGCTTACCTTGGAT 1560
Db 748 GCCAACCAAGTCTGGGCTGAGTGCATGCAATTCCTGGGCGCAGCACACATGCTTACCTTGGAT 807
Qy 1561 CCCAACGTCACCGGTGCTTCTCGGAGCCCTAACCCCTTGGCATCGATCTTATTTGGAGC 1620
Db 808 CCCAACGTCACCGGTGCTTCTCGGAGCCCTAACCCCTTGGCATCGATCTTATTTGGAGC 867
Qy 1621 CTGGGTCGCAACCACTGAGCTTCTCAACTCTTCAAGATGAAGTGTCCGTTCATCTG 1680
Db 868 CTGGGTCGCAACCACTGAGCTTCTCAACTCTTCAAGATGAAGTGTCCGTTCATCTG 927
Qy 1681 GCGCTGTCGACATGGCC--TTTGGGGT--GGTCTCGGAGTCTTCAACCAAGTGCATCTT 1738
Db 928 GCGCTGTCGACATGGCCCTTTTGGGGTGGGTCTCTCGGAGTCTTCAACCAAGTGCATCTT 987
Qy 1739 GCCAGAGGACCGGCTGCTGCTGAGAGACGCTGCGGAGCTCACCTTCTGCTGGGACTCT 1798
Db 988 GCCAGAGGACCGGCTGCTGCTGAGAGACGCTGCGGAGCTCACCTTCTGCTGGGACTCT 1047
Qy 1799 TCGGTTACTCTGCTGTTCTAGTCACTACAGTGGCTGTGTCTGCGGCTGCGGCGCG 1858
Db 1048 TCGGTTACTCTGCTGTTCTAGTCACTACAGTGGCTGTGTCTGCGGCTGCGGCGCG 1107
Qy 1859 CCTCG---CCCAGCATCTCTCATCCATCAAGATGTTCTTCTTCTCCCAAGAGCCCA 1915
Db 1108 CTTCCGCGCCCAAGCATCTCTCATCCATCAAGATGTTCTTCTTCTCCCAAGAGCCCA 1167
Qy 1916 GCACAGGCTGCTTACCCCGGAGGAGGTGCTCAGGCGACGCTGTGTGTCTGGGCT 1975
Db 1168 GCACAGGCTGCTTACCCCGGAGGAGGTGCTCAGGCGACGCTGTGTGTCTGGGCT 1227
Qy 1976 TGGCCATGCTGCGCCCTCTGCTGCTTGGCACACCTGTCACCTGCTGACCGCCACCGCC 2035
Db 1228 TGGCCATGCTGCGCCCTCTGCTGCTTGGCACACCTGTCACCTGCTGATGACCGCCACCGCC 1287
Qy 2036 GCGGCTGCGGAGGAGGCGCGCTGACCGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 2095

Db 1288 GCCGCTGCGGAGGCGCGCTGACCGACAGGAGGAAAAAAGGCGGGTGTCTGGACC 1347
Qy 2096 TGCCTGACGCATCTGTGAATGGCTGGAGCTCCGATGAGGAAAAAGGCGGGCCCTGGATG 2155
Db 1348 TGCCTGACGCATCTGTGAATGGCTGGAGCTCCGATGAGGAAAAAGGCGGGCCCTGGATG 1407
Qy 2156 ATGAAGAGGAGCGCGAGCTGCTCCCTCCGAGGTGCTCATGACAGGCGCCATCCACACCA 2215
Db 1408 ATGAAGAGGAGCGCGAGCTGCTCCCTCCGAGGTGCTCATGACAGGCGCCATCCACACCA 1467
Qy 2216 TCGAGTTCTGCTGGGCTGCGCTCTCCACACCGCCTCTACCTGCGGCTGTGGGCGCCCTGA 2275
Db 1468 TCGAGTTCTGCTGGGCTGCGCTCTCCACACCGCCTCTACCTGCGGCTGTGGGCGCCCTGA 1527
Qy 2276 GCCTGGGCGGCGCC 2290
Db 1528 GCCTGGGCGGCGCC 1542

RESULT 4

US-11-266-748A-129440/c
; Sequence 129440, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129440
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-129440

Query Match 29.4%; Score 775; DB 7; Length 1696;

Best Local Similarity 99.3%; Pred. No. 1.2e-212;

Matches 1505; Conservative 0; Mismatches 5; Indels 5; Gaps 3;

Qy 781 CAGCTCTTCGCTTCTGACGAGGAGGCGCGCTCGGGGCGCTGACGAGCTGCAA 840
Db 1669 CAGCTCTTCGCTTCTGACGAGGAGGCGCGCTCGGGGCGCTGACGAGCTGCAA 1610
Qy 841 CAGCAGAGCCAGGAGCTGACGAGGAGTCTTCGGGAGACAGAGCGGTTCTGAGCAGGTG 900
Db 1609 CAGCAGAGCCAGGAGCTGACGAGGAGTCTTCGGGAGACAGAGCGGTTCTGAGCAGGTG 1550
Qy 901 CTAGGCGGGTGTGACGCTGCTGCGCCAGGCGAGGTGCAAGATGAAGGCC 960
Db 1549 CTAGGCGGGTGTGACGCTGCTGCGCCAGGCGAGGTGCAAGATGAAGGCC 1490
Qy 961 GTGTACTGCGCCCTGAACACAGTGCAGCGGTGAGCACAGGCAAGTGCCTCATTTGCCGAG 1020

Db 1489 GTGTACTGCGCCCTGAAACAGTGCAGCGTGAAGCAACAGCAAAAGTGCCTCATTTGCCGAG 1430
Qy 1021 GCCTGCTGCTCTGTGCGAGAGCTGCGCGCCCTGCGAGAGGCGCTGCGGAGACAGCTCGATG 1080
Db 1429 GCCTGCTGCTCTGTGCGAGAGCTGCGCGCCCTGCGAGAGGCGCTGCGGAGACAGCTCGATG 1370
Qy 1081 GAGAGGAGTGTGAGTGCCTGCTGACCGCATTCCTGCGGAGACATGCCGCCACATC 1140
Db 1369 GAGAGGAGTGTGAGTGCCTGCTGACCGCATTCCTGCGGAGACATGCCGCCACATC 1310
Qy 1141 ATCCGACCAACCGCTTACCGGCGAGCTTCCAGGAGACATGCCGCTAGCGGCGTGGG 1200
Db 1309 ATCCGACCAACCGCTTACCGGCGAGCTTCCAGGAGACATGCCGCTAGCGGCGTGGG 1250
Qy 1201 CGCTACAGGAGGTCAACCGCGCTCCCTACACCATCATCATCTTCCCTTCTGTTTGT 1260
Db 1249 CGCTACAGGAGGTCAACCGCGCTCCCTACACCATCATCATCTTCCCTTCTGTTTGT 1190
Qy 1261 GTGATTTGGGGATGTGGGCGACGCGCTGCTCATGTTCTCTTCGCGCTGGCCATGTC 1320
Db 1189 GTGATTTGGGGATGTGGGCGACGCGCTGCTCATGTTCTTCTTCGCGCTGGCCATGTC 1130
Qy 1321 CTTGCGGAGAACCGACCGGCTGTGAAGCGCGCAGAACGAGATCTGGCAGACTTCTTC 1380
Db 1129 CTTGCGGAGAACCGACCGGCTGTGAAGCGCGCAGAACGAGATCTGGCAGACTTCTTC 1070
Qy 1381 AGGGCGCGCTACCTGCTCCTGCTTATGGGCGCTGTTCTCCATCTACACCGGCTTATCTAC 1440
Db 1069 AGGGCGCGCTACCTGCTCCTGCTTATGGGCGCTGTTCTCCATCTACACCGGCTTATCTAC 1010
Qy 1441 AACGAGTGTTCAGTTCGCGGCGACAGCATTTTCCCTCGGCTGGAGTGTGGCGCCATG 1500
Db 1009 AACGAGTGTTCAGTTCGCGGCGACAGCATTTTCCCTCGGCTGGAGTGTGGCGCCATG 950
Qy 1501 GCCAACAGTCTGGCTGGAGTGTGATTCCTGCGCGCAGCACAGATCTTACCTGAGT 1560
Db 949 GCCAACAGTCTGGCTGGAGTGTGATTCCTGCGCGCAGCACAGATCTTACCTGAGT 890
Qy 1561 CCCAACGTCACCGGTGCTTCTCGGAGCCCTTACCGCTTGGCATCGATCTTATTTGGAGC 1620
Db 889 CCCAACGTCACCGGTGCTTCTCGGAGCCCTTACCGCTTGGCATCGATCTTATTTGGAGC 830
Qy 1621 CTGCTGCCAAACCACTTGTGAGTTCCTCAACTCTTCAAGATGAAGATGTCGCTCATCTG 1680
Db 829 CTGCTGCCAAACCACTTGTGAGTTCCTCAACTCTTCAAGATGAAGATGTCGCTCATCTG 770
Qy 1681 GGGTGTGTCACATGGCC-TTTGGGGT-GGTCTCGGAGTCTTCAACACGTCGACTTGG 1738
Db 769 GGGTGTGTCACATGGCC-TTTGGGGTGGGTCTTCAACACGTCGACTTGG 710
Qy 1739 GCCAGAGGCGACCGGCTGCTGCTGAGAGCGCTGCGGAGCTCACCTTCTGCTGGAGCTCT 1798
Db 709 GCCAGAGGCGACCGGCTGCTGCTGAGAGCGCTGCGGAGCTCACCTTCTGCTGGAGCTCT 650
Qy 1799 TCGGTTACTGCTGCTTCTAGTTCATCTCAAGTGGCTGTGTGCTGGGCTGCCAGGCGCG 1858
Db 649 TCGGTTACTGCTGCTTCTAGTTCATCTCAAGTGGCTGTGTGCTGGGCTGCCAGGCGCG 590
Qy 1859 CTTGCG---CCCAGCATCTCATCCACTTTCATCAAGTGGCTTCTTCTTCCACAGCCCA 1915
Db 589 CTTGCGCGCCCGAGCATCTCATCCACTTTCATCAAGTGGCTTCTTCTTCCACAGCCCA 530
Qy 1916 GCAACAGGCTGCTTACCGCGGAGGAGTGTGTCAGGCGCACGCTGCTGCTGCTGGCT 1975
Db 529 GCAACAGGCTGCTTACCGCGGAGGAGTGTGTCAGGCGCACGCTGCTGCTGCTGGCT 470
Qy 1976 TGGCCATGTGCCCCATCCTGCTGTGGCAACCCCTGCACTGCTGCAACCGCCACCGCC 2035
Db 469 TGGCCATGTGCCCCATCCTGCTGTGGCAACCCCTGCACTGCTGCAACCGCCACCGCC 410
Qy 2036 GCGGCTTGGGAGGCGCGCTGACCGACAGGAGGAAAAAAGGCGGGTGTCTGAGCC 2095

Db 409 GCCTGCGAGGAGGCGCGTGAACGACAGGAGGAAACAAAGCGCGGTTGCTGGACC 350
QY 2096 TGCTGACCGCATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGGACAGGGGCTGGATG 2155
Db 349 TGCTGACCGCATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGGACAGGGGCTGGATG 290
QY 2156 ATGAAGAGGAGGCGGAGCTCGTCCCTCCGAGGTGCTCATGACACCGGCGCATCCACACCA 2215
Db 289 ATGAAGAGGAGGCGGAGCTCGTCCCTCCGAGGTGCTCATGACACCGGCGCATCCACACCA 230
QY 2216 TCGAGTTCTGCTGGGCTGGCTCCCAACACCGCTTCTACCTGCGGCTGTGGGCGCTGA 2275
Db 229 TCGAGTTCTGCTGGGCTGGCTCCCAACACCGCTTCTACCTGCGGCTGTGGGCGCTGA 170
QY 2276 GCCTGGCCACGCCC 2290
Db 169 GCCTGGCCACGCCC 155

RESULT 5

US-11-266-748A-221798
; Sequence 221798, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 221798
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-221798

Query Match 28.8%; Score 760; DB 7; Length 1000;
Best Local Similarity 100.0%; Pred. No. 2.6e-208;
Matches 760; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1864 CCAGCATCTCATCCATTCATCAACATGTTCTCTCCACAGCCCGCCAGCAACAGG 1923
Db 218 CCAGCATCTCATCCATTCATCAACATGTTCTCTCCACAGCCCGCCAGCAACAGG 277
QY 1924 CTGCTTACCCCGGAGAGGTGTCAGGCCACGCTGGTGGTCTTGGCCCTTGGCCATG 1983
Db 278 CTGCTTACCCCGGAGAGGTGTCAGGCCACGCTGGTGGTCTTGGCCCTTGGCCATG 337
QY 1984 GTGCCCATCTCTGCTGGCACACCCCTGTCACCGCCGCGCCGCGCCCTG 2043
Db 338 GTGCCCATCTCTGCTGGCACACCCCTGTCACCGCCGCGCCGCGCCCTG 397
QY 2044 CCGAGGAGGCGCGCTGACCGACAGGAGGAAACAAAGGCGCGGTTGCTGGACCTGCGCTGAC 2103

Db 398 CCGAGGAGGCGCGCTGACCGACAGGAGGAAACAAAGGCGCGGTTGCTGGACCTGCGTAC 457
QY 2104 GCATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGGACAGGGGCTTGGATGATGAAGAG 2163
Db 458 GCATCTGTGAATGGCTGGAGCTCCGATGAGGAAAGGACAGGGGCTTGGATGATGAAGAG 517
QY 2164 GAGGCGGAGCTCGTCCCTCCGAGGTGCTCATGACACCGGCGCATCCACACCATCGAGTTC 2223
Db 518 GAGGCGGAGCTCGTCCCTCCGAGGTGCTCATGACACCGGCGCATCCACACCATCGAGTTC 577
QY 2224 TGCTGGGCTGGCTTCCCAACACCGCTTCTACCTGCGGCTGTGGGCGCTTGGAGCTTGGCC 2283
Db 578 TGCTGGGCTGGCTTCCCAACACCGCTTCTACCTGCGGCTGTGGGCGCTTGGAGCTTGGCC 637
QY 2284 CACGCGGAGCTGTCGAGGTCTGTGGGCGCATGCGGATAGCGCTTGGGCGCTTGGGCG 2343
Db 638 CACGCGGAGCTGTCGAGGTCTGTGGGCGCATGCGGATAGCGCTTGGGCGCTTGGGCG 697
QY 2344 CCGGAGGTGGGCGTGGGCGCTGTGGTGTGCTGCTCCCATCTTTGCGCGCTTGGCGGTGATG 2403
Db 698 CCGGAGGTGGGCGTGGGCGCTGTGGTGTGCTGCTGCTGCGCTTCTGCAAGCTTGGCGGTG 757
QY 2404 ACCGTGGCTATCTGCTGTGATGAGGAGGACTCTCAGCGCTTCTGCAAGCTTGGCGGTG 2463
Db 758 ACCGTGGCTATCTGCTGTGATGAGGAGGACTCTCAGCGCTTCTGCAAGCTTGGCGGTG 817
QY 2464 CACTGGGTGAATTCAGAAACAAAGTTCTACTCAGGCAAGGCTTACAGCTGAGTCCCTTC 2523
Db 818 CACTGGGTGAATTCAGAAACAAAGTTCTACTCAGGCAAGGCTTACAGCTGAGTCCCTTC 877
QY 2524 ACCTTCGCTGCCACAGATGACTAGGGCCACTGCAAGTCTTCTGCGGAGCTTCTTCTGAC 2583
Db 878 ACCTTCGCTGCCACAGATGACTAGGGCCACTGCAAGTCTTCTGCGGAGCTTCTTCTGAC 937
QY 2584 CTCTGAGGCGAGGAGGAAATAAGACGCTCCGCGCTTGGCA 2623
Db 938 CTCTGAGGCGAGGAGGAAATAAGACGCTCCGCGCTTGGCA 977

RESULT 6

US-11-266-748A-287153
; Sequence 287153, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 287153
; LENGTH: 1000

Qy	2524	ACCTTGGCTGGCCACAGATGACTAGGGGCCACTGTGAGGTCTCTGCAGACAGCTCCTTCTCTGAC	2583
Db	123	ACCTTGGCTGGCCACAGATGACTAGGGGCCACTGTGAGGTCTCTGCAGACAGCTCCTTCTCTGAC	64
Qy	2584	CTCTGAGGCGAGGAGGAATAAAGACCGTCCGCCCTGGCA	2623
Db	63	CTCTGAGGCGAGGAGGAATAAAGACCGTCCGCCCTGGCA	24

RESULT 8
US-11-266-748A-397768
/ Sequence 397768, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnston, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcryptome Microarray Technology and
/ TITLE OF INVENTION: Methods of Using the Same
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ CURRENT FILING DATE: 2005-11-03

Query Match	28.8%	Score 760;	DB 7;	Length 1000;
Best Local Similarity	100.0%;	Pred. No. 2.6e+08;		
Matches 760; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1864	CCGAGATCCTCATCGACCTTCATCAACATGTTCTCTTCTCCACAGCCCCAGCAACAGG	1923
Db	218	CCGAGATCCTCATCGACCTTCATCAACATGTTCTCTTCTCCACAGCCCCAGCAACAGG	277
Qy	1924	CTGCTCTACCCCGGACGAGGAGTGGTCCAGGCCACCGCTGGTGGTCTCTGGCCTTGGCCATG	1983
Db	278	CTGCTCTACCCCGGACGAGGAGTGGTCCAGGCCACCGCTGGTGGTCTCTGGCCTTGGCCATG	337
Qy	1984	GTGCCCATCTCTGTCTTGTGGCACACCCCTCGACCTGTGTGACACCGCCACCCGCGCGCGCTG	2043
Db	338	GTGCCCATCTCTGTCTTGTGGCACACCCCTCGACCTGTGTGACACCGCCACCCGCGCGCGCTG	397
Qy	2044	CGGAGGAGGCCGCTGACCCGACAGGAGGAAAAAAGGCGGGGTGTCTGGACCTGCCTGCAC	2103
Db	398	CGGAGGAGGCCGCTGACCCGACAGGAGGAAAAAAGGCGGGGTGTCTGGACCTGCCTGCAC	457
Qy	2104	GCATCTGTGAATCGCTGGAGCTCCGATGAGGAAAAAGCAGGGGGCTGGATGATGAAGAG	2163
Db	458	GCATCTGTGAATCGCTGGAGCTCCGATGAGGAAAAAGCAGGGGGCTGGATGATGAAGAG	517
Qy	2164	GAGGCCGAGCTGTGCCCTCCGAGGTGCTCATGCAACAGGCCCATCCACACCATCGAGTTC	2223
Db	518	GAGGCCGAGCTGTGCCCTCCGAGGTGCTCATGCAACAGGCCCATCCACACCATCGAGTTC	577

Qy	2224	TGCTGGGCTGCGTCTCCAAACA	CGGCTCTCTACTCGGCTGTGGGCCCTTGAGCCCTGGCC	2283	
Db	578	TGCTGGGCTGCGCTCTCCAAACA	CGGCTCTCTACTCGGCTGTGGGCCCTTGAGCCCTGGCC	637	
Qy	2284	CAGCCGAGCTGTCGAGGTTCTG	TGGGCATGGCATAGCCCTGGGCCCTGGGC	2343	
Db	638	CAGCCGAGCTGTCGAGGTTCTG	TGGGCATGGCATAGCCCTGGGCCCTGGGC	697	
Qy	2344	CGGAGGTGGGCGTGGCGGCTGT	GTCGGTCCCATCTTTGCGCGCTTTGCGGTGATG	2403	
Db	698	CGGAGGTGGGCGTGGCGGCTGT	GTCGGTCCCATCTTTGCGCGCTTTGCGGTGATG	757	
Qy	2404	ACGCTGCTATCTGCTGTGTGAT	TGGAGGACTCTCAGCCTTCTGCA	CGCCCTGCGGCTG	2463
Db	758	ACGCTGCTATCTGCTGTGTGAT	TGGAGGACTCTCAGCCTTCTGCA	CGCCCTGCGGCTG	817
Qy	2464	CACCTGGTGAAATTCAGAACAA	GTGTTACTCAGGCACGGGCTACA	AGCTGAGTCCCTTC	2523
Db	818	CACCTGGTGAAATTCAGAACAA	GTGTTACTCAGGCACGGGCTACA	AGCTGAGTCCCTTC	877
Qy	2524	ACCTTCGCTGCCACAGATGACT	TAGGGCCCACTGCAGGTCTCTG	CCAGACCTCTCTTCCTGAC	2583
Db	878	ACCTTCGCTGCCACAGATGACT	TAGGGCCCACTGCAGGTCTCTG	CCAGACCTCTCTTCCTGAC	937
Qy	2584	CTCTGAGGCAGGAGAGGAATAA	AGACGGTCCGCCCTTGGCA	2623	
Db	938	CTCTGAGGCAGGAGAGGAATAA	AGACGGTCCGCCCTTGGCA	977	

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RESULT 9
US-11-266-748A-468814/c
; Sequence 468814, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
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; PRIOR APPLICATION NUMBER: EP 04105507.0
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; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 468814
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-468814

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Query Match	28.8%	Score 760;	DB 7;	Length 1000;
Best Local Similarity	100.0%;	Pred. No. 2.6e-208;		
Matches 760;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1664	CCGAGCATCCTCATCCCATCTTCATCAATGTTCTCTTTCTCCACAGCCCCCACACAGG	1923	


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Db 783 CCCAGCATCTCATCCACTTTCATCAACATGTTCTCTCTCTCCACAGCCCCAGCAACAGG 724
Qy 1924 CTGCTCTACCCCGGCGAGAGGTGGTCCAGGCCACGCTGGTGGTCTTGGCCCTTGGCCATG 1983
Db 723 CTGCTCTACCCCGGCGAGAGGTGGTCCAGGCCACGCTGGTGGTCTTGGCCCTTGGCCATG 664
Qy 1984 GTGCCCATCTGCTGCTTGGCACACCCCTGCACCTGCTGCACCGCCACCGCCGCGCTG 2043
Db 663 GTGCCCATCTGCTGCTTGGCACACCCCTGCACCTGCTGCACCGCCACCGCCGCGCTG 604
Qy 2044 CGGAGGAGGCGCTGACCGACAGGAGGAAAAAACAAGGCCGGGTGCTGGACCTCCCTGCAC 2103
Db 603 CGGAGGAGGCGCTGACCGACAGGAGGAAAAAACAAGGCCGGGTGCTGGACCTCCCTGCAC 544
Qy 2104 GCATCTGTGAATGCTGAGCTCCGATGAGGAAAAAGGAGGCGCCCTGGATGATGAAGAG 2163
Db 543 GCATCTGTGAATGCTGAGCTCCGATGAGGAAAAAGGAGGCGCCCTGGATGATGAAGAG 484
Qy 2164 GAGGCCAGCTGCTCCCTCCGAGGTGCTCATGACACGAGGCCATCCACACCATCGAGTTC 2223
Db 483 GAGGCCAGCTGCTCCCTCCGAGGTGCTCATGACACGAGGCCATCCACACCATCGAGTTC 424
Qy 2224 TGCTGGGCTGCTCTCAACACCGCTCTCTTACCTGGCCCTGTGGGCCCTTGAGCCTGGCC 2283
Db 423 TGCTGGGCTGCTCTCAACACCGCTCTCTTACCTGGCCCTGTGGGCCCTTGAGCCTGGCC 364
Qy 2284 CAGCCAGCTGCTCCGAGTTCGTGGGCAATGATGCGCATGAGCCTGGGCTGGCC 2343
Db 363 CAGCCAGCTGCTCCGAGTTCGTGGGCAATGATGCGCATGAGCCTGGGCTGGCC 304
Qy 2344 CGGAGGTGGGCTGGGCGCTGGTGTGCTGCTCCCATCTTGGCCGCTTGGCGTGATG 2403
Db 303 CGGAGGTGGGCTGGGCGCTGGTGTGCTGCTCCCATCTTGGCCGCTTGGCGTGATG 244
Qy 2404 ACCGTGCTATCTCTGCTGGTGAAGGAGGACTCTCAGCCTTCTGACGCTTGGCGCTG 2463
Db 243 ACCGTGCTATCTCTGCTGGTGAAGGAGGACTCTCAGCCTTCTGACGCTTGGCGCTG 184
Qy 2464 CACTGGGTGAATTCAGAAACAAGTTCTACTAGGCAAGGCTTCTGACGCTTGGCGCTG 2523
Db 183 CACTGGGTGAATTCAGAAACAAGTTCTACTAGGCAAGGCTTCTGACGCTTGGCGCTG 124
Qy 2524 ACCTTCGCTCCACAGATGACTAGGCGCCACTGCGAGTCTGCGAGACCTCTTCTGAC 2583
Db 123 ACCTTCGCTCCACAGATGACTAGGCGCCACTGCGAGTCTGCGAGACCTCTTCTGAC 64
Qy 2584 CTCTGAGGCAAGGAGGAATAAGACGGTCCGCCCTGGCA 2623
Db 63 CTCTGAGGCAAGGAGGAATAAGACGGTCCGCCCTGGCA 24

RESULT 10
US-11-266-748A-76627
; Sequence 76627, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
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; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76627
; LENGTH: 1042
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: n is a, c, g, or t
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (251)..(251)
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; NAME/KEY: misc feature
; LOCATION: (284)..(284)
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; NAME/KEY: misc feature
; LOCATION: (312)..(312)
; OTHER INFORMATION: n is a, c, g, or t
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/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (461)..(461)
/ OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-76627

Query Match      22.0%; Score 581; DB 7; Length 1042;
Best Local Similarity 100.0%; Pred. No. 2.9e-157;
Matches 581; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2042 TGGGAGGAGGCGCGTGCACGAGGAGAAACAAGCCGGGTTGCTGGACCTGCCTG 2101
Db      |||||
QY 462 TGGGAGGAGGCGCGTGCACGAGGAGAAACAAGCCGGGTTGCTGGACCTGCCTG 521
Db      |||||
QY 2102 AGCATCTCTGAATGCTGGAGCTCGATGAGAAAGCAGGGGCTTGGATGATGAG 2161
Db      |||||
QY 522 AGCATCTCTGAATGCTGGAGCTCGATGAGAAAGCAGGGGCTTGGATGATGAG 581
Db      |||||
QY 2162 AGGAGCCGAGCTCGTCCCTCCGAGGTGCTATGCACAGGCCATCCACACCATCGAGT 2221
Db      |||||
QY 582 AGGAGCCGAGCTCGTCCCTCCGAGGTGCTATGCACAGGCCATCCACACCATCGAGT 641
Db      |||||
QY 2222 TCTGCTGGGCTGCTCTCAACACCGCTCTCTACCTGGGCTTGGGCTGAGCCTGG 2281
Db      |||||
QY 642 TCTGCTGGGCTGCTCTCAACACCGCTCTCTACCTGGGCTTGGGCTGAGCCTGG 701
Db      |||||
QY 2282 CCCAGCCGAGCTGTCGAGGTTCTGTGGGCCATGGTGATGGCATAGGCTTGGGCTGG 2341
Db      |||||
QY 702 CCCAGCCGAGCTGTCGAGGTTCTGTGGGCCATGGTGATGGCATAGGCTTGGGCTGG 761
Db      |||||
QY 2342 GCCGGAGGTGGGCGCTGGGCGCTGTGGTGTGCTGCCATCTTTGGCGCTTTGCCGTGA 2401
Db      |||||
QY 762 GCCGGAGGTGGGCGCTGGGCGCTGTGGTGTGCTGCCATCTTTGGCGCTTTGCCGTGA 821
Db      |||||
QY 2402 TGACCTGTGCTATCTCTGTGGTGATGAGGAGTCTTCAGCCTTCTGTCAGCCCTTCCCTG 2461
Db      |||||
QY 822 TGACCTGTGCTATCTCTGTGGTGATGAGGAGTCTTCAGCCTTCTGTCAGCCCTTCCCTG 881
Db      |||||
QY 2462 TGACCTGTGCTATCTCTGTGGTGATGAGGAGTCTTCAGCCTTCTGTCAGCCCTTCCCTG 2521
Db      |||||
QY 882 TGACCTGTGCTATCTCTGTGGTGATGAGGAGTCTTCAGCCTTCTGTCAGCCCTTCCCTG 941
Db      |||||
QY 2522 TCACCTTCTGCTCCACAGATGACTAGGGCCCACTGCAGGTCTCTGTCAGACCTTCTTCCCTG 2581
Db      |||||
QY 942 TCACCTTCTGCTCCACAGATGACTAGGGCCCACTGCAGGTCTCTGTCAGACCTTCTTCCCTG 1001
Db      |||||
QY 2582 ACCTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2622
Db      |||||
QY 1002 ACCTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1042
Db      |||||

RESULT 11
US-11-266-748A-109487
/ Sequence 109487, Application US/11266748A
/ Publication No. US20060134663A1
/ GENERAL INFORMATION:
/ APPLICANT: Harkin, Paul
/ APPLICANT: Johnston, Patrick
/ APPLICANT: Mulligan, Karl
/ TITLE OF INVENTION: Transcriptome Microarray Technology and
/ TITLE OF INVENTION: Methods of Using the Same
/ FILE REFERENCE: 55815-0102 (319189)
/ CURRENT APPLICATION NUMBER: US/11/266,748A
/ CURRENT FILING DATE: 2005-11-03
/ PRIOR APPLICATION NUMBER: EP 04105479.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105482.6
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105483.4
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105507.0
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105485.9
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/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: EP 04105484.2
/ PRIOR FILING DATE: 2004-11-03
/ PRIOR APPLICATION NUMBER: US 60/662,276
/ PRIOR FILING DATE: 2005-03-14
/ PRIOR APPLICATION NUMBER: US 60/700,293
/ PRIOR FILING DATE: 2005-07-18
/ NUMBER OF SEQ ID NOS: 483996
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 109487
/ LENGTH: 1042
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (16)..(16)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (21)..(21)
/ OTHER INFORMATION: n is a, c, g, or t
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/ NAME/KEY: misc feature
/ LOCATION: (65)..(65)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (80)..(80)
/ OTHER INFORMATION: n is a, c, g, or t
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/ NAME/KEY: misc feature
/ LOCATION: (155)..(155)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (169)..(170)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (181)..(181)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (186)..(186)
/ OTHER INFORMATION: n is a, c, g, or t
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/ NAME/KEY: misc feature
/ LOCATION: (191)..(191)
/ OTHER INFORMATION: n is a, c, g, or t
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/ NAME/KEY: misc feature
/ LOCATION: (205)..(205)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (241)..(241)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (248)..(248)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (251)..(251)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (284)..(284)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc feature
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/ OTHER INFORMATION: n is a, c, g, or t
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[illegible]

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RESULT 13
US-11-266-748A-54130
; Sequence 54130, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9

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; PRIOR FILING DATE: 2004-11-03									
; PRIOR APPLICATION NUMBER: EP 04105484.2									
; PRIOR FILING DATE: 2004-11-03									
; PRIOR APPLICATION NUMBER: US 60/662,276									
; PRIOR FILING DATE: 2005-03-14									
; PRIOR APPLICATION NUMBER: US 60/700,293									
; PRIOR FILING DATE: 2005-07-18									
; NUMBER OF SEQ ID NOS: 483996									
; SOFTWARE: PatentIn version 3.3									
; SEQ ID NO 54130									
; LENGTH: 671									
; TYPE: DNA									
; ORGANISM: Homo Sapiens									
US-11-266-748A-54130									
Query Match	20.2%;	Score 532;	DB 7;	Length 671;					
Best Local Similarity	99.8%;	Pred.No. 3e-143;							
Matches 582; Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;		
Qy	2041	CTCGGAGGAGGCCGCTGACCCGACAGGAGGAAAA	CAAGGCCGGGTGTCTGGACCTGCCT	2100					
Db	89	CTCGGAGGAGGCCGCTGACCGACAGGAGGAAAA	CAAGGCCGGGTGTCTGGACCTGCCT	148					
Qy	2101	GAGCGATCTGTGAATGCTTGBAGCTTCGATGAGGAAAAGCAGGGGCTTGATGATGAA		2160					
Db	149	GAGCGATCTGTGAATGCTTGBAGCTTCGATGAGGAAAAGCAGGGGCTTGGATGATGAA		208					
Qy	2161	GAGGAGGCGGAGCTCGTGCCCTCCGAGGTGCTCATGCACAGGCCATTCACACCATCGAG		2220					
Db	209	GAGGAGGCGGAGCTCGTGCCCTCCGAGGTGCTCATGCACAGGCCATTCACACCATCGAG		268					
Qy	2221	TTCGTGCTGGGTGCGTCTCCAACACCGCTCTACTCGCGCTGTGGGCCCCGTGAGCCTG		2280					
Db	269	TTCGTGCTGGGTGCGTCTCCAACACCGCTCTACTCGCGCTGTGGGCCCCGTGAGCCTG		328					
Qy	2281	GCCCAGCCGAGTGTCCGAGTTCTGTGGGCGATGGTATGCGCATAGGCCCTGGGCGCTG		2340					
Db	329	GCCCAGCCGAGTGTCCGAGTTCTGTGGGCGATGGTATGCGCATAGGCCCTGGGCGCTG		398					
Qy	2341	GGCGGGGAGTGGGCGTGGCGGCTGTGGTGCTGGTCCCATCTTTTGGCCGCTTTTGCCGTG		2400					
Db	389	GGCGGGGAGTGGGCGTGGCGGCTGTGGTGCTGGTCCCATCTTTTGGCCGCTTTTGCCGTG		448					
Qy	2401	ATGACCGTGGCTATCTCTGTGTGATGAGGAGGACTCTCAGCCTTCTCGCACGCCCTGCGG		2460					
Db	449	ATGACCGTGGCTATCTCTGTGTGATGAGGAGGACTCTCAGCCTTCTCGCACGCCCTGCGG		508					
Qy	2461	CTGCATGGGTGGAAATTCCAGAACAGTTCTACTCAGGCACGGGCTACAGCTGAGTCCC		2520					
Db	509	CTGCATGGGTGGAAATTCCAGAACAGTTCTACTCAGGCACGGGCTACAGCTGAGTCCC		568					
Qy	2521	TTCACCTTCGCTGCCACAGATGACTAGGGGCCACTGCAAGTCTCTGCGACCTCTCTCT		2580					
Db	569	TTCACCTTCGCTGCCACAGATGACTAGGGGCCACTGCAAGTCTCTGCGACCMCTCTCTCT		628					
Qy	2581	GACCTCTGAGCGGAGAGAGAATAAAGACGGTCCGCCCTGGCA		2623					
Db	629	GACCTCTGAGCGGAGAGAGAATAAAGACGGTCCGCCCTGGCA		671					

RESULT 14
US-11-266-748A-76628
; Sequence 76628, Application US/11366748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03

QY	2381	TCCTTCCGCTTTGCGTGATGACCGTGGCTATCCTGCTGGTGATGGAGGACTCTCAG	2440
Db	497	TCCTTGGCGCTTTGCGTGATGACCGTGGCTATCCTGCTGGTGATGGAGGACTCTCAG	556
QY	2441	CCTTCTGTGACGCGCTTGGCGTGCTGCACTGGGTGGAATTCAGAAACAAGTTCTACTCAGGCA	2500
Db	557	CCTTCTGTGACGCGCTTGGCGTGCTGCACTGGGTGGAATTCAGAAACAAGTTCTACTCAGGCA	616
QY	2501	CGGGCTACAAAGCTGAGTCCCTTCACCTTCGCTGCCACAGATGACTAGGGCCCACTGCAGG	2560
Db	617	CGGGCTACAAAGCTGAGTCCCTTCACCTTCGCTGCCACAGATGACTAGGGCCCACTGCAGG	676
QY	2561	TCCTGCCAGACCTCCTTCTGACCTCTGAGGAGGAGGAAATAAAGACGGTCCGCCCTG	2620
Db	677	TCCTGCCAGACCTCCTTCTGACCTCTGAGGAGGAGGAAATAAAGACGGTCCGCCCTG	736
QY	2621	GC	2622
Db	737	GC	738

Search completed: June 30, 2006, 06:49:30
Job time : 310 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - protein search, using sw model

Run on: June 29, 2006, 12:59:20 ; Search time 198 Seconds
(without alignments)
1898.141 Million cell updates/sec

Title: US-10-783-519-2
Perfect score: 4266
Sequence: 1 MGSMPFSEVALVQLFLPTA.....HWVEFQNKFYSGTGKLSDF 822

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: A_Geneseq_8:*
- 2: Geneseq1980s:*
- 3: Geneseq1990s:*
- 4: Geneseq2000s:*
- 5: Geneseq2001s:*
- 6: Geneseq2002s:*
- 7: Geneseq2003as:*
- 8: Geneseq2003bs:*
- 9: Geneseq2004s:*
- 10: Geneseq2005s:*
- 11: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4266	100.0	822	2 AAW41943	AAW41943 Human OC-
2	4266	100.0	822	5 ABB81811	Abb81811 Human OC-
3	4266	100.0	822	8 ADR44119	Adr44119 Human 116
4	4266	100.0	822	9 ADY92606	Ady92606 Human 116
5	4235.5	99.3	830	8 ADI28834	Adi28834 Human mod
6	4235.5	99.3	830	8 ADP12465	Adp12465 Protein e
7	4235.5	99.3	830	8 ABM81281	Abm81281 Tumour-as
8	3996	93.7	787	8 ABM82516	Abm82516 Human tra
9	3982	93.3	787	8 ABM84820	Abm84820 Human dia
10	3131.5	73.4	614	2 AAW98112	Aaw98112 T-cell me
11	3131.5	73.4	614	2 ABM81282	Abm81282 Tumour-as
12	3127.5	73.3	614	2 AAW98113	Aaw98113 T-cell me
13	3127.5	73.3	614	6 ABR43098	Abm43098 Human T-c
14	2917.5	68.4	643	5 ABP41524	Abp41524 Human ova
15	2119	49.7	856	8 ADH09950	Adh09950 Human hos
16	2118.5	49.7	856	2 AAR33281	Aar33281 Tsf1 enco
17	2116	49.6	856	8 ADH09951	Adh09951 Human hos
18	2116	49.6	856	8 ADI28835	Adi28835 Human mod
19	2116	49.6	856	8 ADP54581	Adp54581 Human PRO
20	2116	49.6	856	8 ADP23897	Adp23897 PRO polyp
21	2116	49.6	856	9 ADY15610	Ady15610 PRO polyp
22	2116	49.6	856	9 ADY19962	Ady19962 PRO polyp
23	2074.5	48.6	839	8 ABM84971	Abm84971 Human dia

24	2066	48.4	818	6 ABR62420	Abm62420 Protein G
25	1931	45.3	840	5 ADP69796	Adp69796 Human pol
26	1931	45.3	840	8 ADH09949	Adh09949 Human hos
27	1931	45.3	840	8 ADI28836	Adi28836 Human mod
28	1926.5	45.2	831	8 ADH09952	Adh09952 Human hos
29	1926.5	45.2	831	8 ADI28837	Adi28837 Human mod
30	1918.5	45.0	831	5 ABB08457	Abb08457 Human tum
31	1918.5	45.0	831	8 ADH09948	Adh09948 Human hos
32	1918.5	45.0	831	8 ADH09953	Adh09953 Human hos
33	1918.5	45.0	841	4 AAB60100	Aab60100 Human tra
34	1912	44.8	830	8 ADH09947	Adh09947 Human hos
35	1882	44.1	777	4 AAB48977	Aab48977 Human imm
36	1801.5	42.2	847	8 ADR44120	Adr44120 Human OC-
37	1801.5	42.2	847	9 ADY92607	Ady92607 116 KD os
38	1720	40.3	855	4 ABB58420	Abb58420 Drosophil
39	1720	40.3	855	10 AEG02510	Aeg02510 Drosophil
40	1701	39.9	834	4 ABB71636	Abb71636 Drosophil
41	1701	39.9	834	4 ABB71569	Abb71569 Drosophil
42	1539.5	36.1	703	6 ABR62416	Abm62416 V_ATPase
43	1539.5	36.1	935	8 ADN23157	Adn23157 Bacterial
44	1538	36.1	814	4 ABB69950	Abb69950 Drosophil
45	1501	35.2	1030	8 ADN23158	Adn23158 Bacterial

ALIGNMENTS

RESULT 1

AAW41943
ID AAW41943 standard; protein; 822 AA.

XX AC AAW41943;

XX 02-JUL-1998 (first entry)

XX Human OC-116 kDa protein.

XX Osteoclast; human; OC-116 kDa; screening; cell surface marker; probe.

XX Homo sapiens.

XX WO9803651-A1.

XX 29-JAN-1998.

XX 10-JUL-1997; 97WO-US012569.

XX 19-JUL-1996; 96US-00684932.

XX (FORS-) FORSYTH DENTAL INFIRMARY FOR CHILDREN.

XX Stashenko P, Li Y, Wucherpfennig AL;

XX WPI; 1998-120776/11.

XX N-PSDB; AAV04529.

XX Osteoclast specific or related DNA sequence - useful as probe to screen

XX genomic DNA or cDNA library, or as osteoclast cell surface marker.

XX Example 8; Page 61-64; 75pp; English.

XX The present sequence represents the human OC-116 kDa protein sequence which is used in an example of the present invention, which describes isolated osteoclast specific or related DNA sequences. The present invention also describes: a DNA construct capable of replicating and optionally expressing, in a host cell, osteoclast specific or related DNA, comprising an osteoclast specific or related DNA sequence and sequences necessary for transforming or transfecting a host cell, and for replicating and optionally expressing an osteoclast specific or related DNA sequence in a host cell; and a cell stably transformed or transfected with the DNA construct. The osteoclast specific or related DNA sequence can be used as a probe to screen a genomic DNA or cDNA library for osteoclast specific or related DNA sequences, or as an osteoclast cell

CC surface marker
XX
SQ Sequence 822 AA;

Query Match 100.0%; Score 4266; DB 2; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSMFRSEVALVQLFLPTAAAYTCVSRGELGLVEFRDLNASVSFAQRRFVVDVWRCSE 60
DB 1 MGSMFRSEVALVQLFLPTAAAYTCVSRGELGLVEFRDLNASVSFAQRRFVVDVWRCSE 60
QY 61 LEKTTFTFLOEEVRRAGLVLPKPKGRLLPAPPPRDLLRIQETERLAQELDRVGNQALRA 120
DB 61 LEKTTFTFLOEEVRRAGLVLPKPKGRLLPAPPPRDLLRIQETERLAQELDRVGNQALRA 120
QY 121 QLHQQLHAAVLRQGHPEPQLAAHTDGASERTPLQAQPGPHQDLRVNPFVAGAVEPHKAP 180
DB 121 QLHQQLHAAVLRQGHPEPQLAAHTDGASERTPLQAQPGPHQDLRVNPFVAGAVEPHKAP 180
QY 181 ALERLLWRACRGFLTASPRELOPLEHPVTGSPATWMTFLISYWGEOIQKIRKITDCPH 240
DB 181 ALERLLWRACRGFLTASPRELOPLEHPVTGSPATWMTFLISYWGEOIQKIRKITDCPH 240
QY 241 CHVFPFLQOEERLALGALQQLQOOSQELQEVLTGASERTPLQAQPGPHQDLRVNPFVAGAVEPHKAP 300
DB 241 CHVFPFLQOEERLALGALQQLQOOSQELQEVLTGASERTPLQAQPGPHQDLRVNPFVAGAVEPHKAP 300
QY 301 AVYLLALNQCSTVTHKCLIAEAWCSVRDLPALQOALRDSMBEGVSVAHAHRIPCRMPPT 360
DB 301 AVYLLALNQCSTVTHKCLIAEAWCSVRDLPALQOALRDSMBEGVSVAHAHRIPCRMPPT 360
QY 361 LIETNRFTASFOGIVDRYGVGRYQEVNRPAPYTIITFPFLFVAMFGDVGHGLMFLFALAM 420
DB 361 LIETNRFTASFOGIVDRYGVGRYQEVNRPAPYTIITFPFLFVAMFGDVGHGLMFLFALAM 420
QY 421 VLAENRPVAKAAQNEIWTQTFRGRYLLMLGLFSIYTGFIYNECFSRATSIFFSGMSVAA 480
DB 421 VLAENRPVAKAAQNEIWTQTFRGRYLLMLGLFSIYTGFIYNECFSRATSIFFSGMSVAA 480
QY 481 MANQSGWSDAFLAQTMLTLDNVTGVLGPPYFGIDPIWLSAANHLSPFNSFKMKMSVI 540
DB 481 MANQSGWSDAFLAQTMLTLDNVTGVLGPPYFGIDPIWLSAANHLSPFNSFKMKMSVI 540
QY 541 LGVVMAGFVGLGVNHNHVFQGRHRLLETLPELTGLFGVLYVLYKWLVCVWAARA 600
DB 541 LGVVMAGFVGLGVNHNHVFQGRHRLLETLPELTGLFGVLYVLYKWLVCVWAARA 600
QY 601 ASPSILIHFINFLFSHSPSNRLLYPRQEVVQATLVVLALAMVPIILLGTPLHLHRHR 660
DB 601 ASPSILIHFINFLFSHSPSNRLLYPRQEVVQATLVVLALAMVPIILLGTPLHLHRHR 660
QY 661 RLRRPADROENKAGLLDLDPASVNGWSSDEKAGGLDDEEAEI LPSEVLVHQAIHTI 720
DB 661 RLRRPADROENKAGLLDLDPASVNGWSSDEKAGGLDDEEAEI LPSEVLVHQAIHTI 720
QY 721 EFCGCVNSTASYLRWALSALHAQISEVLMWVMRIGLGLRGVGVAAVLPVIPAFA 780
DB 721 EFCGCVNSTASYLRWALSALHAQISEVLMWVMRIGLGLRGVGVAAVLPVIPAFA 780
QY 781 VMTVAILLVMEGLSAPFLHALRLHWVEFQNKFSYSGTYKLSPPF 822
DB 781 VMTVAILLVMEGLSAPFLHALRLHWVEFQNKFSYSGTYKLSPPF 822

RESULT 2

ABB81811
ID ABB81811 standard; protein; 822 AA.

AC ABB81811;

XX

DT 16-SEP-2002 (first entry)

XX

DE Human OC-116KDa.
XX
KW Human; osteoclast; gene therapy; aberrant bone resorption; OC-116KDa.
XX
OS Homo sapiens.
XX
PN US6403304-B1.
XX
PD 11-JUN-2002.
XX
PF 19-JUL-1996; 96US-00684932.
XX
PR 06-APR-1993; 93US-00045270.
PR 23-FEB-1995; 95US-00392678.
PR 20-JUL-1995; 95US-00012922.
PR 22-FEB-1996; 96US-00605378.
XX
PA (FORS-) FORSYTH DENTAL INFIRMARY FOR CHILDREN.

XX Staehenko P, Li Y, Wuchterpfennig AL;

XX WPI; 2002-536031/57.

DR N-PSDB; ABN86735.

XX Novel isolated osteoclast-specific or -related DNA sequence, useful for producing gene products useful in the therapeutic treatment or diagnosis of disorders involving aberrant bone resorption.

XX Example 8; Fig 3; 34pp; English.

XX The invention relates to novel human osteoclast-specific or -related cDNA sequences. The sequence represents human osteoclast 116KDa (OC-116KDa). The sequences may have a use in gene therapy. The sequences of the invention are useful in the production of gene products useful in the therapeutic treatment or diagnosis of disorders involving aberrant bone resorption, for generating peptides which are useful for producing CC antibodies for identifying osteoclast-specific or -related peptides or CC gene products

XX Sequence 822 AA;

Query Match 100.0%; Score 4266; DB 5; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSMFRSEVALVQLFLPTAAAYTCVSRGELGLVEFRDLNASVSFAQRRFVVDVWRCSE 60
DB 1 MGSMFRSEVALVQLFLPTAAAYTCVSRGELGLVEFRDLNASVSFAQRRFVVDVWRCSE 60
QY 61 LEKTTFTFLOEEVRRAGLVLPKPKGRLLPAPPPRDLLRIQETERLAQELDRVGNQALRA 120
DB 61 LEKTTFTFLOEEVRRAGLVLPKPKGRLLPAPPPRDLLRIQETERLAQELDRVGNQALRA 120
QY 121 QLHQQLHAAVLRQGHPEPQLAAHTDGASERTPLQAQPGPHQDLRVNPFVAGAVEPHKAP 180
DB 121 QLHQQLHAAVLRQGHPEPQLAAHTDGASERTPLQAQPGPHQDLRVNPFVAGAVEPHKAP 180
QY 181 ALERLLWRACRGFLTASPRELOPLEHPVTGSPATWMTFLISYWGEOIQKIRKITDCPH 240
DB 181 ALERLLWRACRGFLTASPRELOPLEHPVTGSPATWMTFLISYWGEOIQKIRKITDCPH 240
QY 241 CHVFPFLQOEERLALGALQQLQOOSQELQEVLTGASERTPLQAQPGPHQDLRVNPFVAGAVEPHKAP 300
DB 241 CHVFPFLQOEERLALGALQQLQOOSQELQEVLTGASERTPLQAQPGPHQDLRVNPFVAGAVEPHKAP 300
QY 301 AVYLLALNQCSTVTHKCLIAEAWCSVRDLPALQOALRDSMBEGVSVAHAHRIPCRMPPT 360
DB 301 AVYLLALNQCSTVTHKCLIAEAWCSVRDLPALQOALRDSMBEGVSVAHAHRIPCRMPPT 360
QY 361 LIETNRFTASFOGIVDRYGVGRYQEVNRPAPYTIITFPFLFVAMFGDVGHGLMFLFALAM 420
DB 361 LIETNRFTASFOGIVDRYGVGRYQEVNRPAPYTIITFPFLFVAMFGDVGHGLMFLFALAM 420

QY 421 VLAENRPAKAAONEIWQTFRGRYLLMLGLPSIYTGFIYNECFSRATSIFFSGWVAA 480
Db 421 VLAENRPAKAAONEIWQTFRGRYLLMLGLPSIYTGFIYNECFSRATSIFFSGWVAA 480
QY 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGPGYPFGIDPIWLSLAANHLSFLNSFKMKMSVI 540
Db 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGPGYPFGIDPIWLSLAANHLSFLNSFKMKMSVI 540
QY 541 LGVWHMAGVVLGVFNHVFQGRHRLLETLPELTFLGLFGYLVFLVIYKMLCVMAARA 600
Db 541 LGVWHMAGVVLGVFNHVFQGRHRLLETLPELTFLGLFGYLVFLVIYKMLCVMAARA 600
QY 601 APSILIHFINMFLFSHPNRLLYPROEVVQATLVVLAAMVPILLGLTPLHLHRRH 660
Db 601 APSILIHFINMFLFSHPNRLLYPROEVVQATLVVLAAMVPILLGLTPLHLHRRH 660
QY 661 RLRRRPADROEENKAGLLDLPDASVNGWSDEEKAGGLDDEEAEELVPSEVLHQAIHTI 720
Db 661 RLRRRPADROEENKAGLLDLPDASVNGWSDEEKAGGLDDEEAEELVPSEVLHQAIHTI 720
QY 721 EFCIGCVSNTASYLRWLWALSLAHQAQSEVLWAMVMRIGLGLGREVGVAAVLVPFAAFA 780
Db 721 EFCIGCVSNTASYLRWLWALSLAHQAQSEVLWAMVMRIGLGLGREVGVAAVLVPFAAFA 780
QY 781 VMTVAILLVMEGLSAPLHRLHWHVFEQNFYSGTGYKLSPP 822
Db 781 VMTVAILLVMEGLSAPLHRLHWHVFEQNFYSGTGYKLSPP 822

RESULT 3

ADR44119
ID ADR44119 standard; protein; 822 AA.

XX ADR44119;

XX 04-NOV-2004 (first entry)

XX Human 116-kDa osteoclast proton pump subunit (OC-116 KDa) protein.

XX Human; OC-116 KD; 116-kDa osteoclast proton pump subunit; therapy;
KW bone degradation; osteoporosis; osteoarthritis.

XX Homo sapiens.

Key	Location/Qualifiers
FT Domain	319..422
FT Domain	/note = Transmembrane domain
FT Domain	438..463
FT Domain	/note = Transmembrane domain
FT Domain	537..558
FT Domain	/note = Transmembrane domain
FT Domain	571..600
FT Domain	/note = Transmembrane domain
FT Domain	632..653
FT Domain	/note = Transmembrane domain
FT Domain	764..796
FT Domain	/note = Transmembrane domain

XX US6777537-B1.

XX 17-AUG-2004.

XX 18-JUL-2000; 2000US-00618304.

XX 22-FEB-1996; 96US-00605378.

XX (FORS-) FORSYTH DENTAL INFIRMARY FOR CHILDREN.

XX Stashenko P, Li Y;

XX WPI; 2004-591304/57.

XX N-PSDB; ADR44118.

XX

PT New isolated human 116-kDa osteoclast (OC-116 KDa) proton pump subunit
PT polypeptide, useful for preventing and/or treating diseases with bone
PT degradation, such as osteoporosis and osteoarthritis.

XX Claim 2; SEQ ID NO 2; 16pp; English.

XX The present invention relates to a human 116-kDa osteoclast proton pump
CC subunit (OC-116 KDa) polypeptide and its encoding polynucleotide. The
CC invention is useful for the prevention and treatment of diseases or
CC conditions associated with aberrant expression or activity of the OC-116
CC KDa protein and bone degradation, such as osteoporosis and
CC osteoarthritis. The present sequence is human OC-116 KDa protein.

XX Sequence 822 AA;

Query Match 100.0%; Score 4266; DB 8; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSNFRSEVALVQLFLPTAAAYTCVSRGELGLVEFRDLNASVAFQRRFVVDVWRCCE 60

Db 1 MGSNFRSEVALVQLFLPTAAAYTCVSRGELGLVEFRDLNASVAFQRRFVVDVWRCCE 60

QY 61 LEKTFLEEVRRAGLVLPKGRLPAPPRDLRIQETERLAQELRDVGRNQQAALRA 120

Db 61 LEKTFLEEVRRAGLVLPKGRLPAPPRDLRIQETERLAQELRDVGRNQQAALRA 120

QY 121 QLHLQLHAALVLRQGHPEPOLAAHTDGASERTPLQAPGPHQDLRVNFVAGAVEPHKAP 180

Db 121 QLHLQLHAALVLRQGHPEPOLAAHTDGASERTPLQAPGPHQDLRVNFVAGAVEPHKAP 180

QY 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEOIGQKIRKITDCPH 240

Db 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEOIGQKIRKITDCPH 240

QY 241 CHVFPELQEEARLGAQLQQLQOQSOELQEVLTGTERFLSVGLRVLQLPQGVQVHKMK 300

Db 241 CHVFPELQEEARLGAQLQQLQOQSOELQEVLTGTERFLSVGLRVLQLPQGVQVHKMK 300

QY 301 AVYALNQCQSVSTTHKCLIAEAWCSVRDLPALQEARLDSMEBGVSAVAHRIPCRDMPPT 360

Db 301 AVYALNQCQSVSTTHKCLIAEAWCSVRDLPALQEARLDSMEBGVSAVAHRIPCRDMPPT 360

QY 361 LIETNRFTASFGIVDRYGVGRYQEVNPAPYTIITPPFLFAMVFGDVGHGLLFLFALAM 420

Db 361 LIETNRFTASFGIVDRYGVGRYQEVNPAPYTIITPPFLFAMVFGDVGHGLLFLFALAM 420

QY 421 VLAENRPAKAAONEIWQTFRGRYLLMLGLPSIYTGFIYNECFSRATSIFFSGWVAA 480

Db 421 VLAENRPAKAAONEIWQTFRGRYLLMLGLPSIYTGFIYNECFSRATSIFFSGWVAA 480

QY 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGPGYPFGIDPIWLSLAANHLSFLNSFKMKMSVI 540

Db 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGPGYPFGIDPIWLSLAANHLSFLNSFKMKMSVI 540

QY 541 LGVWHMAGVVLGVFNHVFQGRHRLLETLPELTFLGLFGYLVFLVIYKMLCVMAARA 600

Db 541 LGVWHMAGVVLGVFNHVFQGRHRLLETLPELTFLGLFGYLVFLVIYKMLCVMAARA 600

QY 601 APSILIHFINMFLFSHPNRLLYPROEVVQATLVVLAAMVPILLGLTPLHLHRRH 660

Db 601 APSILIHFINMFLFSHPNRLLYPROEVVQATLVVLAAMVPILLGLTPLHLHRRH 660

QY 661 RLRRRPADROEENKAGLLDLPDASVNGWSDEEKAGGLDDEEAEELVPSEVLHQAIHTI 720

Db 661 RLRRRPADROEENKAGLLDLPDASVNGWSDEEKAGGLDDEEAEELVPSEVLHQAIHTI 720

QY 721 EFCIGCVSNTASYLRWLWALSLAHQAQSEVLWAMVMRIGLGLGREVGVAAVLVPFAAFA 780

Db 721 EFCIGCVSNTASYLRWLWALSLAHQAQSEVLWAMVMRIGLGLGREVGVAAVLVPFAAFA 780

QY 781 VMTVAILLVMEGLSAPLHRLHWHVFEQNFYSGTGYKLSPP 822

Db 781 VMTVAILLVMEGLSAPLHRLHWHVFEQNFYSGTGYKLSPP 822

Db 781 VMTVAILLVMEGLSAPFLHALRLHWVEFQNKFSYSGTGKLSPPF 822

RESULT 4

ADY92606
ID ADY92606 standard; protein; 822 AA.

XX AC
ADY92606;

XX 02-JUN-2005 (first entry)

XX DE Human 116 kD osteoclast proton pump OC-116 subunit protein.

XX KW cloning; osteopathic; antiarthritic; gene therapy;
XX KW osteoclast proton pump; bone disease; osteoporosis; osteoarthritis.

XX OS Homo sapiens.

XX PN US2005064448-A1.

XX XX 24-MAR-2005.

XX XX 20-FEB-2004; 2004US-00783519.

XX PR 22-FEB-1996; 96US-00605378.

XX PR 18-JUL-2000; 2000US-00618304.

XX XX (STAS/) STASHENKO P.

XX PA (LIYY/) LI Y.

XX PI Stashenko P, Li Y;

XX DR WPI; 2005-241271/25.

XX DR N-PSDB; ADY92605.

XX PT New isolated genes and encoded human 116-kDa osteoclast proton pump
XX PT subunit polypeptides useful for treating bone mass disorders associated
XX PT with aberrant rate of bone degradation (e.g. osteoporosis or
XX PT osteoarthritis).

XX PS Claim 18; SEQ ID NO 2; 17pp; English.

XX SS The invention relates to an isolated gene encoding a polypeptide which is
XX CC a human 116-kD osteoclast proton pump subunit. The composition and
XX CC methods are useful for treating bone mass disorders characterized by
XX CC aberrant rate of bone degradation (e.g. osteoporosis or osteoarthritis).
XX CC The protein may also be used as cell surface markers for osteoclasts.
XX CC This sequence corresponds to the novel OC-116 proton pump subunit. The
XX CC encoding cDNA was isolated by differential screening of a human
XX CC osteoclastoma cDNA library.

XX SQ Sequence 822 AA;

Query Match 100.0%; Score 4266; DB 9; Length 822;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSMFSEVALVQLFLPTAAAYTCVSRIGELGLVEFRDLNASVAFQRRFVVDVWRCCE 60

Db 1 MGSMFSEVALVQLFLPTAAAYTCVSRIGELGLVEFRDLNASVAFQRRFVVDVWRCCE 60

Qy 61 LEKTFTLQEEVRRAGLVLPKPKRLPAPPPRDLRLIOETERLAQELRDVGNQALRA 120

Db 61 LEKTFTLQEEVRRAGLVLPKPKRLPAPPPRDLRLIOETERLAQELRDVGNQALRA 120

Qy 121 QLHQQLHAAVLRQGHPEQLAAATDASERTPLQAPGGPHQDLRVNFVAGAVEPHKAP 180

Db 121 QLHQQLHAAVLRQGHPEQLAAATDASERTPLQAPGGPHQDLRVNFVAGAVEPHKAP 180

Qy 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATMTFLISYWGEOIGQKIRK1TDCFH 240

Db 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATMTFLISYWGEOIGQKIRK1TDCFH 240

Qy 241 CHVEPFLQOEERLGLALQOQOQOEVLGETERFELSOVLGRVLQLLPPGOVQVHKMK 300
Db 241 CHVEPFLQOEERLGLALQOQOQOEVLGETERFELSOVLGRVLQLLPPGOVQVHKMK 300
Qy 301 AVYLAALNQCSVSTTHKCLIAEAWCSVRDLPALQOEALRDSSMEEGVSAAVHRIPCRDMPPT 360
Db 301 AVYLAALNQCSVSTTHKCLIAEAWCSVRDLPALQOEALRDSSMEEGVSAAVHRIPCRDMPPT 360
Qy 361 LIITNRFTASFOGIVDRYGVGRYQEVNPAPYTIITFPFLFPAVMFGDVGHLLMFLPALAM 420
Db 361 LIITNRFTASFOGIVDRYGVGRYQEVNPAPYTIITFPFLFPAVMFGDVGHLLMFLPALAM 420
Qy 421 VLAENRPVAKAAQNEIWOTFFRGRYLLLLMGLFSYITGTFIYNECFSRATSIIPSGWSVAA 480
Db 421 VLAENRPVAKAAQNEIWOTFFRGRYLLLLMGLFSYITGTFIYNECFSRATSIIPSGWSVAA 480
Qy 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGYPFGIDPIWSLAANHLSEFNSFKMKMSVI 540
Db 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGYPFGIDPIWSLAANHLSEFNSFKMKMSVI 540
Qy 541 LGVVMAGFVVLGVFNHVFHQHRLLETTLPETFLGLFGLVFLVYKMLCVWAAARA 600
Db 541 LGVVMAGFVVLGVFNHVFHQHRLLETTLPETFLGLFGLVFLVYKMLCVWAAARA 600
Qy 601 ASPSILIHFINMFLSPSNELLYPROBVQATLVVLALAMVPTILLGTPLHLHLRHR 660
Db 601 ASPSILIHFINMFLSPSNELLYPROBVQATLVVLALAMVPTILLGTPLHLHLRHR 660
Qy 661 RLRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLHQAIHTI 720
Db 661 RLRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLHQAIHTI 720
Qy 721 EFCGCVNTASYLRWLWALSIAHAQSEVLWAMVNRIGLGLGREVGVAADVLPVIPAAPA 780
Db 721 EFCGCVNTASYLRWLWALSIAHAQSEVLWAMVNRIGLGLGREVGVAADVLPVIPAAPA 780
Qy 781 VMTVAILLVMEGLSAPFLHALRLHWVEFQNKFSYSGTGKLSPPF 822
Db 781 VMTVAILLVMEGLSAPFLHALRLHWVEFQNKFSYSGTGKLSPPF 822

RESULT 5

AD128834

ID AD128834 standard; protein; 830 AA.

XX AC AD128834;

XX DT 22-APR-2004 (first entry)

XX DE Human modifier of p53 (MP53) TCIRG-1.

XX KW Human; MP53; modifier of p53; p53; cytosolic; gene therapy;

XX KW T-cell immune regulator 1; TCIRG-1.

XX OS Homo sapiens.

XX PN WO2004004766-A1.

XX PD 15-JAN-2004.

XX PF 09-JUL-2003; 2003WO-US021378.

XX PR 10-JUL-2002; 2002US-0394992P.

XX PR 07-AUG-2002; 2002US-0401604P.

XX PR 16-SEP-2002; 2002US-0410988P.

XX PR 25-NOV-2002; 2002US-0428837P.

XX PA (EXEL-) EXELIXIS INC.

XX PI Costa MA, Maxwell ME, Lackner MR, Hung T, O'Brien CL, Jin Y;

XX PI Nicoll M, Hai B, Zhang H, Lickteig K, Amundsen CD;

XX DR WPI; 2004-142922/14.

DR N-PSDB; ADI28820.
XX GENBANK; 1924145.
PT Identifying a candidate p53 pathway modulating agent for treating e.g.,
PT cancer, comprises contacting an assay system comprising a MP53
PT polypeptide or nucleic acid with a test agent and detecting a test agent-
PT biased activity.
XX
XX
XX Example 2; SEQ ID NO 25; 139pp; English.
XX
CC In the present invention, genetic screens were designed to identify
CC modifiers of the p53 pathway in caenorhabditis elegans, where a
CC homozygous p53 deletion mutant was used. Various specific genes were
CC silenced by RNA inhibition. Genes causing altered phenotypes in the worms
CC were identified as modifiers of the p53 pathway. Human orthologs, denoted
CC modifiers of p52 (MP53), of these modifiers were identified. These
CC include the present sequence, characterised as T-cell immune regulator 1,
CC ATPase, H+ transporting, or lysosomal V0 protein a isoform 3. MP53
CC nucleic acids and polypeptides are attractive drug targets for the
CC treatment of pathologies associated with a defective p53 signalling
CC pathway, such as cancer. Methods for modulating MP53 function and/or the
CC p53 pathway in a mammalian cell involve contacting the cell with an agent
CC that specifically binds a MP53 polypeptide or nucleic acid. The agent may
CC be a small molecular modulator, a nucleic acid modulator or an antibody.
XX
XX Sequence 830 AA;
Query Match 99.3%; Score 4235.5; DB 8; Length 830;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 MGSMPFSEVALVQLFLPTAAATCVSRGELGLVEFRDLNVSAPQRRFVVDVRRCEE 60
DB 1 MGSMPFSEVALVQLFLPTAAATCVSRGELGLVEFRDLNVSAPQRRFVVDVRRCEE 60
QY 61 LEKFTFLOEVRAGLVLPPLPPGRLPAPPDRLLRQETRLAQELRDVRGNQOALRA 120
DB 61 LEKFTFLOEVRAGLVLPPLPPGRLPAPPDRLLRQETRLAQELRDVRGNQOALRA 120
QY 121 QLHQLQHLAAVLROGHEPQLAAHTDGASERTLLQAPGGPHQDLRVNFVAGAVEPHKAP 180
DB 121 QLHQLQHLAAVLROGHEPQLAAHTDGASERTLLQAPGGPHQDLRVNFVAGAVEPHKAP 180
QY 181 ALERLLWRACRGFLIASFRELEQPLEHPTVGTGEPAWTMTFLISYWGEOIGQIKIRITDCFH 240
DB 181 ALERLLWRACRGFLIASFRELEQPLEHPTVGTGEPAWTMTFLISYWGEOIGQIKIRITDCFH 240
QY 241 CHVFPELQBEARLQALQQLQOQSOELQEVLTGERPLSOVLGRVLQLLPPGOVQVHKM 300
DB 241 CHVFPELQBEARLQALQQLQOQSOELQEVLTGERPLSOVLGRVLQLLPPGOVQVHKM 300
QY 301 AVYLALNQCSTVSTHKLIAEAWCSVRDLPALQEARLDSMREGVSAVAHRIPCRDMPT 360
DB 301 AVYLALNQCSTVSTHKLIAEAWCSVRDLPALQEARLDSMREGVSAVAHRIPCRDMPT 360
QY 361 LIRNRTASFGQIVDRYGVGRVQEVNPAPTYITTPFLFVAVMGDVGHGLMLFALAM 420
DB 361 LIRNRTASFGQIVDRYGVGRVQEVNPAPTYITTPFLFVAVMGDVGHGLMLFALAM 420
QY 421 VLAENRPAKAAQNEITWQTFRCGRYLLMLGLFSYTGFIYNECFSRATSIFFSGWSVAA 480
DB 421 VLAENRPAKAAQNEITWQTFRCGRYLLMLGLFSYTGFIYNECFSRATSIFFSGWSVAA 480
QY 481 MANQSGWDAFLAQHTMLTLDPNVTGVFLGYPFGIDPILWSLAANHLFLNSFKMKMSVI 540
DB 481 MANQSGWDAFLAQHTMLTLDPNVTGVFLGYPFGIDPILWSLAANHLFLNSFKMKMSVI 540
QY 541 LGVHMAFGVVLGVFNHVFQGRHRLLETLPELTLGLFGYLVFLVIYKMLCVWAARA 600
DB 541 LGVHMAFGVVLGVFNHVFQGRHRLLETLPELTLGLFGYLVFLVIYKMLCVWAARA 600
QY 601 AS-PSLIIHFNNFLFSHSPSNLLYPRQEVQATLVVLALAMVPILLGLTFLHLHRRH 659
DB 601 AS-PSLIIHFNNFLFSHSPSNLLYPRQEVQATLVVLALAMVPILLGLTFLHLHRRH 659

DB 601 ASAPSILIIHFNNFLFSHSPSNLLYPRQEVQATLVVLALAMVPILLGLTFLHLHRRH 660
QY 660 RLRRRPPADQREENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEALVPSEVLHQAIHT 719
DB 661 RLRRRPPADQREENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEALVPSEVLHQAIHT 720
QY 720 IEFCLGCVSNATSYLRWLWALSLAHQALSEVLNWMVMRIGLGLGREVGVAAVLVPFAAF 779
DB 721 IEFCLGCVSNATSYLRWLWALSLAHQALSEVLNWMVMRIGLGLGREVGVAAVLVPFAAF 780
QY 780 AVMTVAILLVMEGLSAPFLHALRLHWVEFQNKFYSGTGKLSPPF 822
DB 781 AVMTVAILLVMEGLSAPFLHALRLHWVEFQNKFYSGTGKLSPPF 823
RESULT 6
ID ADP12465 standard; protein; 830 AA.
XX ADP12465;
XX ADP12465;
XX 12-AUG-2004 (first entry)
XX Protein encoded by mRNA of the invention #75.
XX transplanted rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX Homo sapiens.
XX WO2004042346-A2.
XX 21-MAY-2004.
XX 24-APR-2003; 2003WO-US012946.
XX 24-APR-2002; 2002US-00131831.
XX 20-DEC-2002; 2002US-00325899.
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX Rosenberg S;
XX WPI; 2004-400724/37.
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX rejection, in an individual, comprises detecting the expression level of
XX the genes.
XX Claim 65; SEQ ID NO 2474; 1762pp; English.
XX The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprising detecting the expression level of one or more genes. The
XX methods, system and kits are useful in diagnosing or monitoring
XX transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX islet, lung, bone marrow or stem cell transplant rejection,
XX xenotransplant rejection or mechanical organ replacement rejection, in an
XX individual. The method is also useful in assessing the immune status of
XX an individual. The methods are also useful in diagnosing and monitoring
XX diseases that involve the immune system, e.g. rheumatoid arthritis,
XX lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX viral, bacterial or fungal infection. The present sequence represents a
XX protein that is encoded by the mRNA of the invention.
XX
XX Sequence 830 AA;
Query Match 99.3%; Score 4235.5; DB 8; Length 830;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 301 AVYALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDRSSMEEGVSAVAHRIPCRDMPPT 360
DB 301 AVYALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDRSSMEEGVSAVAHRIPCRDMPPT 360
QY 361 LIRNRTASFGQIVDYGVRGYEVNPAVPYTIITFFPFLFAVMFGDVGHGLMLFALAM 420
DB 361 LIRNRTASFGQIVDYGVRGYEVNPAVPYTIITFFPFLFAVMFGDVGHGLMLFALAM 420
QY 421 VLAENRPAVKAQAQNEIWQTFRGRYLLMLGLFSIYTGFIYNECFSRATSIFFPSGWSVAA 480
DB 421 VLAENRPAVKAQAQNEIWQTFRGRYLLMLGLFSIYTGFIYNECFSRATSIFFPSGWSVAA 480
QY 481 MANQSGWSDAFLAQHTMLTLDPNVTGVLGPIPGIDPIWLSLAANHLSFNLSPKQKMSVI 540
DB 481 MANQSGWSDAFLAQHTMLTLDPNVTGVLGPIPGIDPIWLSLAANHLSFNLSPKQKMSVI 540
QY 541 LGVVMFAFGVVLGVFNHVFHQHRLLETLPELTFLGLFGYLVFLVYKWLVCWAARA 600
DB 541 LGVVMFAFGVVLGVFNHVFHQHRLLETLPELTFLGLFGYLVFLVYKWLVCWAARA 600
QY 601 AS-PSILIHFINMFLPSHSNRLLYPRQEVQATLVVLALAMVPIILLGTPLHLHRH 659
DB 601 ASAPSILIHFINMFLPSHSNRLLYPRQEVQATLVVLALAMVPIILLGTPLHLHRH 660
QY 660 RLRRRPPADQENKAGLLDLPDASVNGSSDEKAGGLDEEAEALVPSEVLHMQAIHT 719
DB 661 RLRRRPPADQENKAGLLDLPDASVNGSSDEKAGGLDEEAEALVPSEVLHMQAIHT 720
QY 720 IEFCLGCVSNTASVLRWLWALSQAOLSEVLWAMVMRIGLGLGREGVGAVALVPIPAAF 779
DB 721 IEFCLGCVSNTASVLRWLWALSQAOLSEVLWAMVMRIGLGLGREGVGAVALVPIPAAF 780
QY 780 AVMTVAILLVMEGLSAPLHALLHWHVBFQNKFGYSGTKYKLSPF 822
DB 781 AVMTVAILLVMEGLSAPLHALLHWHVBFQNKFGYSGTKYKLSPF 823
RESULT 8
ID ADH22516 standard; protein; 787 AA.
XX
AC ADH22516;
XX
XX
DT 11-MAR-2004 (first entry)
XX
DE Human transporter & ion channel (TRICH) protein SeqID14.
XX
KW human; transporters and ion channel; TRICH; cell proliferative;
KW arteriosclerosis; cancer; autoimmune/inflammatory; AIDS; asthma;
KW neurological; epilepsy; stroke; developmental; Cushing's syndrome;
KW hypothyroidism; infection; gene therapy; cytostatic; antiinflammatory;
KW immunosuppressive; antiasthmatic; anticonvulsant; nootropic;
KW neuroprotective; single nucleotide polymorphism; SNP.
XX
OS Homo sapiens.
XX
XX WO2003093444-A2.
XX
XX 13-NOV-2003.
XX
XX 02-MAY-2003; 2003WO-US014026.
XX
XX 03-MAY-2002; 2002US-0377435P.
PR 03-MAY-2002; 2002US-0377444P.
PR 05-JUN-2002; 2002US-0386497P.
PR 11-JUN-2002; 2002US-0388180P.
XX
XX (INCY-) INCYTE CORP.
XX
PI Baughn MR, Becha SD, Bulloch SA, Chang H, Elliott VS;
PI Emerling BM, Griffin JA, Hafalia AJA, Ison CH, Jackson AA, Jiang X;
PI Jin P, Kable AE, Khare R, Lee SY, Lee S, Mason PM, Marquis JP;
PI Ramkumar J, Richardson TW, Swarnakar A, Tran UK, Chawla NK;

PI Wilson AD;
XX
DR WPI; 2004-022655/02.
DR N-PSDB; ADH22582.
XX
XX New human transporters and ion channels (TRICH), useful for diagnosing,
PT treating and preventing diseases or conditions associated with the
PT aberrant TRICH expression e.g. cancer, AIDS, arteriosclerosis, epilepsy,
PT or infections.
XX
XX Claim 1; SEQ ID NO 14; 448pp; English.
XX
CC This invention relates to novel isolated polynucleotides identified as
CC human transporters and ion channels (TRICH), and the encoded polypeptides
CC thereof. Specifically, it describes using these TRICH molecules, as well
CC as agonists, antagonists, antibodies, expression vectors and host cells,
CC in appropriate screening and toxicity assays to assess the effects of
CC exogenous compounds on TRICH expression. The present invention describes
CC TRICH compositions that are useful in the diagnosis, treatment and
CC prevention of various disorders such as cell proliferative (e.g.
CC arteriosclerosis, cancer), autoimmune/inflammatory (e.g. AIDS, asthma),
CC neurological (e.g. epilepsy, stroke) and developmental (e.g. Cushing's
CC syndrome hypothyroidism) and for infections. Accordingly, these TRICH
CC molecules can be used for gene therapy purposes and exhibit various
CC activities such as cytostatic, antiinflammatory, immunosuppressive,
CC antiasthmatic, anticonvulsant, nootropic and neuroprotective.
CC Furthermore, a microarray is useful in monitoring or measuring protein-
CC protein interactions, drug-target interactions and gene expression
CC profiles. This polypeptide sequence is a human TRICH protein of the
CC invention.
XX
SQ Sequence 787 AA;

Query Match 93.7%; Score 3996; DB 8; Length 787;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 778; Conservative 0; Mismatches 1; Indels 44; Gaps 2;
QY 1 MGSNFRSEVALVOLFLPTAAAYTCVSRGLGELGLVEPRDLNASVSARFPPVVDWRCCE 60
DB 1 MGSNFRSEVALVOLFLPTAAAYTCVSRGLGELGLVEPRDLNASVSARFPPVVDWRCCE 60
QY 61 LEXTFTFLOEEVRAGLVLPKGRLPAPPRLRLRQETRLAQLERLDRVGRNQOALRA 120
DB 61 LEXTFTFLOEEVRAGLVLPKGRLPAPPRLRLRQETRLAQLERLDRVGRNQOALRA 120
QY 121 QLHLQLHAAVLRLQGHPEPQLAAAHDCASERTPLQAPGGPHODLRVNFVAGAVEPHKAP 180
DB 121 QLHLQLHAAVLRLQGHPEPQLAAAHDCASERTPLQAPGGPHODLRVNFVAGAVEPHKAP 180
QY 181 ALERLLWRACRGFLIASFRELEQPLBHPVTGEPATWMTFLISYWGEGIQKIRKITDCFH 240
DB 181 ALERLLWRACRGFLIASFRELEQPLBHPVTGEPATWMTFLISYWGEGIQKIRKITDCFH 240
QY 241 CHVFPELQBEARLQALQQLQOQSOELQEVLGTERFLSQVLGRVQLQLLPPGQVQVHKM 300
DB 241 CHVFPELQBEARLQALQQLQOQSOELQEVLGTERFLSQVLGRVQLQLLPPGQVQVHKM 300
QY 301 AVYALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDRSSMEEGVSAVAHRIPCRDMPPT 360
DB 301 AVYALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDRSSMEEGVSAVAHRIPCRDMPPT 360
QY 361 LIRNRTASFGQIVDYGVRGYEVNPAVPYTIITFFPFLFAVMFGDVGHGLMLFALAM 420
DB 361 LIRNRTASFGQIVDYGVRGYEVNPAVPYTIITFFPFLFAVMFGDVGHGLMLFALAM 420
QY 421 VLAENRPAVKAQAQNEIWQTFRGRYLLMLGLFSIYTGFIYNECFSRATSIFFPSGWSVAA 480
DB 421 VLAENRPAVKAQAQNEIWQTFRGRYLLMLGLFSIYTGFIYNECFSRATSIFFPSGWSVAA 480
QY 481 MANQSGWSDAFLAQHTMLTLDPNVTGVLGPIPGIDPIWLSLAANHLSFNLSPKQKMSVI 540
DB 481 MANQSGWSDAFLAQHTMLTLDPNVTGVLGPIPGIDPIWLSLAANHLSFNLSPKQKMSVI 540

QY 541 LGVHMAFGVGVNFHVFQGRHRLLELTPELTLLGLFGYLVFLVYKMLCVWAARA 600
 Db |||||
 QY 541 LGVHMAFGVGVNFHVFQGRHRLLELTPELTLLGLFGYLVFLVYKMLCVWAARA 600
 |||||
 QY 601 AS-PSILIHFMFLPSHSPSNRLLYPROEVQATLVVLALAMVPILLGLTPLLHRRH 659
 Db |||||
 QY 601 ASAPSILIHFMFLPSHSPSNRLLYPROEVQATLVVLALAMVPILLGLTPLLHRRH 660
 |||||
 QY 660 RLRLRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLMHQAIHT 719
 Db |||||
 QY 661 RLRLRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLMHQAIHT 705
 |||||
 QY 720 IEFCLGCVSNTASYLRMLWALSALHAQLSEVLWAMVMRIGLGLGREVGVAALVLPFAAF 779
 Db |||||
 QY 706 -----EVLWAMVMRIGLGLGREVGVAALVLPFAAF 737
 |||||
 QY 780 AVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPP 822
 Db |||||
 QY 738 AVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPP 780
 |||||

RESULT 9

ABM84820

ID ABM84820 standard; protein; 787 AA.

AC ABM84820;

XX 18-NOV-2004 (first entry)

DT

XX Human diagnostic and therapeutic pprotein SEQ ID NO:5069.

DE

XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

KW

XX Homo sapiens.

OS

XX WO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2003; 2002US-0410259P.

XX 12-SEP-2003; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

XX Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;

XX Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

XX Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

XX Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton BS;

XX Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX Patry S, Shi X, Suarez C;

XX WPI; 2004-329368/30.

XX N-PSDB; ACN43472.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful

XX in diagnosing a condition, disease or disorder associated with human

XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

XX in gene mapping.

XX Claim 27; Page; 190pp; English.

XX

XX The invention relates to novel diagnostic and therapeutic polynucleotides

XX selected from one of the 2722 sequences defined in the specification. A

XX polynucleotide of the invention may have a use in gene therapy. The human

XX diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be

XX used to diagnose a particular condition, disease or disorder associated

XX with human molecules, e.g. cell proliferative disorders,

XX autoimmune/inflammatory disorder, developmental disorder, endocrine

XX disorder, neurological disorders, gastrointestinal disorders, or

XX

XX

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CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX

SQ Sequence 787 AA;

Query Match 93.3%; Score 3982; DB 8; Length 787;

Best Local Similarity 94.4%; Pred. No. 0;

Matches 777; Conservative 0; Mismatches 2; Indels 44; Gaps 2;

QY 1 MGSMFRSEVALVQLPPTAAAYTCVSRIGELGLVEPRDLNASVSFAQRFFVVDVNRCEE 60

Db |||||

QY 1 MGSMFRSEVALVQLPPTAAAYTCVSRIGELGLVEPRDLNASVSFAQRFFVVDVNRCEE 60

Db |||||

QY 61 LEKTFTEFLQEEVRRAGLVLPKGRIPAPPPRDLARIQETTERLAQELDRVGNQALRA 120

Db |||||

QY 61 LEKTFTEFLQEEVRRAGLVLPKGRIPAPPPRDLARIQETTERLAQELDRVGNQALRA 120

Db |||||

QY 121 QLHQLQLHAAVLROGHEPQLAAATDASERTPLQAQPGPHQDLRVNFVAGAVEPHKAP 180

Db |||||

QY 121 QLHQLQLHAAVLROGHEPQLAAATDASERTPLQAQPGPHQDLRVNFVAGAVEPHKAP 180

Db |||||

QY 181 ALERLLWRACROFLIASPRELEQPLEHPVTGSPATMTFLISYWGEBIQOKIRKITDCPH 240

Db |||||

QY 181 ALERLLWRACROFLIASPRELEQPLEHPVTGSPATMTFLISYWGEBIQOKIRKITDCPH 240

Db |||||

QY 241 CHVFPLQOEERARLQALQOQSOELQEVLTETEFUSOVLGRVLTLLPGOVQVHKMK 300

Db |||||

QY 241 CHVFPLQOEERARLQALQOQSOELQEVLTETEFUSOVLGRVLTLLPGOVQVHKMK 300

Db |||||

QY 301 AVYLAALNQCSTTHKCLIAEAWCSVRDLPALQEAALRDSMEEGVSAAVAHRIPCRDMPPT 360

Db |||||

QY 301 AVYLAALNQCSTTHKCLIAEAWCSVRDLPALQEAALRDSMEEGVSAAVAHRIPCRDMPPT 360

Db |||||

QY 361 LIITNRFTASFOGIVDRYGVGRYQEVNPAPYTIITFPFLFAVMPGDVGHLMLFALAM 420

Db |||||

QY 361 LIITNRFTASFOGIVDRYGVGRYQEVNPAPYTIITFPFLFAVMPGDVGHLMLFALAM 420

Db |||||

QY 421 VLAENRPAVKAQNEIMOTFFRGRYLLMLLMLGFLSYITGFIYNECFSRATSIIPSGMSVAA 480

Db |||||

QY 421 VLAENRPAVKAQNEIMOTFFRGRYLLMLLMLGFLSYITGFIYNECFSRATSIIPSGMSVAA 480

Db |||||

QY 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGYPFGIDPIWSLAANHLSPFNSFKMKMSVI 540

Db |||||

QY 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGYPFGIDPIWSLAANHLSPFNSFKMKMSVI 540

Db |||||

QY 541 LGVHMAFGVGVNFHVFQGRHRLLELTPELTLLGLFGYLVFLVYKMLCVWAARA 600

Db |||||

QY 541 LGVHMAFGVGVNFHVFQGRHRLLELTPELTLLGLFGYLVFLVYKMLCVWAARA 600

Db |||||

QY 601 AS-PSILIHFMFLPSHSPSNRLLYPROEVQATLVVLALAMVPILLGLTPLLHRRH 659

Db |||||

QY 601 ASAPSILIHFMFLPSHSPSNRLLYPROEVQATLVVLALAMVPILLGLTPLLHRRH 660

Db |||||

QY 660 RLRLRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLMHQAIHT 719

Db |||||

QY 661 RLRLRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLMHQAIHT 705

Db |||||

QY 720 IEFCLGCVSNTASYLRMLWALSALHAQLSEVLWAMVMRIGLGLGREVGVAALVLPFAAF 779

Db |||||

QY 706 -----EVLWAMVMRIGLGLGREVGVAALVLPFAAF 737

Db |||||

QY 780 AVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPP 822

Db |||||

QY 738 AVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPP 780

Db |||||

RESULT 10

AAW98112
ID AAW98112 standard; protein; 614 AA.
XX
AC AAW98112;
XX
21-JUN-1999 (first entry)
XX
T-cell membrane protein TIRC7.
XX
TIRC7; T-cell immune response cDNA 7; T-cell membrane protein; human;
KW immunosuppressive; organ transplantation; graft rejection;
KW transplant rejection; autoimmune disease; allergy; infection; tumour;
KW cancer; rheumatoid arthritis; lupus erythematosus; multiple sclerosis;
KW encephalitis; vasculitis; diabetes mellitus; pancreatitis; gastritis;
KW thyroiditis; asthma; lepramotosis; therapy.
XX
Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Protein 1..601
FT Domain /note= "separately claimed in Claim 1"
FT Domain 173..209
FT Domain /note= "transmembrane domain"
FT Domain 229..246
FT Domain /note= "transmembrane domain"
FT Domain 319..346
FT Domain /note= "transmembrane domain"
FT Domain 356..400
FT Domain /note= "transmembrane domain"
FT Domain 413..437
FT Domain /note= "transmembrane domain"
FT Domain 513..532
FT Domain /note= "transmembrane domain"
FT Domain 544..585
FT Domain /note= "transmembrane domain"
XX
WO9911782-A1.
XX
11-MAR-1999.
XX
28-AUG-1998; 98WO-EP005462.
XX
29-AUG-1997; 97DE-01038710.
XX
12-FEB-1998; 98DE-02002653.
XX
(BGM) BRIGHAM & WOMENS HOSPITAL.
XX (UTKU/) UTKU N.
XX
Utku N, Gullans SR, Milford EL;
XX
WPI; 1999-205186/17.
XX N-PSDB; AAX24912.
XX
A novel T-cell transmembrane protein (TIRC7) - useful for modulating
PT immune responses, for use in organ transplantations and treatment of
PT infectious disease.
XX
Claim 1(i); Page 84-86; 97pp; English.
XX
The present sequence is TIRC7, a novel T-cell transmembrane protein that
XX exhibits a central role in T-cell activation in vitro and in vivo. TIRC7
XX mRNA is transiently up-regulated in the early phase of T-cell activation
XX via a calcineurin-dependent pathway. TIRC7 cDNA (see AAX24912) was
XX identified following a screen for genes that are differentially expressed
XX in alloactivated human T cells. A second TIRC7 protein (see AAW98113) is
XX identical except for one amino acid substitution (Arg121 to Gln),
XX suggesting 2 alleles of the TIRC7 gene. The invention provides vectors,
XX host cells, antibodies, TIRC7 peptides, polypeptides and polynucleotides
XX that are useful in diagnostic compositions for identifying T-cell
XX activating or co-stimulating compounds, or for identifying inhibitors of
XX T-cell activation and stimulation. TIRC7 peptides or polypeptides,
XX vectors and antibodies are useful in the preparation of pharmaceutical
XX compositions for treatment of acute and chronic diseases involving T-cell

CC activation and Th1 and Th2 immune response, for the treatment of acute
CC and chronic rejection of allo- and xeno organ transplants and bone marrow
CC transplantation, for the treatment of rheumatoid arthritis, lupus
CC erythematosus, multiple sclerosis, encephalitis, vasculitis, diabetes
CC mellitus, pancreatitis, gastritis, thyroiditis, for the treatment of
CC malign disorders of T, B or NK cells, for the treatment of asthma,
CC lepramotosis, Helicobacter pylori associated gastritis, or for the
XX treatment of skin, adrenal or lung tumors (claimed)
XX
SQ Sequence 614 AA;
Query Match 73.4%; Score 3131.5; DB 2; Length 614;
Best Local Similarity 99.7%; Pred. No. 7.1e-301;
Matches 605; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 217 MTFLLSYWGEIQIGQIRKIDTCFCHVFPFLQOEAEALGALQQLQQQSQELQVLGTER 276
DB 1 MTFLLSYWGEIQIGQIRKIDTCFCHVFPFLQOEAEALGALQQLQQQSQELQVLGTER 60
QY 277 FLSQVLGRVLQQLPPGQVQVHKMAYLALNQSVSTTHKCLIAEAWCSVRDLPALQAL 336
DB 61 FLSQVLGRVLQQLPPGQVQVHKMAYLALNQSVSTTHKCLIAEAWCSVRDLPALQAL 120
QY 337 RDSSMBEGVSVAHRIPCRDMPTLIRTNRFTASFOGIVDRYGVGRYQVNPAPYTIITF 396
DB 121 RDSSMBEGVSVAHRIPCRDMPTLIRTNRFTASFOGIVDRYGVGRYQVNPAPYTIITF 180
QY 397 PFLFAVMFGDVGHGLLMFLFALAWLAENRPAVKAQNEIWQTFFRGRYLLMLGLFSIY 456
DB 181 PFLFAVMFGDVGHGLLMFLFALAWLAENRPAVKAQNEIWQTFFRGRYLLMLGLFSIY 240
QY 457 TGFYINCEFSRATSIFFSGWSVAAMANQSGWSDAFLAQHTMLTLDPNVTGVFLGPYPFGI 516
DB 241 TGFYINCEFSRATSIFFSGWSVAAMANQSGWSDAFLAQHTMLTLDPNVTGVFLGPYPFGI 300
QY 517 DPIWSLAANHLSEFLNSFKMKMSVILGVWMAFGVILGVFNHVFQGRHRLLETLPLTLF 576
DB 301 DPIWSLAANHLSEFLNSFKMKMSVILGVWMAFGVILGVFNHVFQGRHRLLETLPLTLF 360
QY 577 LLGLFGVLYFLVIYKWLVCVWAARAAS-PSILIHFINMFLPSHSPSNRLLYPROEVVQATL 635
DB 361 LLGLFGVLYFLVIYKWLVCVWAARAASPSILIHFINMFLPSHSPSNRLLYPROEVVQATL 420
QY 636 VVLALAMVPILLGTPHLHLHRRRLRRPADRQENKAGLLDPDASVNGWSSDSEKA 695
DB 421 VVLALAMVPILLGTPHLHLHRRRLRRPADRQENKAGLLDPDASVNGWSSDSEKA 480
QY 696 GGLDDEEAELVPSEVLMEHQAHTIEFCIGCVSNTASYLRLWALSALAHQSEVLWAMVM 755
DB 481 GGLDDEEAELVPSEVLMEHQAHTIEFCIGCVSNTASYLRLWALSALAHQSEVLWAMVM 540
QY 756 RIGLGLGREVGVAADVLPVIFAFAFVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGT 815
DB 541 RIGLGLGREVGVAADVLPVIFAFAFVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGT 600
QY 816 GYKLSPP 822
DB 601 GYKLSPP 607
RESULT 11
ABM81282
ID ABM81282 standard; protein; 614 AA.
XX
AC ABM81282;
XX
18-NOV-2004 (first entry)
DT
XX Tumour-associated antigenic target (TAT) polypeptide PRO24831, SEQ:3307.
DE
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;

KW	central nervous system cancer; bladder cancer; pancreatic cancer;
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;
KW	chromosome identification; chromosome mapping; gene mapping;
KW	gene therapy; cytostatic.
OS	Homo sapiens.
XX	
PN	WO2004030615-A2.
XX	
PD	15-APR-2004.
XX	
PF	29-SEP-2003; 2003WO-US028547.
XX	
PR	02-OCT-2002; 2002US-0414971P.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Wu TD, Zhang Z, Zhou Y;
XX	
DR	WPI; 2004-347921/32.
DR	N-PSDB; ACN39268.
XX	
PT	New tumor-associated antigenic target polypeptides and nucleic acids,
PT	useful in preparing a medicament for treating or detecting a
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT	prostate cancer or tumor.
XX	
PS	Claim 12; SEQ ID NO 3307; 7273pp; English.
XX	
CC	The invention relates to human tumour-associated antigenic target (TAT)
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are
CC	overexpressed in cancer tissues compared to normal tissues, and may thus
CC	serve as effective targets for the diagnosis and treatment of cancer in
CC	mammals. The invention also relates to nucleic acid and polypeptide
CC	sequences at least 80% identical to the TAT nucleic acids and
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC	TAT polypeptide; and methods and compositions for the treatment or
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC	antibodies, antagonists, binding molecules and compositions are useful
CC	for diagnosing or treating a cell proliferative disorder associated with
CC	increased TAT expression, particularly cancers such as breast cancer,
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC	used as hybridisation probes, in chromosome and gene mapping, in
CC	chromosome identification and in gene therapy. The present sequence
CC	represents a TAT polypeptide of the invention
XX	
SQ	Sequence 614 AA;
	Query Match 73.4%; Score 3131.5; DB 8; Length 614;
	Best Local Similarity 99.7%; Pred. No. 7.1e-301;
	Matches 605; Conservative 0; Mismatches 1; Indels 1; Gaps 1
QY	217 MTFPLISYWGEOIGOKIRKIDCFCHVFPFQQEAREALGALQLOOQSQEQLVGETER 276
Db	1 MTFPLISYWGEOIGOKIRKIDCFCHVFPFQQEAREALGALQLOOQSQEQLVGETER 60
QY	277 FLSQVLGRVLQLLPPGQVQVHKMAVYLALNQCSVSTTHKCLIAEAWCSVRDLPALQAL 336
Db	61 FLSQVLGRVLQLLPPGQVQVHKMAVYLALNQCSVSTTHKCLIAEAWCSVRDLPALQAL 120
QY	337 RDSMSEGVSAVAHRIPCRDNMPPTLIRNRRFTASQGIIVRGYGVGVENPAPYTIITF 396
Db	121 RDSMSEGVSAVAHRIPCRDNMPPTLIRNRRFTASQGIIVRGYGVGVENPAPYTIITF 180
QY	397 PFLFAVMFGDVGHGLLMLFLFALAMVLAENRPAVKAQNEIWOTFFRGYVILLMLGLFSY 456
Db	181 PFLFAVMFGDVGHGLLMLFLFALAMVLAENRPAVKAQNEIWOTFFRGYVILLMLGLFSY 240
QY	457 TGFITYNECFSRATSIFFSGWSVAAMANQSGWSDAPLAQHTMLTLDPNVTGVLGPYPFGI 516

XX	(BGHM) BRIGHAM & WOMENS HOSPITAL.
PA	(UTKU/) UTKU N.
PA	
XX	Utku N, Gullans SR, Milford EL;
PI	
XX	WPI; 1999-205186/17.
DR	N-PSDB; AAX24913.
DR	
XX	A novel T-cell transmembrane protein (TIRC7) - useful for modulating
PT	immune responses, for use in organ transplantations and treatment of
PT	infectious disease.
XX	
XX	Claim 1(i); Page 93-95; 97pp; English.
PS	
XX	
CC	The present sequence is TIRC7, a novel T-cell transmembrane protein that
CC	exhibits a central role in T-cell activation in vitro and in vivo. TIRC7
CC	mRNA is transiently up-regulated in the early phase of T-cell activation
CC	via a calcineurin-dependent pathway. TIRC7 cDNA (see AAX24912) was
CC	identified following a screen for genes that are differentially expressed
CC	in alloactivated human T cells. A second TIRC7 protein (see AAX98112) is
CC	identical except for one amino acid substitution (Gln121 to Arg).
CC	suggesting 2 alleles of the TIRC7 gene. The invention provides vectors,
CC	host cells, antibodies, TIRC7 peptides, polypeptides and polynucleotides
CC	that are useful in diagnostic compositions for identifying T-cell
CC	activating or co-stimulating compounds, or for identifying inhibitors of
CC	T-cell activation and stimulation. TIRC7 peptides or polypeptides,
CC	vectors and antibodies are useful in the preparation of pharmaceutical
CC	compositions for treatment of acute and chronic diseases involving T-cell
CC	activation and Th1 and Th2 immune response, for the treatment of acute
CC	and chronic rejection of allo- and xeno organ transplants and bone marrow
CC	transplantation, for the treatment of rheumatoid arthritis, lupus
CC	erythrematosus, multiple sclerosis, encephalitis, vasculitis, diabetes
CC	melitus, pancreatitis, gastritis, thyroiditis, for the treatment of
CC	malign disorders of T, B or NK cells, for the treatment of asthma,
CC	lepramatosis, Helicobacter pylori associated gastritis, or for the
CC	treatment of skin, adrenal or lung tumors (claimed)
XX	
XX	Sequence 614 AA;
SQ	

Query Match 73.3%; Score 3127.5; DB 2; Length 614;

Best Local Similarity 99.5%; Pred. No. 1.8e-300;

Matches	604;	Conservative	1;	Mismatches	1;	Indels	1;	Gaps	1;
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217	QY	MTFLISYWGEOIGQKIRK1TDCFFCHVFPFLQOEERLQALQLOQSOBELQEVLGETER	276
	Db	1 MTFLISYWGEOIGQKIRK1TDCFFCHVFPFLQOEERLQALQLOQSOBELQEVLGETER	60
277	QY	FLSQVLGRVQLQLPPGVQVHKMAKVYALNQCOSVSTTHKCLIAEAWCSVRDLPALQOAL	336
	Db	61 FLSQVLGRVQLQLPPGVQVHKMAKVYALNQCOSVSTTHKCLIAEAWCSVRDLPALQOAL	120
337	QY	RDSSEEGVSAVAHRI PCRMPPTLI RTNRF TASFQI VDRYGVGRYQEVNPAPYTIITFF	396
	Db	121 QDSSMEEGVSAVAHRI PCRMPPTLI RTNRF TASFQI VDRYGVGRYQEVNPAPYTIITFF	180
397	QY	PFLFVPMFGDVGHGLMFLPALAMVLAENPAVKAAQNEITWOTFFRGRYLLMLGLFSY	456
	Db	181 PFLFVPMFGDVGHGLMFLPALAMVLAENPAVKAAQNEITWOTFFRGRYLLMLGLFSY	240
457	QY	TGFIYNECFSRATSI PFSGMSVAAMANQSGWDAFLAQHTMLTLDPNVTGVFLGPYPFGI	516
	Db	241 TGFIYNECFSRATSI PFSGMSVAAMANQSGWDAFLAQHTMLTLDPNVTGVFLGPYPFGI	300
517	QY	DP1WSLANHLSFLNSFKWMSVILGVVHMAFGVVLGVFNHVFHQHRLLLETLP1ELTFF	576
	Db	301 DP1WSLANHLSFLNSFKWMSVILGVVHMAFGVVLGVFNHVFHQHRLLLETLP1ELTFF	360
577	QY	LLGLFGYLVFLVYKWLVCWAARAAS - PS1LIHF1NMFLFSHSPSNRLLYPRQEVVQATL	635
	Db	361 LLGLFGYLVFLVYKWLVCWAARAASPS1LIHF1NMFLFSHSPSNRLLYPRQEVVQATL	420
636	QY	VVLAMAVP1ILLGTPLHLHRRHRRRRLRRPADRQENKAGLLDLPDASVNGWSDEBKA	695

Matches	604;	Conservative	1;	Mismatches	1;	Indels	1;	Gaps	1;
QY	217	MTFLSYMGEOIGQKIRKLTDCFHCHVFPFLOQEEARLALGALQOQSOELOEVIGETER	276						
Db	1	MTFLSYMGEOIGQKIRKLTDCFHCHVFPFLOQEEARLALGALQOQSOELOEVIGETER	60						
QY	277	FLSQVLGRVLQLPPQGVQVHRKAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQEAL	336						
Db	61	FLSQVLGRVLQLPPQGVQVHRKAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQEAL	120						
QY	337	RSSMEEGVSAVAHRIPCDMDPTLIRNRTFASFGIVDRVGVGRYQVNPAPYTIITP	396						
Db	121	QDSMEEGVSAVAHRIPCDMDPTLIRNRTFASFGIVDRVGVGRYQVNPAPYTIITP	180						
QY	397	PFLFAMFGDVGHLLMFLPALAMVLAENRPVAKAAQNEIMOTFERGRVLLLMGLFSY	456						
Db	181	PFLFAMFGDVGHLLMFLPALAMVLAENRPVAKAAQNEIMOTFERGRVLLLMGLFSY	240						
QY	457	TGFIYNECFSRATSIFFPSGWSVAAMANQSGWSDAFLAQHTMLTLDPNVTGVFLGPYPFGI	516						
Db	241	TGFIYNECFSRATSIFFPSGWSVAAMANQSGWSDAFLAQHTMLTLDPNVTGVFLGPYPFGI	300						
QY	517	DIWLSLAANHLFSLSFKMKQSVILGVVHMAFGVVLGVVNHVHFGQRHRLLETLPELTP	576						
Db	301	DIWLSLAANHLFSLSFKMKQSVILGVVHMAFGVVLGVVNHVHFGQRHRLLETLPELTP	360						
QY	577	LLGLFGYLVFLVIYKWLVCVWAARAAS-PSILIHFINMFLFSPNSRLLYPROEVVQATL	635						
Db	361	LLGLFGYLVFLVIYKWLVCVWAARAASPSILIHFINMFLFSPNSRLLYPROEVVQATL	420						
QY	636	VVLAWAMPILLGLTPLHLHRRRLRRRPPADROEENKAGLLDLPDASVNGWSSDEEKA	695						
Db	421	VVLAWAMPILLGLTPLHLHRRRLRRRPPADROEENKAGLLDLPDASVNGWSSDEEKA	480						
QY	696	GGLDEEAEALVPSEVLMHQAIHTTEPCGVCVNTASYRLWALSIAHAQLSEVLWAMVM	755						
Db	481	GGLDEEAEALVPSEVLMHQAIHTTEPCGVCVNTASYRLWALSIAHAQLSEVLWAMVM	540						
QY	756	RIGLGLGREGVGAUVLPIFAAPAVMTVAILLVMEGLSAPFLHALRLHWHVFQNKFSCT	815						
Db	541	RIGLGLGREGVGAUVLPIFAAPAVMTVAILLVMEGLSAPFLHALRLHWHVFQNKFSCT	600						
QY	816	GKYLSPF 822							
Db	601	GKYLSPF 607							

RESULT 14
ID ABP41524
AC ABP41524 standard; protein; 643 AA.

DT 22-AUG-2002 (first entry)

DE Human ovarian antigen HTAES83, SEQ ID NO:2656.

KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; chromosome 11q13.4-13.5.

OS Homo sapiens.

PN WO200200677-A1.

XX 03-JAN-2002.

XX PF 07-JUN-2001; 2001WO-US018569.
 XX PR 07-JUN-2000; 2000US-0209467P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX BI Birse CB, Rosen CA;
 XX WI WPI; 2002-147878/19.
 XX DR N-PSDB; ABQ54601.
 XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 XX PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 XX PT cancer), immune disorders, cardiovascular disorders and neurological
 XX PT diseases.
 XX PS Claim 11; SEQ ID NO 2656; 2922pp; English.
 XX CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prophesying or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 643 AA;

Query Match 68.4%; Score 2917.5; DB 5; Length 643;
 Best Local Similarity 99.3%; Pred. No. 1.3e-279;
 Matches 559; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY	67	FLQEEVRVAGLVLPKGRLLPAPPRDLRIQEETERLAQELDRVGNQALRAQLHQLO	126						
Db	35	FLQEEVRVAGLVLPKGRLLPAPPRDLRIQEETERLAQELDRVGNQALRAQLHQLO	94						
QY	127	LHAAVLRQGHFPQLAAHTDASERTPLQAPGPHQDLRVNFAVAGVEPHKAPALERLL	186						
Db	95	LHAAVLRQGHFPQLAAHTDASERTPLQAPGPHQDLRVNFAVAGVEPHKAPALERLL	154						
QY	187	WRACGFLIASPRELEQPLEHPVTGEPATWMTFLISYMGEOIGQKIRKLTDCFHCHVFPF	246						
Db	155	WRACGFLIASPRELEQPLEHPVTGEPATWMTFLISYMGEOIGQKIRKLTDCFHCHVFPF	214						
QY	247	LQOEEARLGAALQOQSOELOEVIGETERFSLQVLGRVLQLPPQGVQVHRKAVYLAL	306						
Db	215	LQOEEARLGAALQOQSOELOEVIGETERFSLQVLGRVLQLPPQGVQVHRKAVYLAL	274						
QY	307	NOCSSVSTTHKCLIAEAWCSVRDLPALQEALRDSMEEGVSAVAHRIPCDMDPTLIRNTR	366						

Db 275 NQCSVSTTHKCLIAEAWCSVRDLPALQALRDSSMEGSAVAXRIPCRDMPPTLIIRTNR 334
QY 367 FTASFGQIVDRYGRVQEVNPAQYITITPPFLPAVNFQDVGHGGLMLPALAMVLAENR 426
Db 335 FTASFGQIVDAYGVGRYQEVNPAQYITITPPFLPAVNFQDVGHGGLMLPALAMVLAENR 394
QY 427 PAKAAQNEIWTQFFRCRYLLMLLGLFSIYTGFIYNECFSRATSIIPSGMSVAMANQSG 486
Db 395 PAKAAQNEIWTQFFRCRYLLMLLGLFSIYTGFIYNECFSRATSIIPSGMSVAMANQSG 454
QY 487 WSDAFLAQHTMLTLDPNVTGVFLGYPFGIDPIWSLAANHLSPNSFKMSVILGVVHM 546
Db 455 WSDAFLAQHTMLTLDPNVTGVFLGYPFGIDPIWSLAANHLSPNSFKMSVILGVVHM 514
QY 547 AFGVVLGVFNHVFHQHRRLLLETLPELTLLGLFGVILVLYIKVLCVWAARAAS-PSI 605
Db 515 AFGVVLGVFNHVFHQHRRLLLETLPELTLLGLFGVILVLYIKVLCVWAARAAS-PSI 574
QY 606 LIHFIMFLSHSPSNRLLYPRQ 628
Db 575 LIHFIMFLSHSPSNRLLYPRQ 597

RESULT 15

ADH09950

ID ADH09950 standard; protein; 856 AA.

XX ADH09950;

XX 11-MAR-2004 (first entry)

XX Human host factor protein, SEQ ID NO 478.

XX antiviral; host factor; retrovirus; HIV; human.

XX Homo sapiens.

XX WO2003094847-A2.

XX 20-NOV-2003.

XX 07-MAY-2003; 2003WO-US014382.

XX 07-MAY-2002; 2002US-037811P.

XX (UYEM-) UNIV EMORY.

XX Devine SE;

XX WPI; 2004-011998/01.

XX The invention relates to a novel method for identifying an antiviral
PT compound. The novel method comprises exposing a cell that expresses a
PT host factor to a candidate compound to identify an agent that inhibits
PT the expression or activity of the host factor. The novel method involves
PT identifying an antiviral compound, comprising exposing a first cell that
PT expresses a host factor to a candidate compound, determining whether the
PT candidate compound inhibits the expression or activity of the host factor
PT in the first cell, where a candidate compound that inhibits the
PT expression or activity of the host factor in the first cell is a
PT potential antiviral compound, exposing a second cell to the potential
PT antiviral compound and a retrovirus, and determining whether the compound
PT inhibits the ability of the retrovirus to infect or replicate within the
PT second cell, where a potential antiviral compound that inhibits the
PT ability of the retrovirus to infect the second cell is an antiviral
CC compound. The method is useful in identifying antiviral agents, including

CC those that are effective against retroviruses, such as HIV. This sequence
CC represents a human host factor protein used in the antiviral
CC identification method of the invention.

XX Sequence 856 AA;

Query Match 49.78; Score 2119; DB 8; Length 856;

Best Local Similarity 50.08; Pred. No. 3.5e-200;

Matches 433; Conservative 137; Mismatches 226; Indels 70; Gaps 15;

QY 1 MGSFMRSEAEVALQFLPTAAATCYVSRCLGELGVFRDLNANASVAFQRFVVDVMRCEE 60

Db 1 MGSFMRSEAEVALQFLPTAAATCYVSRCLGELGVFRDLNANASVAFQRFVVDVMRCEE 60

QY 61 LEKTFPLOBEVRRAGLVLPKGRPLPAPPRDLRIQEETERLAQELRQVNRGNQALRA 120

Db 61 LERILVYLQEIINRADIPLEGEASPPAPPLKQVLEMQEQQLKLEVELEVTNKEKLRK 120

QY 121 QL-----HQLQLHAANVLRQCHE-----PQLAAAHDTGASERTPLLOAPGPHQDL 165

Db 121 NLLELIEYTHMLRVTKTFVKNRVEPEPTYEEFESL-----ESDLSLDYSCMQRLGA 171

QY 166 RVNFVAGAVEPHKAPALERLLWRAACRGFLIASFRELEOPLHVPVTGSPATMTFLISYWG 225

Db 172 KLGFSVGLNQGVKAEFEKMLWRCVGYTIVSAELDESLEDGETGEVWKVYVFLISFWG 231

QY 226 EQIGQKIRKITDCFHCHVFPFLQOEEARLQALQOQSQOELQOELQOELQOELQOELQOEL 285

Db 232 EQIGHKVKKICDCYCHVYPPNTAEERREIQGLNTRIQLDLYTLVHLKTEDYLRQLCKA 291

QY 286 LQLLPFGQVQVHKMAVYLAALNOCVSSTTHKCLIAEAWCSVRDLPALQALRDSSMEEG- 344

Db 292 AESVYSRVIVQVKKQKAIYHMLNMCSPDVTNKLIAEYVWCPEADLQDLRLALEEGRESGA 351

QY 345 -VSAVAHRIPCRDMPPTLIIRTNRTASFGQIVDRYGRVQEVNPAQYITITPPFLPAM 403

Db 352 TIPSFNWIIPTKETPTPTIRTNKFTGQFQIVDAYGVGSYREVNPAQYITITPPFLPAM 411

QY 404 FGDVGHGLMLPALAMVLAENRPAVKAQNEIWTQFFRCRYLLMLLGLFSIYTGFIYNE 463

Db 412 FGDVGHGLMLPALAMVLAENRPAVKAQNEIWTQFFRCRYLLMLLGLFSIYTGFIYNE 470

QY 464 CFSRATSIIPSGMSVAMANQSG-----WSDAFLAQHTMLTLDPNVTGVFLGYP 513

Db 471 CFSKSNVLFSGMNVSAVMSYSSHPHAKKQVLMNDSVVRHNSILQLDPSIPGVRGYP 530

QY 514 FGDVGHGLMLPALAMVLAENRPAVKAQNEIWTQFFRCRYLLMLLGLFSIYTGFIYNE 573

Db 531 LGIDPIWNLATNRLITFLNSFKMSVILGVVHMAFGVVLGVFNHVFHQHRRLLLETLPE 590

QY 574 LTFLLGLFGVFLVLYIKVLCVWAARA--SPSILHFINMFLSHSPSNRLLYPROEVV 631

Db 591 LTFMLCIGVLIPIFYKWL-VFSAETSRVAPSILIEFINMFLPASKTSG-LYTQGEYV 648

QY 632 QATLVVALAMVPILLGLTPLLHHRHR-----LRRPADROEENKAGLLDL 680

Db 649 QRVLLVVTALSVPLFLGKPLFLLMLHNGRSCFVNRSGYTLIRK--DSEEE----- 698

QY 681 PDASVNGSSDEKAGGLDD--EEEA--ELVPEVLMHQAHTIETCLGCVSNATSVLRL 736

Db 699 --VSLGSDQDIEGNHQVEDGCREMACBENFGEILMTQVTHSIEYCLGICISNTASVRL 756

QY 737 WALSLAHQAQLSEVLMAMVNRIGLGLGREGVAAVLPVFAAFVMTVAILLVMGLSASF 796

Db 757 WALSLAHQAQLSDVLMAMVNRIGLGLGREGVAAVLPVFAAFVMTVAILLVMGLSASF 814

QY 797 LHALRLHWEFQNKFGYSGYKLSPP 822

Db 815 LHALRLHWEFQNKFGYSGYKLSPP 840

Search completed: June 29, 2006, 13:02:58
Job time : 203 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 29, 2006, 13:03:14 ; Search time 44 Seconds
(without alignments)
1797.504 Million cell updates/sec

Title: US-10-783-519-2
Perfect score: 4266
Sequence: 1 MGSMPFSEEEVALVQLFLPTA.....HWVEFQNKFYSGTGKLSPF 822

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2143.5	50.2	855	2 JH0287	immune regulatory
2	1954	45.8	838	2 A54163	vacuolar ATPase (E
3	1931	45.3	838	2 B38556	vacuolar proton pu
4	1539.5	36.1	935	2 S15795	vacuolar proton pu
5	1491.5	35.0	865	2 T18565	probable H ⁺ -export
6	1406.5	33.0	873	2 T16282	hypothetical prote
7	1375	32.2	1236	2 T19492	hypothetical vacuol
8	1331	31.2	821	2 H84600	probable vacuolar
9	1323.5	31.0	843	2 T06068	probable vacuolar
10	1318	30.9	840	1 A42970	H ⁺ -exporting ATPas
11	1280.5	30.0	805	2 T37787	probable vacuolar
12	1210	28.4	780	2 H84685	probable vacuolar
13	1190	27.9	775	2 T46719	H ⁺ -exporting ATPas
14	1144	26.8	890	2 S54554	hypothetical prote
15	448	10.5	163	2 T46449	hypothetical prote
16	301	7.1	686	2 F72655	ATP synthase, subu
17	283.5	6.6	658	2 E69228	H ⁺ -transporting tw
18	281.5	6.6	649	2 T45102	probable V-type so
19	280.5	6.6	659	2 E71214	H ⁺ -transporting AT
20	273.5	6.4	659	2 A75029	ATP synthase subun
21	270.5	6.3	701	2 E90202	H ⁺ -transporting AT
22	269.5	6.3	676	2 F69394	H ⁺ -transporting tw
23	259.5	6.1	695	2 G64327	H ⁺ -transporting AT
24	255.5	6.0	722	2 F84364	ntpi protein - Ent
25	235.5	5.5	664	2 B53610	probable V-type AT
26	203.5	4.8	622	2 B71326	probable V-type AT
27	182	4.3	454	2 F71313	probable V-type AT
28	168.5	3.9	649	2 G71530	ATP synthase, chai
29	167.5	3.9	649	2 C81867	

30 163 3.8 690 2 D75487 v-type ATP synthas
31 155.5 3.6 660 2 E81549 ATP synthase, chai
32 155.5 3.6 660 2 C86502 ATP synthase subun
33 154.5 3.6 660 2 E72121 ATP synthase chain
34 141.5 3.3 663 2 C95153 v-type sodium ATP
35 128.5 3.0 378 2 S55634 glycoprotein M - e
36 119 2.8 608 2 C70111 v-type ATPase, sub
37 117.5 2.8 1119 2 AC0045 probable membrane
38 117 2.7 594 2 D95286 hypothetical prote
39 116.5 2.7 704 2 D82227 conserved hypothet
40 113.5 2.7 431 2 AF2635 exopolysaccharide
41 113.5 2.7 435 2 E97417 exoQ-like protein
42 112.5 2.6 1037 2 A36096 Ca²⁺-transporting
43 112 2.6 669 2 E71127 hypothetical prote
44 111.5 2.6 627 2 B44409 gamma-aminobutyric
45 111.5 2.6 730 2 E75387 NADH dehydrogenase

ALIGNMENTS

RESULT 1

JH0287

immune regulatory protein precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004

C:Accession: JH0287

R:Lee, C.K.; Ghoshal, K.; Beaman, K.D.

Mol. Immunol. 27, 1137-1144, 1990

A:Title: Cloning of a cDNA for a T cell produced molecule with a putative immune regul

A:Reference number: JH0287; MUID:91061805; PMID:2247090

A:Accession: JH0287

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-855 <LEE>

A:Cross-references: UNIPROT:P15920; UNIPARC:UPI00000161FAB; GB:X55184; NID:g52754; PIDN

C:Superfamily: vacuolar ATP synthase 95K chain

Query Match 50.2%; Score 2143.5; DB 2; Length 855;

Best Local Similarity 51.4%; Pred. No. 3.3e-148;

Matches 441; Conservative 129; Mismatches 233; Indels 55; Gaps 15;

Qy	1	MGSMPFSEEEVALVQLFLPTAAYTCVSRGELGLVFRDLNASVSARQRFVVDVWRC	60
Db	1	MGSLFRSESCLAQLFQSGTAYECLSGKGLVQFRDLNQNVSSPQRFVGEVKRCE	60
Qy	61	LEKTFTFLOEVRERAGLVLPKGRPLPAPPRLRLRIQETRIQAOLRDVRGNQOALRA	120
Db	61	LERILVYLQETITRADIPPEGEASPAPPLKLVLEMQEQLKLELREVTNNKEKLK	120
Qy	121	QL-----HQLQHAALVRQGH-----PQLAAHTDGAERTPLLAQPGPHQDLRVN	168
Db	121	NLLELVEYTHMLRVTKTFLKRVNFEPTVEEFPALENDSLDYS-CMQLGA-----KL	174
Qy	169	FVAGAVEPKAPALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLSYWGEQ	228
Db	175	FVSGLLIQQRVEAFERMLWRACKGYITVYAELEDECLDPETGEVIMKYVFLISFWGEQ	234
Qy	229	GQKIRKITDCHVFHPFPLQEEEARLGALQOLQOQSOELQELVETGTERFLSOVLGRVLQ	288
Db	235	GHKVKIKDCYCHYIYPNPTAERREIQEGLNTRIQDLTVLHKETDYRQLVCKAAES	294
Qy	289	LPFGQVQVHKMKAVALALNQCSVSTTHKCLIAEAWCSVRDLPAQELRDSMBEG--VS	346
Db	295	VCSRVVQVRKMKAIYHMLNWCSPDVTNKCLIAEAWCPEVDLPGLRRALSGSREGATIP	354
Qy	347	AVAHRIPCDMPPTLIRTRWFTASFGQIVDVRGVGRYQEVNPAFYITITPPFLFANVFGD	406
Db	355	SPMNTIPTKETPTTLIRTNKFTGEGQNIYDAYGVGSYREVNPAFTIITITPPFLFANVFGD	414
Qy	407	VGHGLMELFALAMVLAENRPAKAAQNETWQTFGRGYLLLMGLPSIYTGTYNCFCS	466
Db	415	FGHGFVWFLFALLLVLENHNPRLSQSQ-EILRMFFDGRYLLLMGLPSVYTGTYNCFCS	473

A:Reference number: Z18977
A:Accession: T18565
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-865 <WIL>
A:Cross-references: UNIPROT:Q17660; UNIPARC:UPI000007E97E; EMBL:AL031269; PIDN:CAA20334.
A:Experimental source: clone VM02B12L
R:Colles, L.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z19084
A:Accession: T19177
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-865 <W12>
A:Cross-references: UNIPARC:UPI000007E97E; EMBL:Z50872; PIDN:CAA90758.1; GSPDB:GN000020;
A:Experimental source: clone C05D12
C:Genetics:
A:Gene: CESP:VM02B12L.1
A:Map position: 2
A:Introns: 66/1; 181/2; 576/2; 648/3; 775/1
C:Superfamily: vacuolar ATP synthase 95k chain
C:Keywords: hydrolase

Query Match 35.0%; Score 1491.5; DB 2; Length 865;
Best Local Similarity 37.0%; Pred. No. 1.2e-100;
Matches 330; Conservative 165; Mismatches 285; Indels 113; Gaps 18;

QY 1 MGSERSEVALVQLFLPTAAAYTCVSRIGELGLVEFPRDLNASVAFQRRFVVDVWRCBE 60
DB 1 MGSYRSEHMKLCQIFFOSESAQCVAELGMAQFIDLNEEQAYTRKFNEVRRCD 60
QY 61 LEKTFQEEVRRAGLVLPPEKGRLPAPPPDLRLRQEBTERLAQELRDVRGNOALRA 120
DB 61 MERKINFEDEITKDLVIPDYDEHPAPQPKHMEANLEKLEELVQINKCKVLXN 120
QY 121 QLHLQOLHAVALRQHEPQLAAHT--DGASERTPLLOAPGQP-----HQDL 165
DB 121 NHVQLLEKMAVLE--HVTSLDHPHSCREAAIMSISAARGAEPISFGMKDEPKVKDBK 178
QY 166 RVNFVAGAVEPHKAPALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWTFLLSYWG 225
DB 179 ELKFTVGVVGRSKAFAFERFLRLSRKVFAPQIQOQTE--LFGNEFEDKCVFLTFSSG 237
QY 226 EQIGKIRKIDTCFH--CHVFPLQOEERLALQLOOQSOELQOEVLGETERFLFSQVLG 283
DB 238 EQLRAKVKICDGFQAKCYTPENPAETKL--LLNIKVTQDMKAVIEKTLDYRSKCIH 295
QY 284 RVQLLPPGQVQVHKAVYALNOCVSTTHKCLIAEAWCSVRDLPALQEAALRDSMBE 343
DB 296 AAATNLKRWGIMLLKLSIFHTLNNFSDVDTOKCLIAECWVPEADIGQVNSLHMGTHS 355
QY 344 G--VSAAVHRIPCRDMPPTLIRNRTASFGQIVDRYGVGRYOEVNPAPYTIITPFLFA 401
DB 356 GSTVPAIUNEMETDKYPTFKLNFQGFQFQFQFQFQFQFQFQFQFQFQFQFQFQFQF 415
QY 402 VMFGDVGHGLMFLPALAVLAENRPVAKAONEIWQTFRRYGLLLMLGFLFSYTGTY 461
DB 416 VMFGDAGHGLIILAAAFVFEKLLISMKIKDEIFNTFFGGRVYVLLMGHFAITGTY 475
QY 462 NECFSRATSIIPSGW-----SVAAANQSGWSDAFLAQHTMLTLDPNVT--GVFLGYP 513
DB 476 NDFYSKSYNI FGSSWVNPYNQTLANMDAQGADSNITLS---LTFPEPIAFNHDYGPY 531
QY 514 FGIDPIWLSAANHLSPKMSVILGVVHMAFGVVLGVNHHVHFGORH--RLLETL 571
DB 532 FGVDVPMNLAINRLNFMKMTSILIGISQAFGIMLSLNNH--GNRSVVDIVFVI 589
QY 572 PELTFLGLFGYLVFLVYKMLCWAAARA-----ASPSTLIHFINMFL----- 614
DB 590 FOCLFLGCI FVYLCIQLVLMKMIFFVVKPAYIFGRLYPGSNCAPSLLIGLNNFMVYKSDA 649
QY 615 -FSHSPSN-----RLLYPRQEVVQATLVVLALAMVPILLG 649

DB 650 SPAHDVGTAAKGEMVIVNGQNVYTTINDQCYLQOWYPNQSLVELILLIIVAVVPVMLLV 709
QY 650 TPLHLLHRRRLRRPPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDDEEAEELVPS 709
DB 710 KPFYIRWRHRSGLH-----IDL-----GHGPDHGEFNF 739
QY 710 EYLMHQAHHTTEFCGVCVSNATSYURLWALSALHAQLSEVLWAMVWRIGLGLGREGVAA 769
DB 740 DIMVHQAHHTTEFCVSHSTASYURLWALSALHAQLSDVLWMLMSLTWGGGSGAA 799
QY 770 VVLVPFAAFVMTVAILLVMEGLSAFLHALRHWVEFQNKFYSGTYKLSPP 822
DB 800 ITIL-FYFIFSILSVICILLMEGLSAFLHAIHLHWVEFQSKFYGGTIGIPEFP 851

RESULT 6
T16282
hypothetical protein F35H10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16282
R:Woessner, J.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F35H10.
A:Reference number: Z18490
A:Accession: T16282
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-873 <WOS>
A:Cross-references: UNIPROT:Q20072; UNIPARC:UPI000008163D; EMBL:U40934; NID:gl072149; P: 4
C:Genetics:
A:Gene: CESP:F35H10.4
A:Introns: 39/3; 709/3; 785/1; 843/2
C:Superfamily: vacuolar ATP synthase 95k chain

Query Match 33.0%; Score 1406.5; DB 2; Length 873;
Best Local Similarity 36.8%; Pred. No. 1.9e-94;
Matches 329; Conservative 158; Mismatches 303; Indels 103; Gaps 23;

QY 1 MGSERSEVALVQLFLPTAAAYTCVSRIGELGLVEFPRDLNASVAFQRRFVVDVWRCBE 60
DB 1 MGSLSRSEMRFCQLIVEKDAAFNVAEIGKQYVQFQKDLNPNVNSFORTFVKDIRRVD 60
QY 61 LEKTFQEEVRRAGLVLPPEKGRLPAP-----PPRDLRLRQEBTERLAQELRDVRGNO 115
DB 61 MERKLRFLSQVVDKDIVP--GRVOTGDYTLPTSEINTLEGTLEKDKDKVMNDS 117
QY 116 QALRAQLHQLQHAVALR-----QGHEPQLAAAHDTGASERTPLLOAPGPHQDLRVNF 169
DB 118 SQLKANFMDLKEDAVLDKTDPEFGQVDDQAELENLDEGAVPRVEKGP-----VNY 172
QY 170 VAGAVEPHKAPALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWTFLLSYGEBQIG 229
DB 173 LVGIRRELNGFERVLWRACHHTAYIRSSDIEELEDPGTGEKVHKSVFIFLFGDRMR 232
QY 230 QKIRKITDCFHVP-----PFLQOEERLALQLOOQSOELQOEVLGET--ERFLSQVL 282
DB 233 SIVEKVCDFKAKFKQCPKTFKERQSAK-----NDVRARIQDLQVLQGTREHFR-- 283
QY 283 GRVLQLLPPGQ-----VQVHKMAVYALNOCVSTTHKCLIAEAWCSVRDLPALQEAALRD 338
DB 284 -RVLQAAANHHQMLKQVRMIKTVFHMNLNFTFDGIGRFFVGEWCWI PLKHVEDVRKAIEV 342
QY 339 SSMEEG--VSAAVHRIPCRDMPPTLIRNRTASFGQIVDRYGVGRYOEVNPAPYTIITP 396
DB 343 GAERSGSVKPVLTILETSVTPPTNYNTKPTAFVQGIQVDSYGIATYATYELNPAPYTIITP 402
QY 397 PFLFAMVPGDVGHGLMFLPALAVLAENRPVAKAONEIWQTFRRYGLVLLMLGFLSTY 456
DB 403 PFLFSCHEFDLGHGCIIMLAGLWFLVRKYNLQARNIKDEIFNMFFGGYIILLMLGFLSH 462
QY 457 TGFYNECFSRATSIIPSGWSVAAMANO--SQWSDAFLAQH---TMLTLDP-----NVTGVF 508

Db 463 AGIINDMEFAKFNIFGSGWKNPNYASEIEGWNR--TEHCKEMLVELAPEDAYDHAG-- 518
Qy 509 LGPYPPGIDPIWSLAANHLSPNSFKMKMSVILGVVHNAFGVILGVVHNFHFGQRHLL 568
Db 519 -GPYSFGVDPIWNAENKLNFLNSMKMLSVILGISQMTFGVILSFNHTYKSKIDIFT 577
Qy 569 ETLPFLTLGLGFLVFLVLYKWLVCWAARA-----ASPSILHFINMFLPSH 617
Db 578 VFIPQMLFMGCFMFLCQLILKWLFWTKZATVFGIYPGSHCAPSLLGLINPMWKO 637
Qy 618 SPNSRL--YPRQEVVQATLVLAAMVPIILLIGTPLHLHR 657
Db 638 RNAGFVVDGKNGEYREVETCYLSQMYPGSVLEMILVIAVLCVPMLEGGDIH--HV 695
Qy 658 HRRRLRRPADRQENKAGLL-DLPDASVNGWSSDEBKA-----GGDDEBEAEVLVPE 710
Db 696 MOOKKAKELHGNATVRANVVSSEIYVNGSKKEGAHEEHGGHGEDES- 750
Qy 711 VLHQAHTHTIEFCICVCSNTASYRLWALSIAHAQLSEVLWAMV-MRIGLGLREVGVAA 769
Db 751 IMVHQAHTIEYVLCVSHSTASYRLWALSIAHAQLSEVLWAMVVFVGGIGISGTAGFIA 810
Qy 770 VLVLPVIAFAVMTVAILLMEGLSAFLHALRLHWEVFNQKFGSGTGYKLSPPF 822
Db 811 VYVV--FFIFVLTISILVMEGLSAFLHALRLHWEVFNQKFGSGTGYKLSPPF 861

RESULT 7
T19492
hypothetical protein C26H9A.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19492
R;Smye, R.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z19131
A;Accession: T19492
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1236 <WIL>
A;Cross-references: UNIPROT:Q9XTS8; UNIPARC:UPI000017B7C6; EMBL:Z99169; PIDN:CAB16306.1
A;Experimental source: clone C26H9A
C;Genetics:
A;Gene: CRSP:C26H9A.1
A;Map position: 4
A;Introns: 50/2; 107/2; 119/3; 151/1; 209/2; 327/3; 432/3; 451/3; 482/2; 524/3; 552/2; 5

Query Match 32.2%; Score 1375; DB 2; Length 1236;
Best Local Similarity 35.8%; Pred. No. 6.1e-92;
Matches 334; Conservative 148; Mismatches 321; Indels 130; Gaps 20;
Qy 3 SMFRSEVALVQLPPTAAAYTCVSRILGELGLVEFRDLNASVSFAFORFVVDVVRCEELE 62
Db 291 SMFRSDPMKLYQMLVKEAFECVBAEIGKHGNQVFDLNKMSLYSTFTVKQWRCEME 350
Qy 63 KTTFTFLOEV--RRAGLVLPKPG---RLPAPPPRDLRLRIQETERLAQELDRVGNQ 116
Db 351 RKLRFLEKQVITCKPGL---DPSIDYDLSAPTQAEMLQLEHKLQDLEREFELDNNDY 407
Qy 117 ALRAQLHQLHAALVLR-----QGHPEOLA-----AAHTDG-----ASE 150
Db 408 ALRKNLSKBEFLQVWRLVDEFFQVHKKEBAKARFERSATDDIEMFSKSGFGGLPSSN 467
Qy 151 RTPLLQAPGPHQDLRVNFVAGAVEPHKAPALERLLWRACRGFLIASFRLEQPLEHPVT 210
Db 468 EMLTLPILG---SDDNANFVAGVLPDLKKESEFVRLWRACRTAFVTSASFTVNDPVT 524
Qy 211 GEPATWMTFLISYWGBOIGQIKIRICTCFHCHVFPFLQOBEARLQALQOQSQELQEV 270
Db 525 LEPLQRCVFTVFFKGSRLRIVEKVCDFGNATQYPCPKSKDRKMKMSETEGRMDLTVV 584
Qy 271 LGTERFLSVLGRVLQLLPPGQVQVHKMKAVYALALNQCSTVTHKCLIAEAWCSVRDLP 330

Db 585 IDTTQTHRYTILKDMSPFPIWLKNIQIQKSVFAVMNFTVD-TNGFLAGECWTAAABED 643
Qy 331 ALOEALRDSMEBEG--VSVAHRIPCDMPTTIRTNRTASTASFOGIVDRYGVGRYQEVNP 388
Db 644 DVRAQLHDGFKASCTEVEPILNELWNA PPTTFRHTNKTFTNVFQSVDSYGVSCYCEVNP 703
Qy 389 APTTIITFPFLPFAVMFGDVGHLLMFLFALAMVLAENRPAVKAAQNEIMWOTFFRGYRLLL 448
Db 704 APTTIITFPFLPFAVMFGDAAHGAILLAAFFIRNERKIESKIRDEIFNTFYGRYIMM 763
Qy 449 LMGFLSYTTCFYNECFSRATSPPSGWSVAAMANQSGWSDAFLA-----OHTMLTLDP 502
Db 764 LMGIFSYTGLYNDAPAKSFNVFGSGWSNSYNETQLDW--WIARSYRKHREYSLSLVP 820
Qy 503 NVTGVFLGPPGIDPIWSLAANHLSPNSFKMKMSVILGVVHNAFGVILGVVHNFHFGQ 562
Db 821 EKSPDIEKTYPPGVDPIWNIADNRLSFLNSMKMKASVLIIGITQMTFCGVFLSVLNHIHFKS 880
Qy 563 RHRLLLETLDELFLGLFGYLVFLVYIKWLCV-----WAARAASPSLIHFIN 611
Db 881 YIDIISNFIPOVIFLSCIFTYLCITQIIVKWIFFSVNAENVFGEYPGSGHCAPSLIGLIN 940
Qy 612 MELFSSHSPSNRL-----LYPREVVQATLVLAAMVPIILLIGTPL----- 652
Db 941 MFMPKRNENGLNENGEVSYNCHLGYWPNQRLVETILISISLACIPIMLFGKPLWRFV 1000
Qy 653 ----HLIHRHR--RRLRR--PADRQENKAGLLDLPDASVNGWSSDEKAGGLDEE 702
Db 1001 TSKRHKLOENKLSKLSLRNGTTVSAPTSPVVDAGPFRFEDAE--LLADE-----LDIGE 1053
Qy 703 EABLVPSEVLHQAIHTIEFCICVCSNTASYRLWALSIAHAQLSEVLWAMVNRIGLGLG 762
Db 1054 DIHHSLSIDIFVHQAIHTIEFVLGCVSHSTASYRLWALSIAHAQLSEVMMHMLVIGIHTV 1113
Qy 763 REV--GVAAVVLPV-----FAAFVMTVAILLV 789
Db 1114 DHIENTIAMCLKPVVACVGYFSASAIFFPCLTSLLYGKTYEKEKAPFFIASUSLSILIM 1173
Qy 790 MEGLSAFLHALRLHWEVFNQKFGSGTGYKLSPPF 822
Db 1174 MEGLSAFLHALRLHWEVFNQKFGSGTGYKLSPPF 1206

RESULT 8
H84600
probable vacuolar proton-ATPase subunit [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84600
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
eusa, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84600
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-821 <STO>
A;Cross-references: UNIPROT:Q9SJ77; UNIPARC:UPI000000A1530; GB:AE002093; NID:94567273;
C;Genetics:
A;Map position: 2
C;Superfamily: vacuolar ATP synthase 95K chain

Query Match 31.2%; Score 1331; DB 2; Length 821;
Best Local Similarity 37.3%; Pred. No. 5.8e-89;
Matches 317; Conservative 142; Mismatches 306; Indels 84; Gaps 20;
Qy 4 MFRSEVALVQLPPTAAAYTCVSRILGELGLVEFRDLNASVSFAFORFVVDVVRCEELE 63
Db 17 LMRSEVALVQLPPTAAAYTCVSRILGELGLVEFRDLNASVSFAFORFVVDVVRCEELE 76

Db 1 MSALGELSTHFKDLPDVPVAFQSFVRIRRLDTERLLRLYHLSIDLNGIHPDNLDP 60
QY 82 P--KGRLPAPPPDRLRLRQETTERLAQELRDVGNQALRAQ-LHQQLHAHV----- 131
Db 61 PSYSVLESSTIEDII---ERITREARVRQVLESSQLDEARYLQOLEFANVLTKADAPF 117
QY 132 -----LROGHEPQLAAAHDTGASERTPLIQ-----APGPHQDLRVNF 169
Db 118 SKSGNTVDFLRNNYETSSIFSGEDDTT--APLIENALELGTGTGTFDSEETSQOMTILDF 175
QY 170 VAGAVEPHKAPALERLLWRACRGFLIASPRELEQPLEHPV-TGEPATWMTFLISYWGEOI 228
Db 176 VSGIITPVKQFLERILMRTLGNLFIHQVRADDSLIHGAENKESKT--IFLVIAHGTQI 233
QY 229 GOKIRKIDTDPCHVPPFPLQEEARLGAQLQOQOQOELOEVLGETERLSQVLGRVLQ 288
Db 234 LURIRKISLSGATUFFVEEDAPGRTSQIQOANVSISDLNVALENTRSALYTELTFIASH 293
QY 289 LPFGQVQVHKMAVYLAALNQCSTVTHKCLIAEAWCSVRDLPALQELARDSS--MBEGVS 346
Db 294 ISAMEAVLHKDTVQVMNLFYDQNHKCLIAEGWCPTANLPVQKTLNLSDLTDSQAP 353
QY 347 AVAHRIPCDMPPTLIRNRTFASFGIVDRYGVGRYQVBNPAPYTIITFPFLFAMFGD 406
Db 354 TILNVHTSEQPTTFRVNKPTEGQSIIDSYGIATYREVNHGIVAIVTFPELFAIMFGD 413
QY 407 VGHGLLMFLFALAMVLAENRPAKAAQNEIMOTFFRGRVLLLMGLFSYITGFIYNECES 466
Db 414 LGHGAIMASVALMFLVYKTLGAKKDLDEIVGMVFYGRYIVLLMGLFSYVGFVNDLFS 473
QY 467 RATSIFFPSGWSVAAMANOSGM---SDAFLAQHTMLTLDPNVTGVFLGPYPFGIDPTWSLA 523
Db 474 KPMISFSSRWV-----WPKSEEAJAR-----AVQVGTYPIDPTWISA 513
QY 524 ANHLSFLNSFKMKSVILGVVHMAFGVILGVNVHVFQGRHLLLETPPELFLGLFGY 583
Db 514 DNNLFMSYKMKLSIILGHVHTFCLFLSLNYRFFKRLDIYAVFVPSLIFLEAIFGY 573
QY 584 LVFLVYKWLVCWAARAASPSLIIHFINMFLSHSPSNRLLYPROEVMQATVLAALAMV 643
Db 574 LVITIVKWCIDWKADLOPPSLNMLILMFLSPGLEQLPGQKYLQVGLVIAALICV 633
QY 644 PILLGTPHLHLHRRRLRRPADRQENKAGLL--DLPDASVNGWSSDEKAGGLDDE 701
Db 634 PWLLIVKPVLRWH-----SNEENKYSLSNDLPNV-----DEADALMAVDS 676
QY 702 EBAELPV---SEVLHQAHTHTIEFCGCVSNTASYLRMLWALSALAHQSEVLWAMVRIG 758
Db 677 QEKQAEPPFELGEVWTHQVHTTIEFCGCVSHTASYLRMLWALSALAHQSSVLWMMTLANG 736
QY 759 LGLGREVGVAAVLVPIFAAFVMTVAIILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYK 818
Db 737 FMGTGIVG--SIFVILFGFWFIATCVLVAMEGTSAMLSLRLHWVEGMSKHFGEGBYA 794
QY 819 LSPF 822
Db 795 FTFF 798
RESULT 12
H84685
probable vacuolar proton-ATPase subunit [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84685
R.Jlin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.
Nature 402, 761-769, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84685
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-780 <STO>
A:Cross-references: UNIPROT:Q9SK06; UNIPARC:UPI00000A9CB0; GB:AE002093; NID:G6598613;
C:Genetics:
A:Gene: At2g28520
A:Map position: 2
C:Superfamily: vacuolar ATP synthase 95K chain
Query Match 28.4%; Score 1210; DB 2; Length 780;
Best Local Similarity 35.3%; Pred. No. 3.6e-80;
Matches 301; Conservative 120; Mismatches 309; Indels 122; Gaps 17;
QY 4 MFRSEVALVOLFLPTAAAYTCVSRIGELGVFEFDLNASVSAFORRVVDVWRCCELEK 63
Db 13 LMRSEKMTVLQIIIPVESAHRSITYLGEGLGLQFLRDLDADKSPFQRTFANQVRCCEMR 72
QY 64 TPTFQEEVRRAGLVLPKGRLPAPPRDLRLRQETTERLAQELRDVGNQALRAQLH 123
Db 73 KLRFPKQIDKAGLRCSPP---RLETEPDIALGDLERQLADHEHEVLENNSENKLRQTYN 129
QY 124 QLOLHAALVLRQ-----GHEPQLAAAHDTGASERTPLQAPGG 160
Db 130 ELLEPKVILEKVGVPAPRLRSISISFLSLIKQLFYSQEMNPGHNSQSLR----- 180
QY 161 PHODLRVNFVAGAVEPHKAPALERLLWRACRGFLIASPRELEQPLEHPVTVGPATWMTFL 220
Db 181 -----FISGIINKDKLLKFERMLFRATRGNMLFNQTTSDDEEIMDPSTSEWVKVVF 232
QY 221 ISYWGEOIGQKIRKIDTCFHCHVFPFLQOEEARLGAQLQOQOQOESLQELVETERFLSQ 280
Db 233 VFFSEQARTKILKICEAFGANCYVPVEDTTKQRLTREVLRLSDELTADAGTHRRNN 292
QY 281 VLGRVLQQLPQOVQVHKMAVYLAALNQCSTVTHKCLIAEAWC-----SVRLPALQEL 336
Db 293 ALNSVGYSLTNWITTVRREKAVYDTLNLMLNFDVTKKLVGEGWCPTFAKTQTHEVLRAT 352
QY 337 ROSSMEEGVSVAHARIPCRDMPTLIRNRTFASFGIVDRYGVGRYQVBNPAPYTIIF 396
Db 353 FDSQSGVGV--IFHVMQAVESPTTYFRNKLNTNAFQEIIDAIVGARYQEANPANSVVTY 410
QY 397 PFLFAMFGDVGHGLLMFLFALAMVLAENRPAKAAQNEIMOTFFRGRVLLLMGLFSYI 456
Db 411 PFLFAMFGDMGHGICLLLGAL-YLLARERKLSQKLGSMEMLFQGRYVILLMALFSYI 469
QY 457 TGFVNECFSRATSIFFPSGWSVAAMANOSGMSDAFLAQHTMLTLDPNVTGV--FLGYPYP 514
Db 470 CGLIYNBFFSVFFHIF--GGS--AYKCRDITCSDAY-----TVGLIKYRDPYFP 514
QY 515 GIDPTWSLAANHLSPNSFKMKSVILGVVHMAFGVILGVNVHVFQGRHLLLETPSEL 574
Db 515 GVDPSNRGSRTELPYLSNLSKMKMSILLGIAQNNLGLIISFFNARFGSSLDTRYQFIPOM 574
QY 575 TFLGLGFLVPLVITYKWLVCWAARAASPSLIIHFINMFLSHSPSNRLLYPROEVMQAT 634
Db 575 IFLNSLFGVLSLLIIKW-C-----TGSQADLYHIV----- 604
QY 635 LVVLALAMVPTILLGTPLHLHRRRLRRRRPADRQENKAGLLDLPDASVNGWSDEEK 694
Db 605 LLLLFAPVAPWMLFPKPFALRKIHMERFQGRTYGVLVSVSEVDLDEPDSA----- 654
QY 695 AGGLDDEBEAEVLPSSEVLHMQAHTIEFCGCVSNTASYLRMLWALSALAHQSEVLWAMV 754
Db 655 RGGGHHBEFFNF--SEIFVHQLIHSIEFVIGSVSNTASYLRMLWALSALAHSELSTVPYEV 712
QY 755 MRIGLG-----LGREVGVAAVLVPIFAAFVMTVAIILLVMEGLSAFLHALRLHWVEFQNK 810
Db 713 LLLAWGYENILTRLIGV-----AVFAFATAPILLMMETLSAFLHALRLHWVEFMGK 763
QY 811 FVSGTGYKLSPP 822
Db 764 FFGDGYKFKPF 775

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 29, 2006, 12:59:44 ; Search time 308 Seconds
(without alignments)
2468.710 Million cell updates/sec

Title: US-10-783-519-2
Perfect score: 4266
Sequence: 1 MGSMPFSEVALVQLFLPTA.....HWVEFQNKFGYGTGYKLSPPF 822

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4249.5	99.6	830	1	VPP3 HUMAN
2	4235.5	99.3	830	2	Q8WVC5 HUMAN
3	3601.5	84.4	834	2	Q91W06 MOUSE
4	3600.5	84.4	834	2	Q9JHF5 MOUSE
5	3597.5	84.3	834	2	Q9JL12 MOUSE
6	3571.5	83.7	834	2	Q216B0 RAT
7	2670.5	62.6	837	2	Q918C8 CHICK
8	2370.5	55.6	823	2	Q5CZ26_XENTR
9	2369	55.5	822	2	Q7ZVM7 BRARE
10	2295.5	53.8	827	2	Q4R2B2_TETNG
11	2188	51.3	838	2	Q4RS23_TETNG
12	2149	50.4	854	1	VPP2_BOVIN
13	2146	50.3	856	1	VPP2_MOUSE
14	2145	50.3	856	2	Q216B1 RAT
15	2138	50.1	897	2	Q4SJ89_TETNG
16	2129	49.9	490	2	Q9CTA9 MOUSE
17	2119	49.7	856	2	G6NUM0 HUMAN
18	2116	49.6	856	1	VPP2_HUMAN
19	2068	48.5	839	2	Q918C9 CHICK
20	1954	45.8	838	1	VPP1_BOVIN
21	1950.5	45.7	831	1	Q8AVM5_XENLA
22	1944.5	45.6	839	1	VPP1_MOUSE
23	1943	45.5	832	2	Q3TWT5_MOUSE
24	1941	45.5	832	2	Q216B2 RAT
25	1940.5	45.5	839	2	Q216B3 RAT
26	1940	45.5	832	2	G6NXK6_MOUSE
27	1939	45.5	838	2	Q216B5 RAT
28	1938.5	45.4	845	2	Q216B4 RAT
29	1935	45.4	838	2	Q918D0_CHICK
30	1931	45.3	838	1	VPP1_RAT
31	1931	45.3	840	1	VPP4_HUMAN
32	1930	45.2	840	2	Q32M47_HUMAN
33	1928.5	45.2	837	1	VPP1_HUMAN
34	1927	45.2	840	2	Q7T1N8_TORMA
35	1927	45.2	846	2	Q6PA83_XENLA
36	1926.5	45.2	839	2	Q502H9_BRARE
37	1926.5	45.2	839	2	Q7T1N9_TORMA
38	1924.5	45.1	831	2	Q53ET5_HUMAN
39	1923.5	45.1	420	2	Q6P735 RAT
40	1921.5	45.0	837	2	Q5RSX1_PONPY
41	1920	45.0	838	2	Q5CZH6_HUMAN
42	1919.5	45.0	837	1	VPP1_PONPY
43	1918.5	45.0	831	2	Q53X12_HUMAN
44	1907.5	44.7	835	2	Q4S964_TETNG
45	1907.5	44.7	837	2	Q5R6N4_PONPY

RESULT 1

VPP3 HUMAN

ID VPP3 HUMAN STANDARD; PRT; 830 AA.

AC Q13488; 075877; integrated into UniProtKB/Swiss-Prot.

DT 01-DEC-2000, sequence version 2.

DT 07-FEB-2006, entry version 49.

DE Vacuolar proton translocating ATPase 116 kDa subunit a isoform 3 (V-

ATPase 116-kDa isoform a3) (Osteoclastic proton pump 116 kDa subunit)

DE (OC-116 kDa) (OC116) (T-cell immune regulator 1) (T cell immune

DE response cDNA7 protein) (TIRC7)

GN Name=TCIRG1; Synonyms=ATP6N1C, ATP6VOA3;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORM LONG).

RC TISSUE=Osteoclastoma;

RX MEDLINE=96158968; PubMed=8579597; DOI=10.1006/bbrc.1996.0145;

RA Li Y.P., Chen W., Stashenko P.;

RT "Molecular cloning and characterization of a putative novel human

osteoclast-specific 116-kDa vacuolar proton pump subunit.";

RL Biochem. Biophys. Res. Commun. 218:813-821(1996).

RN [2]

RP NUCLEOTIDE SEQUENCE (ISOFORM SHORT).

RA Utoku N., Heinemann T., Bulwin C.-G., Beinke S., Beato F., Randall J.,

Busconi L., Delphire E., Robertson E.R., Kojima R., Volk H.D.,

Malford B.L., Gullans S.R.;

RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE (ISOFORM SHORT).

RX MEDLINE=99263502; PubMed=10329006; DOI=10.1006/geno.1999.5751;

RA Heinemann T., Bulwin G.C., Randall J., Schnieders B., Sandhoff K.,

Volk H.D., Milford E., Gullans S.R., Ucku N.;

RT "Genomic organization of the gene coding for TIRC7, a novel membrane

protein essential for T cell activation.";

RL Genomics 57:398-406(1999).

RN [4]

RP VARIANTS OPTB1 ARG-405 AND LEU-444.

RX PubMed=11532986; DOI=10.1093/hmg/10.17.1767;

RA Sobacchi C., Frattini A., Orchard P., Porras O., Texcan I.,

Andolina M., Babul-Hirji R., Baric I., Canham N., Chitayat D.,

Dupuis-Girod S., Ellis I., Etzioni A., Fath A., Fisher A.,

Gerlitsen B., Gulino V., Horwitz E., Klamroth V., Lanino E.,

Mirollo M., Musio A., Matthijs G., Nonomaya S., Nocarangelo L.D.,

Ochs H.D., Superti Furga A., Valiaho J., van Hove J.L.K., Vihinen M.,

Vujic D., Vezzoni P., Villa A.;

RT "The mutational spectrum of human malignant autosomal recessive

osteopetrosis.";

RL Hum. Mol. Genet. 10:1767-1773(2001).

RN [5]

RP VARIANT OPTB1 ARG-405.

RX PubMed=12552563; DOI=10.1002/humu.10165;
 RA Scineca J.-C., Quincey D., Parrinello H., Romatet D., Grosgeorge J.,
 RA Guenday P., Philip N., Fischer A., Carle G.F.,
 RT "Novel mutations in the TCIRG1 gene encoding the a3 subunit of the
 RT vacuolar proton pump in patients affected by infantile malignant
 RT osteopetrosis.";
 RL Hum. Mutat. 21:151-157(2003).
 RN [6]
 RP VARIANTS OPTB1 PRO-141; ARG-405; ASN-462 DEL; ASN-517 AND ARG-775.
 RX PubMed=15300850; DOI=10.1002/humu.20076;
 RA Subani L., Pangrazio A., Sobacchi C., Taranta A., Mortier G.,
 RA Savarirayan R., Villa A., Orchard P., Vezzoni P., Albertini A.,
 RA Frattini A., Pagani F.,
 RT "TCIRG1-dependent recessive osteopetrosis: mutation analysis,
 RT functional identification of the splicing defects, and in vitro rescue
 RT by U1 snRNA.";
 RL Hum. Mutat. 24:225-235(2004).
 CC -|- FUNCTION: Part of the proton channel of V-ATPases (By similarity).
 CC Seems to be directly involved in T cell activation.
 CC -|- SUBUNIT: The V-ATPase is an heteromultimeric enzyme composed of at
 CC least thirteen different subunits. It has a membrane peripheral V1
 CC sector for ATP hydrolysis and an integral V0 for proton
 CC translocation. The V1 sector comprises subunits A-H, whereas V0
 CC includes subunits a, d, c, c', and c''.
 CC -|- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
 CC similarity).
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=Q13488-1; Sequences=Displayed;
 CC Name=Short;
 CC IsoId=Q13488-2; Sequences=VSP 000345;
 CC Note=No experimental confirmation available;
 CC -|- TISSUE SPECIFICITY: The long isoform is highly expressed in
 CC osteoclasts. The short isoform is highly expressed in thymus.
 CC -|- DISEASE: Defects in TCIRG1 are a cause of autosomal recessive
 CC osteopetrosis (OPTB1) [MIM:259700]; also called autosomal
 CC recessive Albers-Schönberg disease. Osteopetrosis is a rare
 CC genetic disease characterized by abnormally dense bone, due to
 CC defective resorption of immature bone. The defect is an
 CC heterogeneous disorder of bone metabolism, which, if untreated, has
 CC a fatal outcome. It occurs in two forms: a severe autosomal
 CC recessive form, occurring in utero, infancy, or childhood, and a
 CC benign autosomal dominant form, occurring in adolescence or
 CC adulthood. However, mild and atypical forms have also been
 CC reported. It is not known whether these latter cases represent
 CC separate nosological entities or a mild form of the recessive
 CC conditions. However, given the large number of genes and gene
 CC mutations associated with this condition a large spectrum of
 CC clinical manifestation is expected as seen in animal studies. The
 CC features of OPTB1 are macrocephaly, progressive deafness and
 CC blindness, hepatosplenomegaly, and severe anemia beginning in
 CC early infancy or in fetal life. Deafness and blindness are
 CC generally thought to represent effects of pressure on nerves.
 CC -|- SIMILARITY: Belongs to the V-ATPase 116 kDa subunit family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL; U45285; AAA97878.1; -; mRNA.
 CC EMBL; AF025374; AAC35742.1; -; mRNA.
 CC EMBL; AF033033; AAD31081.2; -; Genomic_DNA.
 CC Ensembl; ENSG00000110719; Homo sapiens.
 CC H-InvDB; HIX0009874; -;
 CC HGNC; HGNC:11647; TCIRG1.
 CC MIM; 259700; phenotype.
 CC MIM; 604592; Gene.
 CC DR GO; GO:005887; C:integral to plasma membrane; TAS.
 CC DR GO; GO:0005886; C:plasma membrane; TAS.
 CC DR GO; GO:0005215; P:transporter activity; TAS.
 CC DR GO; GO:0006968; P:cellular defense response; TAS.
 CC DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 CC DR GO; GO:0015992; P:proton transport; TAS.

DR InterPro: IPR002490; V_ATPase_sub116.
 DR PANTHER; PTHR11629; V_ATPase_sub116; 1.
 DR Pfam; PF01496; V_ATPase_1; 1.
 KW Alternative splicing; Disease mutation; Glycoprotein;
 KW Hydrogen ion transport; Ion transport; Membrane; Transmembrane;
 KW Transport.
 FT CHAIN 1 830 Vacuolar proton translocating ATPase 116
 FT kDa subunit a isoform 3.
 FT /FTId=PRO 0000119218.
 FT Extracellular (Potential).
 FT TOPO DOM 1 397 Potential.
 FT TRANSMEM 398 418 Potential.
 FT TRANSMEM 445 465 Potential.
 FT TRANSMEM 504 524 Potential.
 FT TRANSMEM 538 558 Potential.
 FT TRANSMEM 576 596 Potential.
 FT TRANSMEM 636 656 Potential.
 FT TRANSMEM 771 791 Potential.
 FT CARBOHYD 41 41 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 483 483 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 503 503 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 1 216 Missing (in isoform Short).
 FT /FTId=VSP 000345.
 FT A -> P (in OPTB1).
 FT VARIANT 141 141 /FTId=VAR 020988.
 FT VARIANT 405 405 G -> R (in OPTB1).
 FT VARIANT 444 444 /FTId=VAR 019589.
 FT VARIANT 462 462 R -> L (in OPTB1).
 FT VARIANT 517 517 /FTId=VAR 019570.
 FT VARIANT 775 775 Missing (in OPTB1).
 FT CONFLICT 377 377 /FTId=VAR 020989.
 FT CONFLICT 603 603 D -> N (in OPTB1).
 FT SEQUENCE 830 AA; 92998 MW; 62ECAF9A22DC698B CRC64;
 Query Match 99.6%; Score 4249.5; DB 1; Length 830;
 Best Local Similarity 99.8%; Pred. No. 1.3e-279;
 Matches 821; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 MGSMRSEVALVQLPPTAAAYTCVSRIGELGVEFRDLNASVSFAQRFPVVDVWRCEE 60
 DB 1 MGSMRSEVALVQLPPTAAAYTCVSRIGELGVEFRDLNASVSFAQRFPVVDVWRCEE 60
 QY 61 LEKTTFTLQEEVRRAGLVLPKPKRLPAPPDRLRIQEETERLAQELRDVRGNQALRA 120
 DB 61 LEKTTFTLQEEVRRAGLVLPKPKRLPAPPDRLRIQEETERLAQELRDVRGNQALRA 120
 QY 121 QLHQLHAAVLRLQGHFOLAAAHYTDGASERTPLLOAGPGPHQDLRVNPFVAGAVEPHKAP 180
 DB 121 QLHQLHAAVLRLQGHFOLAAAHYTDGASERTPLLOAGPGPHQDLRVNPFVAGAVEPHKAP 180
 QY 181 ALERLLWRACRGLFIASPRELEQPLEHPVTGPATWMTFLISYWGBOIGQKTKTKDCPH 240
 DB 181 ALERLLWRACRGLFIASPRELEQPLEHPVTGPATWMTFLISYWGBOIGQKTKTKDCPH 240
 QY 241 CHVFPFLQEEARLQALQQLQSQSQELQVGLGTERFLISQVLGRVLQLLPPQGVQVHKMK 300
 DB 241 CHVFPFLQEEARLQALQQLQSQSQELQVGLGTERFLISQVLGRVLQLLPPQGVQVHKMK 300
 QY 301 AVYLAHQCSVSTTHKCLIAEAWCSVRDLPALQELALRSSMEEGVSVAHRRIPCDMPPT 360
 DB 301 AVYLAHQCSVSTTHKCLIAEAWCSVRDLPALQELALRSSMEEGVSVAHRRIPCDMPPT 360
 QY 361 LIITNRFTASFGIVDRYGVGRYQEVNPAPYTIITFPFLFAVMFGDVGHGLMFLPALAM 420
 DB 361 LIITNRFTASFGIVDRYGVGRYQEVNPAPYTIITFPFLFAVMFGDVGHGLMFLPALAM 420
 QY 421 VLAENRPVAKAQNIEWTFFRGRYLLLMGLFSYTGFIYNECFSRATSIFFSGMSVAA 480
 DB 421 VLAENRPVAKAQNIEWTFFRGRYLLLMGLFSYTGFIYNECFSRATSIFFSGMSVAA 480

Qy 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGYPGIDPIWLSLAANHL SFLNSFKMKMSVI 540
 Db 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGYPGIDPIWLSLAANHL SFLNSFKMKMSVI 540
 Qy 541 LGVVMFAFVGVVGVFNHVFQQRHLLLETLPELTFLLGLFGYLVFLVIYKWLVCWAARA 600
 Db 541 LGVVMFAFVGVVGVFNHVFQQRHLLLETLPELTFLLGLFGYLVFLVIYKWLVCWAARA 600
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 Db 601 ASAPSILIHFNMFSLFHSNRLLYPRQEVVQATLVVLALAMVPIILLGLTPLHLHRRH 660
 Qy 660 RLRRRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLHQAIHT 719
 Db 661 RLRRRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLHQAIHT 720
 Qy 720 IEFCLGCVSNTASYLRWLWLSLAHAQQLSEVLWAMVMRIGLGLREVGVAAVVLPIPAAF 779
 Db 721 IEFCLGCVSNTASYLRWLWLSLAHAQQLSEVLWAMVMRIGLGLREVGVAAVVLPIPAAF 780
 Qy 780 AVMTVAILLVMEGLSAFLHALRLHWHVEFQNKFSYSGTGKLSPP 822
 Db 781 AVMTVAILLVMEGLSAFLHALRLHWHVEFQNKFSYSGTGKLSPP 823

RESULT 2

Q8WVC5 HUMAN
 ID Q8WVC5 HUMAN PRELIMINARY; PRT; 830 AA.
 AC Q8WVC5;
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 21-FEB-2006, entry version 10.
 DE T-cell, immune regulator 1, isoform a.
 GN Names=TCIRG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung and Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J.J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek A., Smailus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pancreas;
 RG NIH MGC Project;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC NIH MGC Project;
 RG

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

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CC
 DR EMBL; BC018133; AAH18133.1; -; mRNA.
 DR EMBL; BC032465; AAH32465.1; -; mRNA.
 DR Ensembl; ENSG00000110719; Homo sapiens.
 DR GO; GO:0016020; P:membrane; IEA.
 DR GO; GO:0015992; C:proton transport; IEA.
 DR InterPro; IPR002490; V ATPase sub116.
 DR PANTHER; PTHR11629; V ATPase sub116; 1.
 DR Pfam; PF01496; V ATPase I; 1.
 DR SQ SEQUENCE 830 AA; 92968 MW; 50751B41B171D9D2 CRC64;

Query Match 99.3%; Score 4235.5; DB 2; Length 830;
 Best Local Similarity 99.6%; Pred. No. 1.2e-278;
 Matches 820; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 Qy 1 MGSNFRSEEVALLVOLFLPTAAAYTCVSRGLGELGLVEFRDLNASVSATQRRFVVDVRCCE 60
 Db 1 MGSNFRSEEVALLVOLFLPTAAAYTCVSRGLGELGLVEFRDLNASVSATQRRFVVDVRCCE 60
 Qy 61 LEKTETFLQEEVRAGLVLPKGRLPAPPPRDLRLIQEETERLAQELRDVGRNQOALRA 120
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 Qy 121 QLHLQLHAAVLRQHEPQLAAAHDTGASERTPLLPQAPGGPHQDLRVNFVAGAVEPHKAP 180
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 Qy 181 ALERLLWRACRGFLIIASFRELEQPLEHPVTGEPATWMTFLISYMGEOIGQKIRKITDCFH 240
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 Qy 241 CHVPPFLQEEEARLQALQQLQOQSOELQEVLGETERFLSVGLRVLQLLPPGVQVHKMK 300
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 Db 661 RLRRRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLHQAIHT 720
 Qy 720 IEFCLGCVSNTASYLRWLWLSLAHAQQLSEVLWAMVMRIGLGLREVGVAAVVLPIPAAF 779
 Db 721 IEFCLGCVSNTASYLRWLWLSLAHAQQLSEVLWAMVMRIGLGLREVGVAAVVLPIPAAF 780
 Qy 780 AVMTVAILLVMEGLSAFLHALRLHWHVEFQNKFSYSGTGKLSPP 822

RP NUCLEOTIDE SEQUENCE
RX MEDLINE=20187595; PubMed=10722719; DOI=10.1074/jbc.275.12.8760;
RA Toyomura T., Oka T., Yamaguchi C., Wada Y., Futai M.;
RT "Three subunit a isoforms of mouse vacuolar H⁺-ATPase. Preferential
RT expression of the a3 isoform during osteoclast differentiation."; J.
RL J. Biol. Chem. 275:8760-8765(2000).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SV;
RX MEDLINE=20173225; PubMed=10709991; DOI=10.1016/S8756-3282(99)00278-1;
RA Scimeca J.-C., Franchi A., Trojani C., Parrinello H., Grosgeorge J.,
RA Robert C., Jaillon O., Poirier C., Gaudray P., Carle G.F.;
RT "The gene encoding the mouse homologue of the human osteoclast-
RT specific 116-kDa V-ATPase subunit bears a deletion in osteosclerotic
RT (oc/oc) mutants."; Bone 26:207-213(2000).
RL Bone 26:207-213(2000).
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CC
CC
CC ENBL; ABO22322; BAA93006.1; -; mRNA.
DR ENBL; AF188702; AAF37193.1; -; Genomic DNA.
DR Ensembl; ENSMUSG0000001750; Mus musculus.
DR MGI; MGI:1350931; Tcirlg1.
DR GO; GO:0016021; C:integral to membrane; RCA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0008553; F:hydrogen-exporting ATPase activity, phospho. .; RCA.
DR GO; GO:0006818; P:hydrogen transport; RCA.
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DR Pfam; PF01496; V_ATPase I; 1.
SQ SEQUENCE 834 AA; 93460 MW; E95ECD70C26367C0 CRC64;
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Matches 696; Conservative 51; Mismatches 74; Indels 7; Gaps 5;
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DB 481 AMANQSGWSDVLSQHSMLTINPNTGVFLGPPYFPGIDPLWSLATNHLSPINSFKKMSV 540

QY 540 ILGVVMAFGVVLGVFNHVFHQHRLLLLETLPELTLGLFGVLYFLVIYKMLCVWAAR 599
DB 541 ILGVVMAFGVFLSIENHVFHQHRLLLLETLPELTLGLFGVLYFLVIYKWNVSAAS 600
QY 600 AAS-PSLIHFIMNLFSPNSRLLYPROEVVQATLVIALAMVPTLLGTLPLHLI--H 656
DB 601 ASSAPSLIHFIMNLFPSQNTNHLHFHGOEVVQVYLVVLALATVPLLGLTPLYLRQH 660
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DB 661 RHRRTQRRPAGQDDEDTDKLASPDASTLNSWSDEEKAGSPGD--EETEFVPEIFMH 719
QY 715 QAIHTTIFELGCVNSNTASYLRWLWALSIAHQAQLSEVLWAMVRIGLGLGREGVAAVVLVP 774
DB 720 QAIHTTIFELGCVNSNTASYLRWLWALSIAHQAQLSEVLWAMVRIGLGLGREGVAAVVLVP 779
QY 775 IFAAFVMTVAIILLVMEGLSAFLHALRLHWVEFQNFYSCTGYKLSPP 822
DB 780 VFAAFVMTVAIILLVMEGLSAFLHALRLHWVEFQNFYSCTGYKLSPP 827
RESULT 5
Q9JUL12 MOUSE
ID Q9JUL12 MOUSE PRELIMINARY; PRT; 834 AA.
AC Q9JUL12;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Vacuolar proton-translocating ATPase 100 kDa subunit isoform a3.
GN Name=Tcirlg1; (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=20167151; PubMed=10702241; DOI=10.1074/jbc.275.10.6824;
RA Nishi T., Forgac M.;
RT "Molecular cloning and expression of three isoforms of the 100-kDa a
RT subunit of the mouse vacuolar proton-translocating ATPase."; J.
RL J. Biol. Chem. 275:6824-6830(2000).
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CC
CC EMBL; AF218253; AAF59822.1; -; mRNA.
DR Ensembl; ENSMUSG00000001750; Mus musculus.
DR MGI; MGI:1350931; Tcirlg1.
DR GO; GO:0016021; C:integral to membrane; RCA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0008553; F:hydrogen-exporting ATPase activity, phospho. .; RCA.
DR GO; GO:0006818; P:hydrogen transport; RCA.
DR InterPro; IPR002490; V_ATPase sub116.
DR PANTHER; PTHR11629; V_ATPase sub116; 1.
DR Pfam; PF01496; V_ATPase I; 1.
SQ SEQUENCE 834 AA; 93506 MW; EB8E42B45163004F CRC64;
Query Match 84.3%; Score 3597.5; DB 2; Length 834;
Best Local Similarity 84.1%; Pred. No. 2.5e-235;
Matches 696; Conservative 50; Mismatches 75; Indels 7; Gaps 5;
QY 1 MGSMFSESEVALVQLFPTAAATCTVSRIGELGLVEFRDLNASVSAPQRRFVVDVNRCEE 60
DB 1 MGSMFSESEVALVQLLPTGSAVNCVSQLGELGLVEFRDLNESVSAPQRRFVVDVNRCEE 60
QY 61 LEKTFPLEQEVRRAGLVLPKPKGRLLPAPPDRLLRIQETRLAQSLRDVVRGNQQAALRA 120
DB 61 LEKTFPLEQEVRRAGLVLPKPKGRLLPAPPDRLLRIQETRLAQSLRDVVRGNQQAALRA 120
QY 121 QLHQLQHLAAVLRQGHPEPQLAAHTDGA-SERTPLLAQPGGPHQDLKRVNFVAGAVEPHKA 179
DB 121 QLHQLRLHSAVLGQSHSPVVAADHTGPRSETTPLLPGTRGPHSDLKRVNFVAGAVEPYKA 180

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Db 121 QLHQLRLHSAVLGQSHSPVAAADHTGPPSETPTLLPGTRGPHSDLKVNFAVAGVEPYKA 180
QY 180 PALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEOIGQKIRKIDCF 239
Db 181 AALERLLWRACRGFLIASPRETEGQLEDVPTGEPATWMTFVSYWGEOIGQKIRKIDCF 240
QY 240 HCHVPPFLQOEBEARLQALQLOQOQOEVLGETERFLSGLVGRVLQLLPPGQVQVHKM 299
Db 241 HCHVPPLEQBEARPTLQLOQOQOQOEVLGETERFLSGLVGRVQVQVQVHKM 300
QY 300 KAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQALRDSSMEEGVSAVAHRIPCRDMP 359
Db 301 KAVYLALNQCSTVTHKCLIAEAWCAARDLPTVQALQSGSSEEGVSAVAHRIPCRDMP 360
QY 360 TLIRNRRPTASFOGIVDRYGVGRYQEVNPAPTYITITFPFLFAMFGDVGHGLMLFALA 419
Db 361 TLIRNRRPTASFOGIVDVGGRYREVNPAPTYITITFPFLFAMFGDVGHGLMLFALA 420
QY 420 MYLAENRPAVKAQAQNEIWQTFPRGRYLLMLGLFSIYTGFIYNECFSRATSIFPFGWSVA 479
Db 421 MYLTENRPAVKAQAQNEIWQTFPGGRYLLMLGLFSYTGFIYNECFSRATITFPFGWSVA 480
QY 480 AMANQSGSDAFLAQHTMLTLDPNVTGVFLGYPFGIDPIMSLAANHLSFLNSFKMKMSV 539
Db 481 AMANQSGSDEYLSQHSMLTNPNITGVFLGYPFGIDPIMSLATNHLNLSFLNSFKMKMSV 540
QY 540 ILGVHMAFGVVLGVFNHVFQORHRLLETLPELTFLGLFGYLVFLVYKWLVCWMAAR 599
Db 541 ILGVTHMAFGVFLSIFNHHVFQAHRLLETLPELTFLGLFGYLVFLVYKWLVCWMAAR 600
QY 600 AAS-PSILIHFINMFLFSGHSPNRLLYPROEVQVQVTLVLAAMVPILLLGTPHLH--H 656
Db 601 ASSAPSLIHFINMFLFSGHSPNTHLLPHQEVQVQVTLVLAAMVPILLLGTPHLHRLH 660
QY 657 RRRRLRRRPAQROBENKAGLLDLPDASV--NGWSSDEKAGGLDDEBEAEVLPSEVLH 714
Db 661 RRRRTORRPAQROBENKAGLLDLPDASV--NGWSSDEKAGGLDDEBEAEVLPSEV 719
QY 715 QAIHTIEFCGCSNTASVLRWALSLAHQSEVLWAMVNRIGLGLGREGVAAVVLVP 774
Db 720 QAIHTIEFCGCSNTASVLRWALSLAHQSEVLWAMVNRIGLGLGREGVAAVVLVP 779
QY 775 IFAPAVMTVAILLVMEGLSAFLHALRHLHWVEFQNKFSYSGTYKLSPP 822
Db 780 VFAAPAVLTVAILLVMEGLSAFLHALRHLHWVEFQNKFSYSGTYKLSPP 827

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RESULT 6

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Q216B0 RAT
ID Q216B0 RAT PRELIMINARY; PRT; 834 AA.
AC Q216B0
DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, sequence version 1.
DT 07-MAR-2006, entry version 1.
DE V-H-ATPase subunit a3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wistar;
RA Guyon S., Amar M., Fossier P., Morel N.;
RL "Neurons coexpress three different v-ATPase subunit a isoforms.";
RT Submitted (NOV-2005) to the EMBL/GenBank/DBSJ databases.
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CC -----
DR EMBL; DQ286426; AB91445.1; --; mRNA.
SQ SEQUENCE 834 AA; 93168 MW; 2E0DCFF9BED3979B CRC64;

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RESULT 7

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Q918C8 CHICK
ID Q918C8 CHICK PRELIMINARY; PRT; 837 AA.
AC Q918C8;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Vacuolar H(+) -transporting ATPase 116 kDa subunit, a3 isoform
DE (EC 3.6.1.35).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

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Query Match 83.7%; Score 3571.5; DB 2; Length 834;
Best Local Similarity 83.7%; Pred. No. 1.5e-233;
Matches 693; Conservative 53; Mismatches 75; Indels 7; Gaps 6;

QY 1 MGSFSEVALVQLFLPTAAAYTCVSRIGELGLVEFRDLNASVAFQRRFVVDVWRCEE 60
Db 1 MGSFSEVALVQLLLLTASAYNCVSQLGELGLVEFRDLNESVAFQRRFVVEVRCSE 60
QY 61 LEKTTFTFOEVRRAGLVLPKPKGRLPAPPPRDLRIQETRLAQELDRVGNQOALRA 120
Db 61 LEKTTFTFLREEVQRAGLTLTPPEGTLPAPPPRDLRIQETRLAQELDRVGNQOALRA 120
QY 121 QLHQLRLHSAVLQCHHEPQLAAAHDTG-ASERTPLQAPGGPHQDLRVNFAVAGVEPYKA 179
Db 121 QHQLQLHSAVLQGSHPAPMAAVHTGPTTERTPLLSATPGPHADLKVNFAVAGVEPYKA 180
QY 180 PALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEOIGQKIRKIDCF 239
Db 181 AALERLLWRACRGFLIASFKETEGQLEDVPTGEPATWMTFVSYWGEOIGQKIRKIDCF 240
QY 240 HCHVPPFLQOEBEARLQALQLOQOQOEVLGETERFLSGLVGRVLQLLPPGQVQVHKM 299
Db 241 HCHVPPLEQBEARLRTLQLOQOQOQOEVLGETERFLSGLVGRVQVQVQVQVHKM 300
QY 300 KAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQALRDSSMEEGVSAVAHRIPCRDMP 359
Db 301 KAVYLALNQCSTVTHKCLIAEAWCAARDLPTVQALQSGSSEEGVSAVAHRIPCRDMP 360
QY 360 TLIRNRRPTASFOGIVDRYGVGRYQEVNPAPTYITITFPFLFAMFGDVGHGLMLFALA 419
Db 361 TLIRNRRPTASFOGIVDVGGRYREVNPAPTYITITFPFLFAMFGDVGHGLMLFALA 420
QY 420 MYLAENRPAVKAQAQNEIWQTFPRGRYLLMLGLFSIYTGFIYNECFSRATSIFPFGWSVA 479
Db 421 MYLTENRPAVKAQAQNEIWQTFPGGRYLLMLGLFSYTGFIYNECFSRATITFPFGWSVA 480
QY 480 AMANQSGSDAFLAQHTMLTLDPNVTGVFLGYPFGIDPIMSLAANHLSFLNSFKMKMSV 539
Db 481 AMANQSGSDEYLSQHSMLTNPNITGVFLGYPFGIDPIMSLATNHLNLSFLNSFKMKMSV 540
QY 540 ILGVHMAFGVVLGVFNHVFQORHRLLETLPELTFLGLFGYLVFLVYKWLVCWMAAR 599
Db 541 ILGVTHMAFGVFLSIFNHHVFQAHRLLETLPELTFLGLFGYLVFLVYKWLVCWMAAR 600
QY 600 AAS-PSILIHFINMFLFSGHSPNRLLYPROEVQVQVTLVLAAMVPILLLGTPHLHRLH- 657
Db 601 ASSAPSLIHFINMFLFSGHSPNTHLLPHQEVQVQVTLVLAAMVPILLLGTPHLHRLH 660
QY 658 HRRRLRRRP-ADROBENKAGLLDLPDASV--NGWSSDEKAGGLDDEBEAEVLPSEVLH 714
Db 661 HRRRTORRPAQROBENKAGLLDLPDASV--NGWSSDEKAGGLDDEBEAEVLPSEV 719
QY 715 QAIHTIEFCGCSNTASVLRWALSLAHQSEVLWAMVNRIGLGLGREGVAAVVLVP 774
Db 720 QAIHTIEFCGCSNTASVLRWALSLAHQSEVLWAMVNRIGLGLGREGVAAVVLVP 779
QY 775 IFAPAVMTVAILLVMEGLSAFLHALRHLHWVEFQNKFSYSGTYKLSPP 822
Db 780 VFAAPAVLTVAILLVMEGLSAFLHALRHLHWVEFQNKFSYSGTYKLSPP 827

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OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=white leghorn; TISSUE=Bone;
RX MEDLINE=20325091; PubMed=10866814;
RA Mattsson J.P., Li X., Peng S.B., Nilsson F., Andersen P.,
RT Lundberg L.G., Stone D.K., Keeling D.J.,
RT "Properties of three isoforms of the 116-kDa subunit of vacuolar H+-
ATPase from a single vertebrate species. Cloning, gene expression and
RT protein characterization of functionally distinct isoforms in Gallus
RT gallus";
RL Eur. J. Biochem. 267:4115-4126 (2000).
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CC -----
CC ENBL; AJ289021; CAB93529.1; -; mRNA.
DR Ensembl; ENSGALG0000003516; Gallus gallus.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0020037; F.heme binding; IEA.
DR GO; GO:0016787; F.hydroxylase activity; IEA.
DR GO; GO:0006118; P.electron transport; IEA.
DR GO; GO:0015992; P.proton transport; IEA.
DR InterPro; IPR012282; Cytochrome_c_r.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR002490; V_ATPase_sub116.
DR PANTHER; PTHR11629; V_ATPase_sub116; 1.
DR Pfam; PF01496; V_ATPase_1; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
KW Hydroxylase.
SQ SEQUENCE 837 AA; 94421 MW; F5E91863B4530300 CRC64;

Query Match 62.6%; Score 2670.5; DB 2; Length 837;
Best Local Similarity 64.2%; Pred. No. 2.2e-172;
Matches 536; Conservative 85; Mismatches 195; Indels 19; Gaps 9;

QY 1 MGSFSESEVALVQLFPTAAATCYSLGELGVFERDLNASVSAPQRFVVDVVRCEE 60
DB 1 MGSFSESEVCLAQFLHSASVCSVSELGERLLEFRDLNPHVSAPQRFVGEVRCEE 60

QY 61 LEKTFTFLOBEVVARAGLVLPPLPPGRPLPAPPRLRLRIQEETERLAELDRVRCNQALRA 120
DB 61 MEKTFTFLOELHAGRGVLGCTENPAPVAREALRVQSEQLARELREVSRRALRG 120

QY 121 QLHLQHLAAVLRQHGHE-----POLAAHTDGASERTPLLPQAGPHQDLRVNFVAGAV 174
DB 121 RLQDLRLYLHLVLRGQRLTSMPPGPGSPSSRAFSSEHEPLDPSVHHLDRKINFVTGVI 180

QY 175 EPHKAPALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEOIGQKIRK 234
DB 181 HPMRVNAFERLLWRACRGVYLVASFVEMPEPLEDPTGTSVTWVIFLISYWGEOIGQKIRK 240

QY 235 ITDCFCHVFPFPLQEQEARLGALQQLQOQSQELQEVLTETTERFLSOVLGRVLQLLPPGV 294
DB 241 ISDCFCHVFPYEPESASRADTLNGVLSQDLVSVLVEETEQLAQVLQDKVIALPSWRV 300

QY 295 QVHKMAVYALNQCQSVSTTHKCLIAEAWCSVRDLPALQELALDSSMEEG--VSVAHRI 352
DB 301 QVQKMAIYLVNLQCSLDVTEKCLIAEAVMCPQDLFQVQELAFQGVKSGSSVECFQRI 360

QY 353 PCEDMPTLIRNRTFTASFGIYDRYGVGRYQVNPAPYITITFPFLPAMFGDVGHGLL 412
DB 361 PTLESPTLIRTNKFTAGFQSIYDAYGVASYQVNPAPYAITITFPFIFAMFGDVGHGLL 420

QY 413 MELPALAMVLAENRPAVKAQNEIMQTEFRGRVYLLLMGLFSITYTGFYNECFSRATSLF 472
DB 421 MELPALAMVLFENSPSLQQSQSNEIMQFFKGRVLIILMGAFSITYTGFYNECFSKATVIF 480

QY 473 PSQSWVAAMNOSGWSDAFLAQHTMLTLDPNVTGVFLGYPFGIDPISLANHLSFLNS 532
DB 481 PSAMSVAATMANHSSWSAYLATHQSLLTLDPNVTGVFRGYPFGIDPISLANHLSFLNS 540

QY 533 FRKMSVILGVVMAFGVVLGVFNHVFHQHRLLELTLELTPLLGLFGVLPVLYYKW 592
DB 541 FRKMSVILGVVHMGVGLGVFNHVFHQHRLLELLELTPLLGLFGVLPVLYYKW 600

QY 593 LCYWAARA-ASPSILIHPIFMFLFSHPNRLYPROEVQATLVIALAMVPTLLGTP 651
DB 601 VKFSAVDSQVAPSIILHIFDMFLFTSNADNLPYRGQVPQMWLVVLLALSVPLLLGTP 660

QY 652 LHLL-HRRHRRRLRRPADROENKAGLLDLPDA--SYNGWSSDEEKAGGLDDEEAEALVP 708
DB 661 LYLKQKRRRRANSIPPAATVEQEP-LLEGQAGNSVNATKEDVESGHHGPDAAHMDF-- 717

QY 709 SEVLMQAIHTIFCIGCVSNTASYLRWALSALHAQLSVLWAMVWRIG-LGLGREVG 767
DB 718 SEVFMQAIHTIFCIGCVSNTASYLRWALSALHAQLSVLWAMVWRIG-LGLGREVG 774

QY 768 AAVLVLPFAAFVAVMTVAILLVMEGLSAFLHRLHWHVEFQNKFSYGTGKLSPPF 822
DB 775 GGVLPVFAAFVAVLTVAILLVMEGLSAFLHRLHWHVEFQNKFSYGTGKLSPPF 829

RESULT 8

Q5CZ26 XENTR PRELIMINARY; PRT; 823 AA.
AC Q5CZ26;
DT 29-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 29-MAR-2005, sequence version 1.
DE 07-FEB-2006, entry version 7.
DE MGC108034 protein.
GN Name=MGC108034;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywicki M.I., Skalek U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole body;
RX Klein S., Kleier D.S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; BC090359; AAH90359.1; -; mRNA.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0015992; P.proton transport; IEA.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR002490; V_ATPase_sub116.

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DR PFam; PF01496; V_ATPase_I; 1.
DR PROSITE; P80041; HTH_ARAC_FAMILY_1; UNKNOWN 1.
SQ SEQUENCE 823 AA; 93940 MW; F88783693BF5C23C CRC64;

Query Match 55.6%; Score 2370.5; DB 2; Length 823;
Best Local Similarity 56.7%; Pred. No. 5.2e-152;
Matches 476; Conservative 121; Mismatches 203; Indels 39; Gaps 10;

QY 1 MGSFRSEVALVOLPLPTAAAYTCVSRGLGELVEFRDLNASVSFAQRRFVVDVNRCEE 60
DB 1 MGSFRSEVALVOLPLPTAAAYTCVSRGLGELVEFRDLNASVSFAQRRFVVDVNRCEE 60
QY 61 LEKTTFFLOEVRAGLVPPKGRLPAPPDRLRIQETERLAQELDRVGNQOALRA 120
DB 61 LEKTTFFLOEVRAGLVPPKGRLPAPPDRLRIQETERLAQELDRVGNQOALRA 120
QY 61 METTFSYLERLRKAGVQAPESMPPALPDRATRMQBEESQLAKELREVSQNRQTLOE 120
DB 61 METTFSYLERLRKAGVQAPESMPPALPDRATRMQBEESQLAKELREVSQNRQTLOE 120
QY 121 QLHQQLLHAALVRQGHGHE---POL-AAAHDTGASERTPLLOAPEGPHQDLRVNFFVAGAVEP 176
DB 121 QLHQQLLHAALVRQGHGHE---POL-AAAHDTGASERTPLLOAPEGPHQDLRVNFFVAGAVEP 176
QY 121 RLRELLEYANILRESQRFPTGLLEGEAQWKDRSEDDPLLDPAVNKQDLRVSMAGVIHP 180
DB 121 RLRELLEYANILRESQRFPTGLLEGEAQWKDRSEDDPLLDPAVNKQDLRVSMAGVIHP 180
QY 177 HKAPALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYMGEOIGQIRKIT 236
DB 177 HKAPALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYMGEOIGQIRKIT 236
QY 181 WMNMFERLLWRACRGFLIVNFMSEPMEDIVTGESVTQIIIFLISYMGKEIKKIXA 240
DB 181 WMNMFERLLWRACRGFLIVNFMSEPMEDIVTGESVTQIIIFLISYMGKEIKKIXA 240
QY 237 DCFHCHVFPFLOQEEARLQALQOQSOELQEVLTGETERFLSQVLGRVLQLLPQGVQV 296
DB 237 DCFHCHVFPFLOQEEARLQALQOQSOELQEVLTGETERFLSQVLGRVLQLLPQGVQV 296
QY 241 NCFHCHVFPYADDETSLRLETNLVQIDQMVKVLLQTEGYSQVLSRAASALHHWRVSV 300
DB 241 NCFHCHVFPYADDETSLRLETNLVQIDQMVKVLLQTEGYSQVLSRAASALHHWRVSV 300
QY 297 HMKAVYIALNOCVSTTHKCLIAEAWCSVRDLPALQEAIRDSSMBE--GVSAAVAHRIPC 354
DB 297 HMKAVYIALNOCVSTTHKCLIAEAWCSVRDLPALQEAIRDSSMBE--GVSAAVAHRIPC 354
QY 301 RMKHVYILNLCSV--RERCCLIGVWCPVVDLPILLQSAITRASESSGGGGSFCHRIPC 358
DB 301 RMKHVYILNLCSV--RERCCLIGVWCPVVDLPILLQSAITRASESSGGGGSFCHRIPC 358
QY 355 RDMPTLTIRTNFTASFGQIDVDRYGVGRYOENVAPYTIITPPFLFAVMFGDVGHLLMF 414
DB 355 RDMPTLTIRTNFTASFGQIDVDRYGVGRYOENVAPYTIITPPFLFAVMFGDVGHLLMF 414
QY 359 AFSPTLTIRTNKTSFGQIDVDRYGVGRYOENVAPYTIITPPFLFAVMFGDVGHLLMF 418
DB 359 AFSPTLTIRTNKTSFGQIDVDRYGVGRYOENVAPYTIITPPFLFAVMFGDVGHLLMF 418
QY 415 LPALAMVLAENRPVAKAQNQETWQTFRRGRYLLMLGLFSIYGTIYNCFSRATSIIPS 474
DB 415 LPALAMVLAENRPVAKAQNQETWQTFRRGRYLLMLGLFSIYGTIYNCFSRATSIIPS 474
QY 419 LPALAMVLAENRPVAKAQNQETWQTFRRGRYLLMLGLFSIYGTIYNCFSRATSIIPS 478
DB 419 LPALAMVLAENRPVAKAQNQETWQTFRRGRYLLMLGLFSIYGTIYNCFSRATSIIPS 478
QY 475 GHSVAMANQSGWSDAFLAQHTMLTLDNPNVTGVFLGPPYFPGIDPTIWSLAANHLSFLNSPK 534
DB 475 GHSVAMANQSGWSDAFLAQHTMLTLDNPNVTGVFLGPPYFPGIDPTIWSLAANHLSFLNSPK 534
QY 479 GHSVAMARANNWTSDSKLPPIPLNPNITGVFTAPYFPGIDPTIWSLAANHLSFLNSPK 538
DB 479 GHSVAMARANNWTSDSKLPPIPLNPNITGVFTAPYFPGIDPTIWSLAANHLSFLNSPK 538
QY 535 MMSVILGVVHMAFGVLGVNHNHFGQHRLLLETLPELTLGLFGVLFLVLYKWL 594
DB 535 MMSVILGVVHMAFGVLGVNHNHFGQHRLLLETLPELTLGLFGVLFLVLYKWL 594
QY 539 MMSVILGVVHMAFGVLGVNHNHFGQHRLLLETLPELTLGLFGVLFLVLYKWL 598
DB 539 MMSVILGVVHMAFGVLGVNHNHFGQHRLLLETLPELTLGLFGVLFLVLYKWL 598
QY 595 VNAARAA--SPSILIHFMFLFSHSPSNRLLYPROQEVQATLVVLALAMVPIILLGTPLH 653
DB 595 VNAARAA--SPSILIHFMFLFSHSPSNRLLYPROQEVQATLVVLALAMVPIILLGTPLH 653
QY 599 LTAEADAENAPSILIHFMFLFTQNGRDLVQGGQVQVTVLIVAILCIPVLLIGDPIC 658
DB 599 LTAEADAENAPSILIHFMFLFTQNGRDLVQGGQVQVTVLIVAILCIPVLLIGDPIC 658
QY 654 LLHRRRRLRRPADQSENKAGLLDLPDASVNGWSSDEEAKAGGLDDE-----BEA 704
DB 654 LLHRRRRLRRPADQSENKAGLLDLPDASVNGWSSDEEAKAGGLDDE-----BEA 704
QY 659 LLIOHRSK-----KDSHQNRCSL-----NNGDREALLEDEITVPTGHGHS 701
DB 659 LLIOHRSK-----KDSHQNRCSL-----NNGDREALLEDEITVPTGHGHS 701
QY 705 ELVPSVLMHQAHITIEFCGCVSNSTASYLRWLALSLAHQOLSEVLMAVMWRIIG-LGR 763
DB 705 ELVPSVLMHQAHITIEFCGCVSNSTASYLRWLALSLAHQOLSEVLMAVMWRIIG-LGR 763
QY 702 KPDREVFPMHMIHTIEYCLGCSINTASYLRWLALSLAHQOLSEVLMAVMWRIIG-SLSL 761
DB 702 KPDREVFPMHMIHTIEYCLGCSINTASYLRWLALSLAHQOLSEVLMAVMWRIIG-SLSL 761
QY 764 EYGVAAVVLVPIFAAFVMTVAILLVMEGLSFAFLHALRLHWFEQNFQYSGTGKLSPPF 822
DB 764 EYGVAAVVLVPIFAAFVMTVAILLVMEGLSFAFLHALRLHWFEQNFQYSGTGKLSPPF 822
QY 762 TWG----IVLVPIFAFVAVLTVAILLMEGLSFAFLHALRLHWFEQNFQYSGTGKLSPPF 817
DB 762 TWG----IVLVPIFAFVAVLTVAILLMEGLSFAFLHALRLHWFEQNFQYSGTGKLSPPF 817

RESULT 9
Q7ZVM7 BRARE PRELIMINARY; PRT; 822 AA.
AC Q7ZVM7
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Zgc:55891.
```

296 VHKMAYVLAALNOCVSSTHKLIAEAWCSVRDLPALQOALRDSSMEEG--VSAVAHRIP 353
292 VQKCAVQTVNLCSPTDKCLIAEAWCPVSQLPALQOALRDSSMEEG--VSAVAHRIP 351
354 CRDMPPTLIRNRTAFSGQIVDRYGRYQEVNPAVYTIITPFLFAVFGDVGHLGM 413
352 ATTSPTLPNTSPTAGFQSDVAYGVASVYVNPVAVYTIITPFLFAVFGDVGHLGM 411
414 FLFALAMVLAENRPAVKAQNEIWQTFPRGRYLLMLLGLFSIYTGFIYNECFSRATIFP 473
412 TLAALMWLENDPKLAKNTNEIWRMFMGGRYLLMLLGLFSIYTGFIYNECFSRATIFP 471
474 SGWSVAAMNOCWSGDAFLAQHTMLTLDPNVTGVFLGPGDIPWLSAANHLSELSNF 533
472 SGHVRNPAEYVNWTESTFKKMYLSLDPNVTGVFTGYPFGDIPWGLANNHLTFLNSY 531
534 KMKMSVILGVVHMAFGVGLVFNHFGQRHRLLETLPELTFLGLGFLVFLVIYKWL 593
532 KMKMSVILGVVHMAFGVGLVFNHFGQRHRLLETLPELTFLGLGFLVFLVIYKWL 591
594 CWAARA-ASPSILIHFINMFLSHSPSNRLLYPRQEVQATLVLAAMVPIILLGTPL 652
592 VYGFVNSDSAPSILIHFINMFLSHSPSNRLLYPRQEVQATLVLAAMVPIILLGTPL 651
653 HLLHRRRRRRRPPADROBENKAGLLDLPDASVNGWSDEKAGGLDDEEAEIIVPSEVL 712
652 QEYLSHKKRRKNTGDRP-----LAEANGSINSQGDVARGGGGGESE-BFDTANVF 704
713 MQQAIHTIEFCGVCNSTASYLRWLWLSLAHAQSEVLWAMVNRIGLGLGREVGVAIVL 772
705 MQQAIHTIEFCGVCNSTASYLRWLWLSLAHAQSEVLWAMVNRIGLGLGREVGVAIVL 762
773 VPIPAFAMVMAVAILMEGLSAPLHARLHWVEFQNKFGYKLSPPF 822
763 ALVFEVGFVAVLTSLVMEGLSAPLHARLHWVEFQNKFGYKLSPPF 812

RESULT 10
Q4R2B2_TETNG
ID Q4R2B2_TETNG PRELIMINARY; PRT; 827 AA.
AC Q4R2B2;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome 1 SCF14944, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG00026564001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphia; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaut S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.,
RA Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Croliis H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX Genoscope; Whitehead Institute Centre for Genome Research;
RP

Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.

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EMBL; CAAE01014944; CAG06270.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR002490; V:ATPase subunit 6.
DR PANTHER; PTHR11629; V:ATPase subunit 6.
DR Pfam; PF01496; V:ATPase_1; 1.
FT NON_TER 827 827
SQ SEQUENCE 827 AA; 93857 MW; DE6E5AF8679C107A CRC64;

Query Match 53.8%; Score 2295.5; DB 2; Length 827;
Best Local Similarity 55.9%; Pred. No. 6.5e-147;
Matches 468; Conservative 120; Mismatches 220; Indels 29; Gaps 11;

QY 1 MGSMPRESEVALVQLFPTAAAYTCVSRGELGLVEFRDLNANASVAFQRRFVVDVMRCEE 60
DB 1 MGSIFRSEEVCLVQLFLOSSAYNCVSELGELGLVEFRDLNPNVAFQRFVGEVRCEE 60
QY 61 LEKTFPTLOEEVRRAGLVLPKGRLP-----APPDRLRIQEETERLAQELRVRG 113
DB 61 LEKTFPTLOEEVRRAGLVLPKGRLP-----APPDRLRIQEETERLAQELRVRG 118
QY 114 NQALRAQLHQLHAALVROGHEPQLAAHTDQASERTPLQAPG--GHQDLRVNFA 171
DB 119 NRDSLRAQLTQLCOYRGVLRTRH-----SITASQAPPPVLESQGLFENRDVRLSFA 172
QY 172 GAYEPHKA PALERLLWRACRGFLIASFRELEQLEHPVTGEPATWTMTFLISYGEQIGQK 231
DB 173 GVVHPKVASFERLLWRACRGFLIASFRELEQLEHPVTGEPATWTMTFLISYGEQIGQK 232
QY 232 IRKTCDFCHVFPFLOQEEARLQALQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 291
DB 233 VKKICDFCHVFPFLOQEEARLQALQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 292
QY 292 GOVQVHKMAVLAALNOCVSSTHKLIAEAWCSVRDLPALQOALRDSSMEEG--VSAVA 349
DB 293 WKVRQCKAVQTVNLCSPTDKCLIAEAWCPVSQLPALQOALRDSSMEEG--VSAVA 352
QY 350 HRPICRDMPTLIRNRTAFSGQIVDRYGRYQEVNPAVYTIITPFLFAVFGDVG 409
DB 353 NRLATSTPTLPNTSPTAGFQSDVAYGVASVYVNPVAVYTIITPFLFAVFGDVG 412
QY 410 GLMLFLFALAMVLAENRPAVKAQNEIWQTFPRGRYLLMLLGLFSIYTGFIYNECFSRAT 469
DB 413 GILMTLAALMWLENDPKLAKNTNEIWRMFMGGRYLLMLLGLFSIYTGFIYNECFSRAT 472
QY 470 STPPSGWSVAAMNOCWSGDAFLAQHTMLTLDPNVTGVFLGPGDIPWLSAANHLSELSNF 529
DB 473 STFNSGHVKRPMDDNNVNSVLSGTQFLPMDVVPVFTSPYFPFGDIPWGLANNHLTFLNSY 532
QY 530 LNSFKMMSVILGVVHMAFGVGLVFNHFGQRHRLLETLPELTFLGLGFLVFLVIYKWL 589
DB 533 LNSYKMSVILGVVHMAFGVGLVFNHFGQRHRLLETLPELTFLGLGFLVFLVIYKWL 592
QY 590 YKWLCVWAARA-SPSILIHFINMFLSHSPSNRLLYPRQEVQATLVLAAMVPIILLGTPL 648
DB 593 FKWIVVTPAQSKFAPSILIHFINMFLSHSPSNRLLYPRQEVQATLVLAAMVPIILLGTPL 652
QY 649 GTPL--HLLHRRRR--PLRRRPPADROBENKAGLLDLPDASVNGWSDEKAGGLDDEEAE 705
DB 653 GKPICKVYTKRRSHVTSGLCKQEDRHLPMG--DSSINTSRSGEVEG--STENEAV 708
QY 706 LVPSEVLHMQAIHTIEFCGVCNSTASYLRWLWLSLAHAQSEVLWAMVNRIGLGLGREVG 765
DB 709 FDTADVLMHQAHTIEFCGVCNSTASYLRWLWLSLAHAQSEVLWAMVNRIGLGLGREVG 768

766 GAAAVLVPIFAFAVMTVAILLVMEGLSAFLHALRLHWVEFQNFYSGTGKLSPP 822
 769 G--AAVLFVPAFAVLTVSIILLMEGLSAFLHALRLHWVEFQNFYSGTGKLSPP 823

RESULT 11

QARSZ3 TETNG
 ID QARSZ3_TETNG PRELIMINARY; PRT; 838 AA.
 AC QARSZ3_TETNG
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Chromosome 12 SCAP14999, whole genome shotgun sequence. (Fragment).
 OS ORFNames=GSTENG0029489001;
 GN Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthopterygii; Acanthopterygii; Perciformes; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OC NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jallion O., Aury J.-M., Brunet P., Petit J.-L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,
 RA Desliva C., Salancoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.-N., Gulgo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype."
 RL Nature 431:946-957(2004).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBSJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

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CC -----
 CC EMBL; CAAG01014999; CAG08489.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0020037; F:heme binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0015992; P:proton transport; IEA.
 DR InterPro; IPR002355; Cu oxidase Cu BS.
 DR InterPro; IPR002490; V:ATPase sub16.
 DR PANTHER; PTHR11629; V:ATPase sub116; 1.
 DR Pfam; PF01496; V:ATPase_1; 1.
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
 DR NON_TER 838
 SQ SEQUENCE 838 AA; 96100 MW; 5B871FC22DA381EA CRC64;

Query Match 51.3%; Score 2188; DB 2; Length 838;
 Best Local Similarity 52.4%; Pred. No. 1.3e-139;
 Matches 437; Conservative 130; Mismatches 247; Indels 20; Gaps 8;

QY 1 MGSMFRSEVALVQLFLPTAAATCVSRIGELGLVEFRDLNASAFQRRFVVDVWRCCE 60
 Db 1 MGSLFRGEICLAQLQAGSAYDCISLSELGLVEFRDLNPTVTFQRYKYSIKKCE 60
 QY 61 LEKTFPQEEVRRAGLVLPKPKGLPAPPDRLRIQETRLAQELRDVGNQOALRA 120
 Db 61 MERILGYLMKEVKKADI SLPEGDVNPPIAPLPKPHILSIMEQLQRLVELGVEVTKNKEQLR 120

QY 121 QL-----HQQLHAAVLRQGHREPOLAAAHDTGAS--ERTPLQAPGPHQDLRVNFA 171
 Db 121 NLLELLEYHMLRITRNFVQSAERNAQLHYEEFFLEKDTMDYSSMRQLGAKLGFVS 180
 QY 172 GAVEPHKAPALRLWRACRGFLIASFRELEOPLBHPVTGBPATWMTFLISYWGEOIGOK 231
 Db 181 GIIQVKTAEFERMLRWCKYITILTYAEVYLENPDGTGETKSVVFLISFWGEIQGK 240
 QY 232 IRKITDCFHCHVFPFLQOEERLALQQLQOQSQELQEVIGETERFLSQVLGRVLQLPP 291
 Db 241 VKKICDCYCHLYPYPSSNEERNDVLEGLKTRIQDLHTVLHRTEDYLRQVLVKASSEIYT 300
 QY 292 GOVQVHKKAVYALALNQCQSVSTTHKCLTAECVSRDLPALQEARLDSMEG--VSAVA 349
 Db 301 WTIQVKMKAIYIILNLCSDFTNKCLTAECVSRDLPALQEARLDSMEG--VSAVA 360
 QY 350 HRIPCRDMPPTLIRNRTFTASFGQIVDRYGVQYOVNAPVYTIITFPFLFAMFGDVGH 409
 Db 361 NRIPTSSPTLIRNRTFTSGFQINVDAYGVQSYREVNPAPFTIITFPFLFAMFGDLGH 420
 QY 410 GLLMFLFALAMVLAENRPAVKAQNEIWQTFGRYLLMLGLFSIYTGFIYNECFSRAT 469
 Db 421 GLIMAFAMVLYENNRKVKXTRNEIWNMPPEGRVYIILMMGLFSIYTGFIYNDGFSKSL 480
 QY 470 SIPTSGMSVAMANQSGHSDAFLAOTHTLTDNPVTGYPGLGYPGIDPINSIAHLSP 529
 Db 481 NIFSGMSVAMAFRENVMQDDVYGNRFLTDNPVTGYPGLGIDPINSIAHLSP 540
 QY 530 LNSPFMKMSVILGVVHMAFGVVLGVNFVHVFQHRHLLETPELTFLGLGFLVFLVI 589
 Db 541 LNSYFKMSVILGVVHMAFGVVLGVNFVHVFQHRHLLETPELTFLGLGFLVFLVI 600
 QY 590 YKWLVCWAAARAA-SPSIIHFINMFLPSHSPSNRLLYPRQEVVQATLVVLAAMVPILL 648
 Db 601 YKWLAFSAKDSKSHAPSVLTHFINMFLMQGS-AMQPLYPQNGQLFVWVIAVLSVPVFL 659
 QY 649 GTPLHLHLHRRRLRRRPAQRQENKAGLLDLPDASVNGWSDEEKAGGLDDEEAEVLP 708
 Db 660 GKPLYLYLWLNHNGNPSTCGIGDEE--LFLLRADDMEGSSHSDPSSG--DHQSENFN 714
 QY 709 SEVLHQHAIHTIEFCVGSNTASYLRWLWALSLAHLAQLSEVLWAMVMRIGLGLREVGA 768
 Db 715 ADELHQHAIHTIEFCVGSNTASYLRWLWALSLAHLAQLSEVLWAMVMRIGLGLREVGA 773
 QY 769 AVLVPIFAFAVMTVAILLVMEGLSAFLHALRLHWVEFQNFYSGTGKLSPP 822
 Db 774 -LFLVPEVGLFAVLTVSIILLMEGLSAFLHALRLHWVEFQNFYSGTGKLSPP 826

RESULT 12

VPP2_BOVIN
 ID VPP2_BOVIN STANDARD; PRT; 854 AA.
 AC Q97681;
 DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-1999, sequence version 1.
 DT 07-FEB-2006, entry version 34.
 DE Vacuolar proton translocating ATPase 116 kDa subunit A isoform 2 (V-ATPase 116-kDa isoform a2).
 GN Name=ATP6V0A2; Synonyms=ATP6N1B;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=99107917; PubMed=9891027; DOI=10.1074/jbc.274.4.2549;
 RA Peng S.-B., Li X., Crider B.P., Zhou Z., Andersen P., Tsai S.J.,
 RA Xie X.-S., Stone D.K.;
 RT "Identification and reconstitution of an isoform of the 116-kDa
 RT subunit of the vacuolar proton translocating ATPase."
 RL J. Biol. Chem. 274:2549-2555(1999).

CC -!- FUNCTION: Part of the proton channel of V-ATPases.
 CC -!- SUBUNIT: The V-ATPase is an heteromultimeric enzyme composed of at
 CC least thirteen different subunits. It has a membrane peripheral V1
 CC sector for ATP hydrolysis and an integral V0 for proton
 CC translocation. The V1 sector comprises subunits A-H, whereas V0
 CC includes subunits a, d, c, c', and c''.
 CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
 CC -!- TISSUE SPECIFICITY: Highly expressed in lung, kidney and spleen.
 CC -!- SIMILARITY: Belongs to the V-ATPase 116 kDa subunit family.
 CC
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC EMBL: AF105016; AA012058.1; ; mRNA.
 CC InterPro: IPR002490; V_ATPase_sub116.
 CC DR PANTHER: PTHR11629; V_ATPase_sub116; 1.
 CC DR Pfam: PF01496; V_ATPase_I; 1.
 CC KW Glycoprotein; Hydrogen ion transport; Ion transport; Membrane;
 CC Transmembrane; Transport.
 CC CHAIN 1 854 Vacuolar proton translocating ATPase 116
 CC kDa subunit A isoform 2.
 CC FTID=PRO_0000119215.
 CC
 CC TOPO_DOM 1 396 Extracellular (Potential).
 CC FT TRANSMEM 397 413 Potential.
 CC FT TRANSMEM 452 472 Potential.
 CC FT TRANSMEM 555 575 Potential.
 CC FT TRANSMEM 591 611 Potential.
 CC FT TRANSMEM 651 671 Potential.
 CC FT TRANSMEM 787 807 Potential.
 CC FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 157 157 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 438 438 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 484 484 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 505 505 N-linked (GlcNAc...) (Potential).
 CC SQ SEQUENCE 854 AA; 98010 MW; 8BD9A128465CCED5 CRC64;
 CC
 CC Query Match 50.48; Score 2149; DB 1; Length 854;
 CC Best Local Similarity 50.68; Pred. No. 6e-137;
 CC Matches 439; Conservative 133; Mismatches 222; Indels 74; Gaps 15;
 CC
 CC QY 1 MGSFMRSEVALVQLFLPTAAATCVSRGELGLVEPRDLNANASAFQRFVVDVNRCEE 60
 CC DB 1 MGSLSRSETNCLAQFLQSTAVECLSVLGEKGLVEPRDLNQNVSFQRFVGVKCEE 60
 CC
 CC QY 61 LEKTFPQBEVRRAGVLVPPKGRLPAPPRLRLRIQETTERLAQELRDVRGNQALRA 120
 CC DB 61 LERILAYLQVEINRADIPLEPGDTPPPAPPLKQVLEMQEQLXLELRELVTKNKEKLR 120
 CC
 CC QY 121 QL-----HQQLHAVALRQGE-----PQLAAAHDTGASERTPLLOAPGGPHQDL 165
 CC DB 121 NLELEIYTHMLRVTKTFVKNVVEFETPEYEPPL-----ENESLLDYSQMQLGA 171
 CC
 CC QY 166 RVNFVAGAVPHKAPALERLLWRACRGFLIASFRELEQPLEHPVTGSPATWMTFLISYWG 225
 CC DB 172 KLGFVSLINGQKVEAFKMLRVCKGYTIVTAELDEPLEDETGEVIKMYVFLISFWG 231
 CC
 CC QY 226 EQTGQIKRKITDCHGHVFPFLQOEAREALGALQLOQSQSEQLGEVETGERFLSLQVGRV 285
 CC DB 232 EQIGHKVKKICDCVCHVYEPYPTAERREIQRGLNTRIQLDVLVHLKTEDYLRQLCKA 291
 CC
 CC QY 286 LQLLPPQOVQVHKMKAIVYALNOCSSVTHKCLIAEAWCSVRDLPAQELRDUSSMEEG- 344
 CC DB 292 AESVYGRVIOVKMKALYHMLNMCSDFTVNKLIAEVMWCPEADHLURRALESGRESGG 351
 CC
 CC QY 345 -VSAAHRIPCRDPPTLIRNFTASFOQIVDRYGVGRYQEVNPAPYTIITPPFLFAVM 403
 CC DB 352 TISFPMNITPKETPTPLINTNFTGQFQINIVAYGVGSQEVNPNALFTIITPPFLFAVM 411
 CC
 CC QY 404 FGDVGHGLMFLPALAMVLAENPAVKAAQNEIWTQFFRGRYLLLLMGLFSYITGYTNE 463
 CC DB 412 FGDVGHGFVFMFALLLVLENHPRLNQSQ-EIWRMFFNGRYILLMGLFSVYTGILYND 470
 CC
 CC QY 464 CFSRATSIFFSGHSAVAMANQSG-----WSDAFLAQHTMLTLDPNVTGVFLGYP 513

Db 471 CFSKSNVLFGRSMNVSAMYSSSHSPEDQRKMWLNDISVRHHSVYLQLDPSVPGVFRGYP 530
 QY 514 FGDIPWLSAANHLFLNSFKMKSIVLGVVHMAFGVVLGVFNHVFQQRHLLLETLPE 573
 Db 531 FGDIPWLNATNRLTFLNSFKMKSIVLGVVHMAFGVVLGVFNHVFQQRHLLLETLPE 590
 QY 574 LTFLLGLFGYLVFLVIYKVLGVMAARAA--SPSILIHFMFLFSHSPSNRLLYPROEV 631
 Db 591 LLEMLCIFGYLFIEMIIYKWL-VYSAETSRTPSILIEFISFLASDTGG-LYPQGEHV 648
 QY 632 QATLVVLAMVPIILLGLTPLHLHRRR-----LRRRPADROENKAGLLDL 680
 Db 649 QRLLLITVLVSVPVLFLGKPLFLWLHGRSCFVGSGYTLVRK--DSEEE----- 698
 QY 681 PDASVNGWSDEEKAGGLDDE-----EEAELVPSEVLMEQAIHTIEFCIGCVSNNTASYL 734
 Db 699 --VSLGGQDIEBGNQMEDGCEVTCEPDF--GEILMTQIHSIYCLGICISNTASYL 754
 QY 735 RLWALSIAHQAQLSEVLWAMVNRIGLGRGVGVAAVLVLPFAFAVMTVAILLVMEGLS 794
 Db 755 RLWALSIAHQAQLSEVLWAMLVHGLRVDTAYGV--LVLLPVIAPFAVLTIFILLMEGLS 812
 QY 795 AFLHALRLHWVFQNKFPYSGTGYKLSPP 822
 Db 813 AFLHALRLHWVFQNKFPYVGAGTKFVPF 840
 RESULT 13
 VPP2_MOUSE
 ID VPP2_MOUSE STANDARD; PRT; 856 AA.
 AC P15920; Q3UX3; Q9UJ02;
 DT 01-APR-1990, integrated into UniProtKB/Swiss-Prot.
 DT 11-JAN-2001, sequence version 2.
 DT 07-FEB-2006, entry version 57.
 DE Vacuolar proton translocating ATPase 116 kDa subunit A isoform 2 (V-
 DE ATPase 116-kDa isoform a2) (Immune suppressor factor J657).
 GN Name=AtP60a2; Synonyms=AtP6n1b, Tj6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=91061805; PubMed=2247090; DOI=10.1016/0161-5890(90)90102-6;
 RA Lee C.-K., Ghoshal K., Beaman K.D.;
 RT "Cloning of a cDNA for a T cell produced molecule with a putative
 RT immune regulatory role.";
 RL Mol. Immunol. 27:1137-1144 (1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=20187595; PubMed=10722719; DOI=10.1074/jbc.275.12.8760;
 RA Toyomura T., Oka T., Yamaguchi C., Wada Y., Futai M.;
 RT "Three subunit A isoforms of mouse vacuolar H+-ATPase. Preferential
 RT expression of the a3 isoform during osteoclast differentiation.";
 RL J. Biol. Chem. 275:8760-8765 (2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Brain, and Heart;
 RX MEDLINE=20167151; PubMed=10702241; DOI=10.1074/jbc.275.10.6824;
 RA Nishi T., Forgac M.;
 RT "Molecular cloning and expression of three isoforms of the 100-kDa a
 RT subunit of the mouse vacuolar proton-translocating ATPase.";
 RL J. Biol. Chem. 275:6824-6830 (2000).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=NOD; TISSUE=Dendritic cell;
 RX PubMed=16141072; DOI=10.1126/science.11112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,

Db 474 KSNVLFSGWNVSAHYSSSHSPERQKMWLVNDSTIRHSTRLQDLPNIPGVFRGYPYFPGI 533
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Db 534 DPTWLSAANHLSPNSFKMKSIVILGVVMAFVGVVGFVNFVHFQGRHRLLELTPBLTF 593
Qy 577 LLGLFGVLYFVLVIYKMLCVMAARA-ASPSILIHFNFLSHSPNSRLLYPRQEVQATL 635
Db 594 MLCIFGVLIFMIIYKMLAYSAAETSRAPSLIEFINFLPFTSKTHG-LYPGQAHVQVRL 652
Qy 636 VVLALAMVPILLGLTPLHLHRRRR-----LRRPADROENKAGLLDLPDAS 684
Db 653 VALTVLAVPVFLGKPLFLWLHNGRCFGMSRSGYTLVRK--DSEEE--VSLGNQDIE 708
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Db 765 QLSVDVWAMLRVGLRVDTTYGV--LLLLPMAFFAVLTIFILLVMEGLSAFLHALRH 822
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Db 823 VEFONKEYVGATKFPVPF 840

RESULT 14
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DT 07-MAR-2006, sequence version 1.
DT V-H+ATPase subunit a2.
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OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Wistar;
RA Guyon S., Amar M., Fossier P., Morel N.;
RT "Neurons coexpress three different v-ATPase subunit a isoforms.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC -----
DR EMBL; DQ286425; ABB91444.1; -; mRNA.
SQ SEQUENCE 856 AA; 98041 MW; B2180D770C133469 CRC64;

Query Match 50.3%; Score 2145; DB 2; Length 856;
Best Local Similarity 50.5%; Pred. No. 1.1e-136;
Matches 436; Conservative 137; Mismatches 226; Indels 64; Gaps 15;

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Db 61 LERILVYLQVEITRADIPLEGEASPPVPKVKHLEMQEQLKLELREVTNKKELRL 120
Qy 121 QL-----HQQLHAVALRQGE-----PQLAAHTDGSERTPPLQAGGPHQDLRVN 168
Db 121 NLLELVEYTHMLVTKTFLKRVNFEPTVEEFPALDESLLDYS-CMQLRGA-----KLG 174
Qy 169 FVAGAVEPHKAPALERLLWRACRGFLTASPRELEQPLEHVPTEGPAWMTFLISYWGEOI 228
Db 175 FVSGLLQQGKVEAFERMLWRACKGYIVTVTAELDEALDEDPETGEVKNYVFLISFWGEOI 234

Qy 229 GQKIRKTTDFCHVFPFLQOEAEALGALQOQOQOEAEVLGETERFISQVLGRVLQL 288
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Qy 289 LPQGVQVHKWKAVALNOCVSTTHKCLIAEAWCSVRDLPAQOEALRDSSEEG--VS 346
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Qy 347 AVAHRICRDMPTLIRNFTASFOGIVDRYGVGRYQEVNPAFYTTIITPPFLFAMVFGD 406
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Qy 407 VGHGLMFLPALAMVLAENRPAKAAQNEIWFQFRGRYLLMLGLSITVGTFTYNECPFS 466
Db 415 LGHGFVNFLLVNLNENHPRLSQSQ-EILRMFFDGRYLLMLGLSITVGTFTYNECPFS 473
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Qy 636 VVLALAMVPILLGLTPLHLHRRRR-----LRRPADROENKAGLLDLPDAS 684
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RESULT 15
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AC Q4SJ89_TETNG
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DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome 4 SCAF14575, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG00017316001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli S., Bouneau L., Fischer S., Lutfalla G., Dossat C., Segurens B.,
RA Nicaut B., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

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OM protein - protein search, using sw model

Run on: June 29, 2006, 13:08:24 ; Search time 52 Seconds
(without alignments)
1383.657 Million cell

US-10-783-519-2
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 Perfect score: 1
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

Database : Issued Patents AA:*

- 1: /EMC Cella SID33/ptodata/2/iaa/5 COMB.pcp.*
- 2: /EMC Cella SID33/pcodata/2/iaa/6 COMB.pcp.*
- 3: /EMC Cella SID33/ptodata/2/iaa/7 COMB.pcp.*
- 4: /EMC Cella SID33/pcodata/2/iaa/8 COMB.pcp.*
- 5: /EMC Cella SID33/ptodata/2/iaa/9 COMB.pcp.*
- 6: /EMC Cella SID33/pcodata/2/iaa/10 COMB.pcp.*
- 7: /EMC Cella SID33/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4266	100.0	822	2	US-08-684-932A-38	Sequence 38, Appl
2	4266	100.0	822	2	US-09-618-304B-2	Sequence 2, Appli
3	4235.5	99.3	849	2	US-09-949-016-8846	Sequence 8846, Ap
4	4235.5	99.3	849	2	US-09-949-016-8847	Sequence 8847, Ap
5	4235.5	99.3	853	2	US-09-949-016-8275	Sequence 8275, Ap
6	4235.5	99.3	853	2	US-09-949-016-8276	Sequence 8276, Ap
7	3394	79.6	750	2	US-09-949-016-7201	Sequence 7201, Ap
8	3394	79.6	750	2	US-09-949-016-7202	Sequence 7202, Ap
9	2143.5	50.2	855	7	5196526-1	Patent No. 5196526
10	1801.5	42.2	847	2	US-09-618-304B-3	Sequence 3, Appli
11	1097.5	25.7	513	2	US-10-094-749-2211	Sequence 2211, Ap
12	892.5	20.9	515	2	US-09-270-767-43227	Sequence 43227, A
13	757.5	17.8	386	2	US-09-248-796A-17451	Sequence 17451, A
14	704	16.5	380	2	US-09-270-767-44518	Sequence 44518, A
15	513	12.0	257	2	US-09-270-767-33142	Sequence 33142, A
16	513	12.0	257	2	US-09-270-767-48359	Sequence 48359, A
17	478	11.2	343	2	US-09-270-767-45290	Sequence 45290, A
18	427	10.0	163	2	US-09-270-767-43040	Sequence 43040, A
19	418.5	9.8	425	2	US-09-248-796A-17452	Sequence 17452, A
20	370	8.7	155	2	US-09-270-767-31642	Sequence 31642, A
21	370	8.7	155	2	US-09-270-767-46859	Sequence 46859, A
22	366	8.6	196	2	US-09-248-796A-17445	Sequence 17445, A
23	319.5	7.5	154	2	US-09-270-767-32407	Sequence 32407, A
24	319.5	7.5	154	2	US-09-270-767-47624	Sequence 47624, A
25	278	6.5	662	2	US-09-134-000C-5682	Sequence 5682, Ap
26	276	6.5	186	2	US-09-248-796A-17453	Sequence 17453, A

ALIGNMENTS

RESULT 1

US-08-684-932A-38
; Sequence 38, Application US/08684932A
; Patent No. 6403304
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; APPLICANT: Li, Yi-ping
; APPLICANT: Wuchterpfennig, Anne L.
; TITLE OF INVENTION: HUMAN OSTEOCLAST-SPECIFIC AND -RELATED
; TITLE OF INVENTION: DNA SEQUENCES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P. C.

Query Match	100.0%;	Score 4266;	DB 2;	Length 822;
Best Local Similarity	100.0%;	Pred. NO. 0;		
Matches 822;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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781 VMTVAILLVMEGLSAPFLHALRLHWVEFQNKFSYGTGYKLSPP 822

RESULT 2

US-09-618-304B-2
; Sequence 2, Application US/09618304B
; Patent No. 677537
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; APPLICANT: Li, Yi-Ping
; TITLE OF INVENTION: Osteoclast Proton Pump Subunit
; FILE REFERENCE: 1564.1006-001
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US/09/618,304B
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-949-016-8846
; Sequence 8846, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8846
; LENGTH: 849
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8846

Query Match 99.3%; Score 4235.5; DB 2; Length 849;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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DB 20 MGSFSESEVALVQLFLPTAAATCTVSRGELGLVEFRDLNASVSFAQRFFVVDVRCCE 79
QY 61 LEKFTFLOEVRAGLVLPPKGRLLPAPPDRLLRIQETERLAQELRDVRGNQOALRA 120
DB 80 LEKFTFLOEVRAGLVLPPKGRLLPAPPDRLLRIQETERLAQELRDVRGNQOALRA 139
QY 121 QLHQLQHAVALRQGHPEQLAAATDGASERTPLQAPGGPHODLRVNFVAGAVEPHKAP 180
DB 140 QLHQLQHAVALRQGHPEQLAAATDGASERTPLQAPGGPHODLRVNFVAGAVEPHKAP 199
QY 181 ALERLLWRCRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEOIGKIRKIDTCFH 240
DB 200 ALERLLWRCRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEOIGKIRKIDTCFH 259
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DB 260 CHVFPFLOQSEARLQALQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 319
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DB 320 AVYALNQC SVSTTHKCLIAEAWCSVRDLPALQOALRDSMERGSAVAHRIPCRMPPT 379
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DB 800 AVMTVAILLVMEGLSAFLHALRLHWFQNKFSYGTGYKLSPP 842

DB 800 AVMTVAILLVMEGLSAFLHALRLHWFQNKFSYGTGYKLSPP 842
RESULT 4
US-09-949-016-8847
; Sequence 8847, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8847
; LENGTH: 849
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8847

Query Match 99.3%; Score 4235.5; DB 2; Length 849;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 MGSFSESEVALVQLFLPTAAATCTVSRGELGLVEFRDLNASVSFAQRFFVVDVRCCE 60
DB 20 MGSFSESEVALVQLFLPTAAATCTVSRGELGLVEFRDLNASVSFAQRFFVVDVRCCE 79
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DB 380 LIETNFTASFOGIVDYGVRQYQVNPAPYITITPPFLFAVMFGDVGHGLMFLFALAM 439
QY 421 VLAENRPAKAAQNEIWTQFFRGYLLMLGLFSIYTGTYNECFSRATSIFFPSGWSVA 480
DB 440 VLAENRPAKAAQNEIWTQFFRGYLLMLGLFSIYTGTYNECFSRATSIFFPSGWSVA 499
QY 481 MANQSGWSDAFLAQHTMLTLDPNVTGVPFGIDPIWLSLAANHLFLNSFKMKMSVI 540
DB 500 MANQSGWSDAFLAQHTMLTLDPNVTGVPFGIDPIWLSLAANHLFLNSFKMKMSVI 559
QY 541 LGVHMAFGVVLGVFNHVFQGRHLLLETLPELTLGLFGYLVFLVIYKMLCVWAARA 600
DB 560 LGVHMAFGVVLGVFNHVFQGRHLLLETLPELTLGLFGYLVFLVIYKMLCVWAARA 619
QY 601 AS-PSLIIHFINMFLSHPSNRLLYPROEVQATLVIALAMVPIILLGTPLHLHRHR 659

Db 620 ASAPGILIHFINMFLSHSPSNRLLYPRQEVVQATLVVLALAMVPIILGTLPLHLHRRH 679
Qy 660 RRLRRPADROENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLMHQAIHT 719
Db 680 RRLRRPADROENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLMHQAIHT 739
Qy 720 IEFCGCVSNTASYLRWLWALSIAHAQSLSEVLWAMVMRIGLGLGREGVAAVVLVPIPAF 779
Db 740 IEFCGCVSNTASYLRWLWALSIAHAQSLSEVLWAMVMRIGLGLGREGVAAVVLVPIPAF 799
Qy 780 AVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPP 822
Db 800 AVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPP 842

RESULT 5
US-09-949-016-8275
; Sequence 8275, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8275
; LENGTH: 853
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8275

Query Match 99.3%; Score 4235.5; DB 2; Length 853;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 1 MGSMFRSEVALVOLFLPTAAAYTCVSRGLGELVFEPRDLNASVSFAFORFVVDVRCCE 60
Db 24 MGSMFRSEVALVOLFLPTAAAYTCVSRGLGELVFEPRDLNASVSFAFORFVVDVRCCE 83
Qy 61 LEKTFPFOEVRVRRAGLVLPKGLPAPPDRDLRIQEEERLAQELRDVRGNOALRA 120
Db 84 LEKTFPFOEVRVRRAGLVLPKGLPAPPDRDLRIQEEERLAQELRDVRGNOALRA 143
Qy 121 QLHLQLHAAVLRQGHPEPOLAAATDASERTPLQAPGGPHQDLRVNFVAGAVEPHKAP 180
Db 144 QLHLQLHAAVLRQGHPEPOLAAATDASERTPLQAPGGPHQDLRVNFVAGAVEPHKAP 203
Qy 181 ALERLLWRACRGFLIASPRELEQPLEHPVTGEPATMTFLISYWGEOIQGKIRK1TDCFH 240
Db 204 ALERLLWRACRGFLIASPRELEQPLEHPVTGEPATMTFLISYWGEOIQGKIRK1TDCFH 263
Qy 241 CHVFPFLOQEARLGALQOQOSELQEVLETGERFLSQVLGRVLQLLPGQOVQVHKM 300
Db 264 CHVFPFLOQEARLGALQOQOSELQEVLETGERFLSQVLGRVLQLLPGQOVQVHKM 323
Qy 301 AVYALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDRSSMEEGSVSAVAHRIPCRDMPPT 360
Db 324 AVYALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDRSSMEEGSVSAVAHRIPCRDMPPT 383
Qy 361 LIRNRTFASFGIVDRYGVGRYQSVNAPYTIITFFPLFAMFGDVGHLLMFLPALAM 420
Db 384 LIRNRTFASFGIVDAVGVGRYQSVNAPYTIITFFPLFAMFGDVGHLLMFLPALAM 443

Qy 421 VLAENRPAVKAQNEIMOTFRGRVYLLMLLGLFSYITGTGYNECFSRATSIIPSGWSVAA 480
Db 444 VLAENRPAVKAQNEIMOTFRGRVYLLMLLGLFSYITGTGYNECFSRATSIIPSGWSVAA 503
Qy 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGPPFGIDPIWLSLAANHLSPFNSFKMKMSVI 540
Db 504 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGPPFGIDPIWLSLAANHLSPFNSFKMKMSVI 563
Qy 541 LGVHMAFGVVLGVNHNHFGQORHLLLETPELTFLGLFGYLVFLVIYKWLVCVWAARA 600
Db 564 LGVHMAFGVVLGVNHNHFGQORHLLLETPELTFLGLFGYLVFLVIYKWLVCVWAARA 623
Qy 601 AS-PSILIHFINMFLSHSPSNRLLYPRQEVVQATLVVLALAMVPIILGTLPLHLHRRH 659
Db 624 ASAPGILIHFINMFLSHSPSNRLLYPRQEVVQATLVVLALAMVPIILGTLPLHLHRRH 683
Qy 660 RRLRRPADROENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLMHQAIHT 719
Db 684 RRLRRPADROENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLMHQAIHT 743
Qy 720 IEFCGCVSNTASYLRWLWALSIAHAQSLSEVLWAMVMRIGLGLGREGVAAVVLVPIPAF 779
Db 744 IEFCGCVSNTASYLRWLWALSIAHAQSLSEVLWAMVMRIGLGLGREGVAAVVLVPIPAF 803
Qy 780 AVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPP 822
Db 804 AVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPP 846

RESULT 6
US-09-949-016-8276
; Sequence 8276, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8276
; LENGTH: 853
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8276

Query Match 99.3%; Score 4235.5; DB 2; Length 853;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 820; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 1 MGSMFRSEVALVOLFLPTAAAYTCVSRGLGELVFEPRDLNASVSFAFORFVVDVRCCE 60
Db 24 MGSMFRSEVALVOLFLPTAAAYTCVSRGLGELVFEPRDLNASVSFAFORFVVDVRCCE 83
Qy 61 LEKTFPFOEVRVRRAGLVLPKGLPAPPDRDLRIQEEERLAQELRDVRGNOALRA 120
Db 84 LEKTFPFOEVRVRRAGLVLPKGLPAPPDRDLRIQEEERLAQELRDVRGNOALRA 143
Qy 121 QLHLQLHAAVLRQGHPEPOLAAATDASERTPLQAPGGPHQDLRVNFVAGAVEPHKAP 180
Db 144 QLHLQLHAAVLRQGHPEPOLAAATDASERTPLQAPGGPHQDLRVNFVAGAVEPHKAP 203
Qy 181 ALERLLWRACRGFLIASPRELEQPLEHPVTGEPATMTFLISYWGEOIQGKIRK1TDCFH 240
Db 204 ALERLLWRACRGFLIASPRELEQPLEHPVTGEPATMTFLISYWGEOIQGKIRK1TDCFH 263

ORGANISM: Human
US-09-949-016-7202

Query Match 79.6%; Score 3394; DB 2; Length 750;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 664; Conservative 6; Mismatches 18; Indels 44; Gaps 3;

```
QY 131 VLROGHEPDLAAHTDGAERTPLAQGGP-----161
DB 16 LQARNFQSALALGG-----SPLVLPRPAPPCGQCGQCAQLPCPCWAGSCPGGLVG 71
QY 162 -----HODLRVNFVAGAVEPHKAPALERLLWRACRGFLIASFRELEOPLEHPVTG 211
DB 72 EAGQEVGAALPSFVAASVAGAVEPHKAPALERLLWRACRGFLIASFRELEOPLEHPVTG 131
QY 212 EPATWMTFLISYWGEOIGQIRKIRKIDTCFCHVFPFLOQBEARLGAQQOQSOEQLQEV 271
DB 132 EPATWMTFLISYWGEOIGQIRKIRKIDTCFCHVFPFLOQBEARLGAQQOQSOEQLQEV 191
QY 272 GETERFLSOVLGRVQLQLPPGOVQVHKMAVYALNOCVSTTHKCLIAEAMCSVRDLPA 331
DB 192 GETERFLSOVLGRVQLQLPPGOVQVHKMAVYALNOCVSTTHKCLIAEAMCSVRDLPA 251
QY 332 LQEARLDSMEGVSVAHRIPCRDMPTLIRTNFTASFOGIVDRYGVGRYQEVNPAPY 391
DB 252 LQEARLDSMEGVSVAHRIPCRDMPTLIRTNFTASFOGIVDRYGVGRYQEVNPAPY 311
QY 392 TITITPFLFVAVMGVGHGLMLPALAMVLAENRPAVKAQNEIWTQTFRGYLLLMG 451
DB 312 TITITPFLFVAVMGVGHGLMLPALAMVLAENRPAVKAQNEIWTQTFRGYLLLMG 371
QY 452 LFSIYTGFIYNECFSRATSIFFSGWSVAAMANOSGSDAFLAQHTMTLDPNVTGVFLGP 511
DB 372 LFSIYTGFIYNECFSRATSIFFSGWSVAAMANOSGSDAFLAQHTMTLDPNVTGVFLGP 431
QY 512 YPFGIDPIWSLAANHLNFLSPKMKMSVILGVVHMAFGVVLGVFNHVFQGRHLLLETL 571
DB 432 YPFGIDPIWSLAANHLNFLSPKMKMSVILGVVHMAFGVVLGVFNHVFQGRHLLLETL 491
QY 572 PELTLLGLFGVLFVLYKWCVAARAAS-PSILIHFINFLFSPHSNRLLYPRQEV 630
DB 492 PELTLLGLFGVLFVLYKWCVAARAAS-PSILIHFINFLFSPHSNRLLYPRQEV 551
QY 631 VQATLVVLALAMPVILLGTPLHLHRRRRRRPADROENKAGLLDLPASVNGWSS 690
DB 552 VQATLVVLALAMPVILLGTPLHLHRRRRRRPADROENKAGLLDLPASVNGWSS 611
QY 691 DEKAGGLDDEEAEELVSEVLMHQAHTIEFCLGCVSNNTASYLRWLALSLAHAQLSEYL 750
DB 612 DEKAGGLDDEEAEELVSEVLMHQAHTIEFCLGCVSNNTASYLRWLALSLAHAQLSEYL 671
QY 751 WAMVMRIIGLGRGVGAVALVPIFAFAMVMTVAILLVMEGLSAFLHALRLHWVFQNK 810
DB 672 WAMVMRIIGLGRGVGAVALVPIFAFAMVMTVAILLVMEGLSAFLHALRLHWVFQNK 731
QY 811 FYSGTGYKLSPPF 822
DB 732 FYSGTGYKLSPPF 743
```

RESULT 9
5196526-1
Patent No. 5196526
APPLICANT: BEAMAN, KENNETH D.
TITLE OF INVENTION: CDNA CLONE FOR T-CELL SUPPRESSOR INDUCER
FACTOR
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/442,116
FILING DATE: 28-NOV-1989
SEQ ID NO.1:
LENGTH: 855
5196526-1

```
Query Match 50.2%; Score 2143.5; DB 7; Length 855;  
Best Local Similarity 51.4%; Pred. No. 3.8e-208;  
Matches 441; Conservative 129; Mismatches 233; Indels 55; Gaps 15;  
QY 1 MGSMPRSEVALVQLPPTAAAYTCVSRIGELGLVEFRDLNASVSFAQRFFVVDVWRCCE 60  
DB 1 MGSMPRSEVALVQLPPTAAAYTCVSRIGELGLVEFRDLNASVSFAQRFFVVDVWRCCE 60  
QY 61 LKRTFTTFOEVRVRLGLVLPKPKRLPAPPDRLRIQEBTERLAQELDRVGNQOALRA 120  
DB 61 LKRTFTTFOEVRVRLGLVLPKPKRLPAPPDRLRIQEBTERLAQELDRVGNQOALRA 120  
QY 121 QL-----HQQLAAAVLRQCHE-----PQLAAHTDGAERTPLAQGGPHQDLRVN 168  
DB 121 NLELVEYTHMLURVTKTFLKRNVEFPETVEEPALENDSLDYS-CMORLGA-----KLG 174  
QY 169 FVAGAVEPHKAPALERLLWRACRGFLIASFRELEOPLEHPVTGEPATWMTFLISYWGEOI 228  
DB 175 FVSGLIQOGRVEAFERMLWRACKGTIVTYAELDSCELPETGEVTKWYVFLISFWGEOI 234  
QY 229 GQIKIRKIDTCFCHVFPFLOQBEARLGAQQOQSOEQLQEVGETERFLSOVLGRVQL 288  
DB 235 GHKVKKICDCHYCHYYPNTAEERREIQEGLNTRIQLDLYTLHKTEDYLRQVLCRAES 294  
QY 289 LPPGOVQVHKMAVYALNOCVSTTHKCLIAEAMCSVRDLPAQELDRVGNQOALRA 346  
DB 295 VCSRVVQVRKMAIYHMLNMCSDVTNKLIAEAMCSVRDLPAQELDRVGNQOALRA 354  
QY 347 AVAHRIPCRDMPTLIRTNFTASFOGIVDRYGVGRYQEVNPAPYTIITFPFLFAVMFGD 406  
DB 355 SPMTNPTIKETPTLIRTNKFTGQNIQVDAVGVSREVNPAFTIITFPFLFAVMFGD 414  
QY 407 VGHGLMLFALAMVLAENRPAVKAQNEIWTQTFRGYLLLMGLFSTIYTFIYNECF 466  
DB 415 FGHGVMFELFALLVLNENHRLSOSQ-EILRMFFDGRYILLMGLFSTIYTFIYNECF 473  
QY 467 RATSIFPSGWSVAAMANOSG-----WSDAFLAQHTMTLDPNVTGVFLGPVPGI 516  
DB 474 KSVNLFSGWNVCMYSSSHSPEEQKMWLMNDSTIRHSRTIQLDPNIPGVFRGPYFPGI 533  
QY 517 DPINSLAANHLNFLSPKMKMSVILGVVHMAFGVVLGVFNHVFQGRHLLLETLPELTF 576  
DB 534 DPINSLAANHLNFLSPKMKMSVILGVVHMAFGVVLGVFNHVFQGRHLLLETLPELTF 593  
QY 577 LLGLFGVLFVLYKWCVAARA-ASPSILIHFINFLFSPHSNRLLYPRQEVVQATL 635  
DB 594 MLCIFGYLIFMIIYKWLAYSATREAPSILIEFINMFLPFTSKTHG-LYPCQAHVQVRL 652  
QY 636 VVALAMPVILLGTPLHLHRRRR-----LRRRPADROENKAGLLDLPAS 684  
DB 653 VALTVLAVPVLFLGKPLFLMLHNGNCFGMSRSGYTLVRK--DSEEE--VSLNGQDLE 708  
QY 685 VNGWSSDEKAGGLDDEEAEELVSEVLMHQAHTIEFCLGCVSNNTASYLRWLALSLAHA 744  
DB 709 -EGNSRMEB---GCREVTCEEFNFGELMTQAIHSIEYCLGICISNTASVLRWLALSLAHA 764  
QY 745 QLSEVLWAMVMRIIGLGRGVGAVALVPIFAFAMVMTVAILLVMEGLSAFLHALRLHW 804  
DB 765 QLSDVLWAMVMRIIGLGRGVGAVALVPIFAFAMVMTVAILLVMEGLSAFLHALRLHW 821  
QY 805 VEFQNKFGYKLSPPF 822  
DB 822 VEFQNKFGYKLSPPF 839
```

RESULT 10
US-09-618-304B-3
Sequence 3, Application US/09618304B
Patent No. 6777537
GENERAL INFORMATION:
APPLICANT: Stashenko, Philip
APPLICANT: Li, Yi-Ping

;; TITLE OF INVENTION: Osteoclast Proton Pump Subunit
;; FILE REFERENCE: 1564.1006-001
;; CURRENT APPLICATION NUMBER: US/09/618,304B
;; PRIOR FILING DATE: 2000-07-18
;; PRIOR APPLICATION NUMBER: 08/605,378
;; PRIOR FILING DATE: 1996-02-22
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 847
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Consensus sequence
;; NAME/KEY: VARIANT
;; LOCATION: (1)...(847)
;; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-618-304B-3

Query Match 42.2%; Score 1801.5; DB 2; Length 847;
Best Local Similarity 46.8%; Pred. No. 2.1e-173;
Matches 391; Conservative 45; Mismatches 384; Indels 15; Gaps 6;

QY 1 MGSMSERSEVALQQLFLPTAAAYTCVSLGELGVEPRDLNASVSAFQRFVVDVNRCEE 60
DB 1 MGFLRSEEXXQLFLXAXXAXCVSLXELGXVFXFDLNXVXXFXQRFVXVRCEE 60
QY 61 LEXTFTFLOEVRAGVLVPPKRLPAPPDRLLRIQEBTERLAQELRDVRGNQOALRA 120
DB 61 MDXXLAFXXEIRAXXXXXXXXXPAPRDMXXXXXXXEXXELXIXNOALXX 120
QY 121 QLHLQLHAAVLROGHEPQLAAAHDTGASERTPLL-QAPGGPHODLRVNFVAGAVEPHKA 179
DB 121 XFXLXAXXAXXILRXXXXXXXAXXDXXEXXLLXXXXXXGXXLRLXXFXVAGXIXXXX 180
QY 180 PALERLLWRACRGFLTASPRELEQPLEHPVTGEPATWMTFLISWGEOIQKIRKIDTCF 239
DB 181 XFERMLWRXCRGXXXXXXXEXPLEXPVTGDXXXXXXXFXIXFGDQXXXXXXKIXEXF 240
QY 240 HCHVFPFLOEAEARLALQLOOQSOEQLGTERFLSQVLGRVLQLLPPQGVQVHKM 299
DB 241 XXXXPXXXXXXXEXXDXXDXXDXLQVLTXXEXXXXXXXVXXXXXXXXXXIXVKM 300
QY 300 XAVYALNQCSTVTHKCLIAEAWCSVRDLPALQELALRDSMEEG--VSAVAHRIPCRDM 357
DB 301 KAIYXXLXNCKIIXXTKCLIAEAWCSVXDLXXQXALRXXXXXXGXXVXIXXKXXXXX 360
QY 358 PPTLIRNRTASFGIVDYGVRQYQVNPAPYTIITFPFLFVAMGVDVGHGLMFLFA 417
DB 361 PPTXXXNTXFTXXFQXIVD-YGIGXYXEINPAPYTIITFPFLFVAMGVDVGHGLMFLFA 419
QY 418 LAMVLAENRPAVAAQNEIWOTFFRGYRLLMLGFLSIYGTFTYNECFSRATSIFFSGWS 477
DB 420 XXVLEXXRXXXXXXXEXFXXFXGRYXXLLMGXFSIYGLIYNDGCFXXXXXIFXSWX 479
QY 478 VAAMANQSGWSDAFLAQHTMLTLDPNVTVGLFGPIPGIDPIWSLAANHLSFLNSFKMKM 537
DB 480 VXXMXXXXXXWEXXKXXXXXXLXKPKVGVFXGPIPGIDPIWXAXNXLKFLNSFKMKM 539
QY 538 SVILGVVHMAFGVILGVFNHVFHQHRLLETLPELTFLLGLFGVILVFLVIYKWLQVWA 597
DB 540 SVILGIIHMKFGVGLXXFNHXXFXXXXXXXFXXXXXXXFGLVGLVLIYKWLQVWA 599
QY 598 A--RAASPSLIHFINNPLFSHSPS-NRLLYPRQVVQATLVVLAAMVPIILLGTPLHL 654
DB 600 XXXXXXPSXLIHFINNPLFSXSSXXMXXMXXQXXIQQXVLVVALXXVFXMXXLXPLXL 659
QY 655 LHRHRR-----RLRRRPAQRQENKAGLLDLPDASVNGWSDEEKAGGLDDEEAE 706
DB 660 XXXXXRXXXXXXXKXXXXXXFXXXXXXXXKXXXXXXXKXXXXXXEXXKDF 719
QY 707 VPSEVLHQAIHTIEFCLGCVSNATSYLRWALSALAHQSEVLWMMWRIGLGLREV 766

DB 720 XXXDXMXHQAIHTIEYCLGCSINTASYLRWALSALAHQSEVLWMMVXXIXGLXXXXXG 779
QY 767 VAAVVLVPIFAAFVAVMTVAILLVMEGLSAPFLHRLHFWVEFQNFYSGTGKYLSP 821
DB 780 XXXXXFXFIFAAFAXLTVAILLMEGLSAPFLHRLHFWVEFQNFYSGTGKFXP 834

RESULT 11

US-10-094-749-2211
; Sequence 2211, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2211
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2211

Query Match 25.7%; Score 1097.5; DB 2; Length 513;
Best Local Similarity 39.0%; Pred. No. 3.2e-102;
Matches 260; Conservative 60; Mismatches 169; Indels 177; Gaps 9;
QY 166 RVNFVAGVPHKAPALERLLWRACRGFLTASPRELEQPLEHPVTGEPATWMTFLISYWG 225
DB 4 KLGFAGVNRNRMASFERLLWRICGNVYLRSEMDAPLEDPTVEEIQKNIIFLYQ 63
QY 226 EQTGQKIRKIDTCFCHVFPFLQOEAEARLALQLOOQSOEQLGTERFLSQVLGRV 285
DB 64 EQLRQKIKKICDGRATVYPCPEPAVERREMLSVNRLEDLITVITQTESHRQLLEA 123
QY 286 LQLLPGQVQVHKMAYLALNQCSTVTHKCLIAEAWCSVRDLPALQELALRDSMEEGV 345
DB 124 AANWHSWLKVKQKMAVYHILNMCNIDVTQOCVIAIBWFFVADATRIKRAL-EGMELSG 182
QY 346 SAVA---HRIPCDEMPPTLIRNRTASFGIVDYGVRQYQVNPAPYTIITFPFLFAV 402
DB 183 SSNAPITVTVQSKTAPPTFRNKNFTAGQNIIVDAVGVSRYREINPAPYTIITFPFLFAV 242
QY 403 MFGDVGHGLLMFLFALAMVLAENRPAVAAQNEIWOTFFRGYRLLMLGFLSIYGTFTY 462
DB 243 MFGDCGHGTVMLLAALMILNERRLLSKQTDNEIWNTFHGRY----- 285
QY 463 ECFSRATSIFFSGWSVAAMANQSGWSDAFLAQHTMLTLDPNVTVGLFGPIPGIDPIWSL 522

Db 286 ----- 285
QY 523 AANHLNFLNSFKMKSVILGVVHMAFGVVLGVFNHVFQGRHLLLETLPELTFLLGLPG 582
Db 286 ----- 285
QY 583 YLVFLVIYKWLVCMAARAASPSILIHFINNLFSSH-PSNRLLYPRQEVVQATLVVLALA 641
Db 286 ----- 285
QY 642 MYPIILLGTP--LHLHRHRRRLRRPADROENKAGLLDLPDASVNGSSDEEKAGGLD 699
Db 323 SVPMMLLIKPFILASHRKSQASRIQEDATENIEGSSSP-SRSGQRTSADTHGALD 381
QY 700 DEEBELVPSEVLHQAIHTIEFCGCVSNTASYLRWLSLAHAQLSEVLWVMVRIGL 759
Db 382 DHGE-EFNGDGVFVQALHTIEYLCISNTASYLRWLSLAHAQLSEVLWVMVNSGL 440
QY 760 ---GLGREYGAUVLVPIFAAFVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTG 816
Db 441 QTRGWGGIVGVFI---IFAVFAVLTVAILLIMEGLSAFLHALRLHWVEFQNKFSYVGDG 495
QY 817 YKLSPP 822
Db 496 YKFSPP 501

RESULT 12

US-09-270-767-43227

; Sequence 43227, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 43227

; LENGTH: 515

; TYPE: PRT

; ORGANISM: *Drosophila melanogaster*

US-09-270-767-43227

Query Match 20.9%; Score 892.5; DB 2; Length 515;
Best Local Similarity 40.0%; Pred. No. 2.1e-81;
Matches 191; Conservative 81; Mismatches 162; Indels 43; Gaps 7;
QY 23 YTCVSRGLGELGLVFEPRDLNASVSQRRFVVDVWRCEELEKTFTLQBEVVRAGLVLP 82
Db 43 YTSVSELGETGVQVRDLNVNVAQRKEVTEVRCDLELRKIRVIEIKDGIPLDI 102
QY 83 KGRLP-APPDRLRIQ---EETE---RLAQ-----ELRDVRGNQALRAQ 121
Db 103 QDDIPRAPNPREIIDLEAHLKTESEMIELAQNEVMKSNYLLELTELKRVLENTQGFSD 162
QY 122 LHQQLHAALVLRQHEPQLAAHTDASERTPLLOAPGPHQDLAVNFVAGAVEPHKAPA 181
Db 163 QEVNLDS--NRAGDNDAAQHRG-----RLGFVAGVNRERVA 202
QY 182 LERLWRACRGLIASFRELEOPLEHPVTGEPATWNTFLISYWGQIGQIKIRKIIDCFHC 241
Db 203 FERMLWRISRGVFLKRSDLDEPLNDPATGHPDIYKTVFAVFGQLKKNRIKVKCTGFA 262
QY 242 HVFPFLOQBEARLQALQOQSQBELQVGLGTERFLSQVLGRVLOQLPPGQVQVHKMA 301
Db 263 SLYPSPSHNREERENVRTRLEDLKLVSQTEDHRSRLVATVSKNLPSPSMVWKMA 322
QY 302 VYLANQCSVSTHKLITAEACWSVRDLPALQEARLDSMEEG--VSAVAHRIPCRDMP 359
Db 323 IYHTLNLFNMDVTKKCLIGECVWPTNDLPVQKALSDGSAAVGSTIPSLNVIDTNEQPP 382

QY 360 TLIRNRFTASQGIQVDRVGRVQYOVNPPAPVTIITPEFLFAVMEFGVGHLLMELFALA 419
Db 383 TNRNKTTRGPNLIDAYGASYRECPALYTCITFFFLFAVMEFGDUGHGUILVLFQAW 442
QY 420 MVLAENRRPAKAAQNEIWTFFGRYLLMLGLFSIYTGFIYNECFSRATSPPSGW 476
Db 443 MVLCKLARIRNGGEIWNIPFGGRYIILLMGLFAMYTGLVYNDVFSKSMNLFGRW 499

RESULT 13

US-09-248-796A-17451

; Sequence 17451, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA

; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT APPLICATION NUMBER: US/09/248,796A

; PRIOR FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 17451

; LENGTH: 386

; TYPE: PRT

; ORGANISM: *Candida albicans*

US-09-248-796A-17451

Query Match 17.8%; Score 757.5; DB 2; Length 386;
Best Local Similarity 41.0%; Pred. No. 7e-68;
Matches 161; Conservative 71; Mismatches 132; Indels 29; Gaps 7;
QY 433 ONEIWTFFRGYRLLMLGLFSIYTGFIYNECFSRATSPFSGMSVAAANQSGSDAFL 492
Db 5 KDEIFDMAYTGRYVLLMGVFSMTYGFYNDVFSISMSIFKSGWE-----WPEKEN 55
QY 493 AQHTMLTLDPNVTGVFLGPPYDIPWLSLAANHLSPFNSFKMKSVILGVVHMAFGVVL 552
Db 56 VGET-----IYAKYVGTYSIGLDPAWHGTENALLFSNYSYKMKLSILMGYHMSYV 108
QY 553 GVFNHVFGRHRLLETLPELTFLLGLFVGLVFIYKWLVCVMAARAASPSILIH-ETN 611
Db 109 SLVNTYFNSMIDVIGNFIPGLLFQGGIFGLSLCIVTKNSVDNWFATGRQPEGLNMLIN 168
QY 612 MFLFSHSPSN--RLLYPRQEVVQATLVVLALAMVPIILLGTPLHLHRRRLRRRPPAD 669
Db 169 MFL---QPGDVPEPLYSQSTIQVFLLIALLICVPMLLLVKPLYM-----KQLEKEANQ 220
QY 670 QEENKAGLLDLPDASVNGSSDEEKAGGLDDEEAEELVPSEVLMHQAIHTIEFCGCVSN 729
Db 221 HGSYSQLANDEESGAVAGQEQENAAEDDDDEEHNFQDITMIHQVHTIEFCLNCVSH 280
QY 730 TASYLRLWALSIAHAQLSEVLWVMVRIGLGIGREVGAAVVLVPIFAAFVMTVAIILV 789
Db 281 TASYLRLWALSIAHAQLSTVLVMSWT--IGNAFGPTGLIGTFMVVFLFAMVFLSV 338
QY 790 MEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPP 822
Db 339 MEGTSAMLHSLRLHWVESMSKYFEGGSAFET 371

RESULT 14

US-09-270-767-44518

; Sequence 44518, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

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OM protein - protein search, using sw model

Run on: June 29, 2006, 13:09:14 ; Search time 181 Seconds
(without alignments)
2103.661 Million cell updates/sec

Title: US-10-783-519-2
Perfect score: 4266
Sequence: 1 MGSFSESEVALVQLFLPTA.....HWFEQNFYSGTGYKLSPF 822

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4266	100.0	822	5	US-10-783-519-2
2	3131.5	73.4	614	4	US-10-145-012-2
3	3131.5	73.4	614	6	US-11-126-866-2
4	3131.5	73.4	614	6	US-11-126-841A-2
5	3127.5	73.3	614	4	US-10-145-012-13
6	3127.5	73.3	614	5	US-10-489-725-5
7	3127.5	73.3	614	6	US-11-126-866-13
8	3127.5	73.3	614	6	US-11-126-841A-13
9	2917.5	68.4	643	4	US-10-264-049-2656
10	2066	48.4	818	4	US-10-495-446-32
11	1918.5	45.0	841	5	US-10-874-706-20
12	1801.5	42.2	847	5	US-10-783-519-3
13	1720	40.3	855	5	US-10-714-995-14
14	1720	40.3	855	6	US-11-097-143-2052
15	1701	39.9	834	6	US-11-097-143-4199
16	1701	39.9	834	6	US-11-097-143-41700
17	1539.5	36.1	703	4	US-10-495-446-28
18	1539.5	36.1	935	4	US-10-369-493-5810
19	1538	36.1	814	6	US-11-097-143-36642
20	1501	35.2	1030	4	US-10-369-493-5811
21	1497	35.1	844	6	US-11-097-143-41496
22	1491.5	35.0	865	4	US-10-369-493-5572
23	1491.5	35.0	865	4	US-10-369-493-5573
24	1406.5	33.0	873	4	US-10-369-493-6070
25	1375	32.2	1236	4	US-10-369-493-6203
26	1325.5	31.1	820	4	US-10-437-963-196349
27	1318	30.9	840	4	US-10-369-493-22409
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					Sequence 2, Appli
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					Sequence 2, Appli
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					Sequence 5, Appli
					Sequence 13, Appli
					Sequence 13, Appli
					Sequence 2656, Ap
					Sequence 32, Appli
					Sequence 20, Appli
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					Sequence 2052, Ap
					Sequence 41499, A
					Sequence 41700, A
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					Sequence 5810, Ap
					Sequence 36642, A
					Sequence 5811, Ap
					Sequence 41496, A
					Sequence 5572, Ap
					Sequence 5573, Ap
					Sequence 6070, Ap
					Sequence 6203, Ap
					Sequence 196349, A
					Sequence 22409, A

ALIGNMENTS

RESULT 1

US-10-783-519-2
; Sequence 2, Application US/10783519
; Publication No. US2005006448A1
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; APPLICANT: Li, Yi-Ping
; TITLE OF INVENTION: Osteoclast Proton Pump Subunit
; FILE REFERENCE: 1564.1006-001
; CURRENT APPLICATION NUMBER: US/10783,519
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/618,304
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 08/605,378
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-519-2

Query Match 100.0%; Score 4266; DB 5; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGSFSESEVALVQLFLPTAAAYTCVSRGELGLVFRDLNASVSASFQRFVVDVWRCEE	60
DB	1	MGSFSESEVALVQLFLPTAAAYTCVSRGELGLVFRDLNASVSASFQRFVVDVWRCEE	60
QY	61	LEKTFTLQEEVVRAGLVLPKGRPLPAPPPRDLRIQETTERLAQLRDLVRGNQQAALRA	120
DB	61	LEKTFTLQEEVVRAGLVLPKGRPLPAPPPRDLRIQETTERLAQLRDLVRGNQQAALRA	120
QY	121	QLHQLGHAALVLRQGHPEPOLAAHTDASERTPLQAQGGPHODLRVNFVAGAVEPHKAP	180
DB	121	QLHQLGHAALVLRQGHPEPOLAAHTDASERTPLQAQGGPHODLRVNFVAGAVEPHKAP	180
QY	181	ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEGIQKIRKTDTCFH	240
DB	181	ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEGIQKIRKTDTCFH	240
QY	241	CHVFPFLQEEARLGLALQLOQSQSGLQVGLGTERFLSQVLRVQLQLPPGQVQVHKMK	300
DB	241	CHVFPFLQEEARLGLALQLOQSQSGLQVGLGTERFLSQVLRVQLQLPPGQVQVHKMK	300
QY	301	AVYLALNQCSVSTTHKCLIAEAWCSVRDLPALQEARLDDSMERGVSVAHRIPCRDMPT	360
DB	301	AVYLALNQCSVSTTHKCLIAEAWCSVRDLPALQEARLDDSMERGVSVAHRIPCRDMPT	360

QY 361 LIRTNRTASFOGIVDRYGVGRYQEVNPAPYITIIIPFLFVAMFGDVGHGLLMFLPALAM 420
DB |||||
DB 361 LIRTNRTASFOGIVDRYGVGRYQEVNPAPYITIIIPFLFVAMFGDVGHGLLMFLPALAM 420
QY 421 VLAENRPAKAAQNEIWTQFFRGRYLLLMGLFSIYTGFIYNECFSRATSIIPSGMSVAA 480
DB |||||
DB 421 VLAENRPAKAAQNEIWTQFFRGRYLLLMGLFSIYTGFIYNECFSRATSIIPSGMSVAA 480
QY 481 MANQSGWSDAFLAQTMLTLDPNVTGVLGPPFGDPTWSLAANHLFSFNSFKMKMSVI 540
DB |||||
DB 481 MANQSGWSDAFLAQTMLTLDPNVTGVLGPPFGDPTWSLAANHLFSFNSFKMKMSVI 540
QY 541 LGVVMHAFGVGVGNVHVFQGRHRLLETLBELTFLGLGVLPVLPVLYKLCVWAARA 600
DB |||||
DB 541 LGVVMHAFGVGVGNVHVFQGRHRLLETLBELTFLGLGVLPVLPVLYKLCVWAARA 600
QY 601 ASPSILIHFINMPLFSHSPSNRLLYPRQEVVQATLVVLAAMVPILLGTPLHLHRHR 660
DB |||||
DB 601 ASPSILIHFINMPLFSHSPSNRLLYPRQEVVQATLVVLAAMVPILLGTPLHLHRHR 660
QY 661 RLRRRPAQREKAGLLDLPASVNGWSSDEEKAGGLDDEEAELVPSEVLMHQAHTI 720
DB |||||
DB 661 RLRRRPAQREKAGLLDLPASVNGWSSDEEKAGGLDDEEAELVPSEVLMHQAHTI 720
QY 721 EFCLGCVSNTASYRLWALSALHAQLSEVLWAMVRIGLGLGREVGVAAVLVLPFAAPA 780
DB |||||
DB 721 EFCLGCVSNTASYRLWALSALHAQLSEVLWAMVRIGLGLGREVGVAAVLVLPFAAPA 780
QY 781 VMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYSGTGYKLSPF 822
DB |||||
DB 781 VMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYSGTGYKLSPF 822

RESULT 2

US-10-145-012-2
; Sequence 2, Application US/10145012
; Publication No. US20030124614A1
; GENERAL INFORMATION:
; APPLICANT: UT KU et al.
; TITLE OF INVENTION: T-CELL MEMBRANE PROTEIN (TIRC7), PEPTIDES AND ANTIBODIES DERIVED
; FILE REFERENCE: 4400-0105P
; CURRENT APPLICATION NUMBER: US/10/145,012
; CURRENT FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-012-2

Query Match 73.4%; Score 3131.5; DB 4; Length 614;
Best Local Similarity 99.7%; Pred. No. 2.4e-265;
Matches 605; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 217 MTFLISYWGEGIQGKIRKIDCFCHVPPFLOQEEARLGAQLQQLQOQSOELQEVIGETER 276
DB |||||
DB 1 MTFLISYWGEGIQGKIRKIDCFCHVPPFLOQEEARLGAQLQQLQOQSOELQEVIGETER 60
QY 277 FLSQVLGRVQLQLPPGQVQVHKMKAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQEA 336
DB |||||
DB 61 FLSQVLGRVQLQLPPGQVQVHKMKAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQEA 120
QY 337 RDSSMEEGVSAVAHRIPCRDMPTLIRNRTFTASFGIVDRYGVGRYQEVNPAPYITITF 396
DB |||||
DB 121 RDSSMEEGVSAVAHRIPCRDMPTLIRNRTFTASFGIVDRYGVGRYQEVNPAPYITITF 180
QY 397 PFLPAMFGDVGHGLLMFLPALAMVLAENRPAKAAQNEIWTQFFRGRYLLLMGLFSIY 456
DB |||||
DB 181 PFLPAMFGDVGHGLLMFLPALAMVLAENRPAKAAQNEIWTQFFRGRYLLLMGLFSIY 240

QY 457 TGFYINECFSRATSIIPSGMSVAAMANQSGWSDAFLAQTMLTLDPNVTGVLGPPYPGI 516
DB |||||
DB 241 TGFYINECFSRATSIIPSGMSVAAMANQSGWSDAFLAQTMLTLDPNVTGVLGPPYPGI 300
QY 517 DPIMSLAANHLFSFNSFKMKMSVILGVVHMAFGVVLGVGNVHVFQGRHRLLETLPELTF 576
DB |||||
DB 301 DPIMSLAANHLFSFNSFKMKMSVILGVVHMAFGVVLGVGNVHVFQGRHRLLETLPELTF 360
QY 577 LGLFGYLVFLVIYKLCVWAARAAS-PSILIHFINMPLFSHSPSNRLLYPROEVVQATL 635
DB |||||
DB 361 LGLFGYLVFLVIYKLCVWAARAASPSILIHFINMPLFSHSPSNRLLYPROEVVQATL 420
QY 636 VVLAAMVPILLGTPLHLHRRLRRRPAQREKAGLLDLPDASVNGWSSDEEKA 695
DB |||||
DB 421 VVLAAMVPILLGTPLHLHRRLRRRPAQREKAGLLDLPDASVNGWSSDEEKA 480
QY 696 GGLDDEEAELVPSEVLMHQAHTIETFCGCVSNTASYRLWALSALHAQLSEVLWAMVM 755
DB |||||
DB 481 GGLDDEEAELVPSEVLMHQAHTIETFCGCVSNTASYRLWALSALHAQLSEVLWAMVM 540
QY 756 RIGLGLGREVGVAAVLVLPFAAPVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYSGT 815
DB |||||
DB 541 RIGLGLGREVGVAAVLVLPFAAPVMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYSGT 600
QY 816 GYKLSPF 822
DB |||||
DB 601 GYKLSPF 607

RESULT 3

US-11-126-866-2
; Sequence 2, Application US/11126866
; Publication No. US20050220789A1
; GENERAL INFORMATION:
; APPLICANT: UT KU, et al., NALAN
; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS TO
; FILE REFERENCE: 1472/71099-2A/JPW/AG
; CURRENT APPLICATION NUMBER: US/11/126,866
; CURRENT FILING DATE: 2005-05-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 2
; LENGTH: 614
; TYPE: PRT
; ORGANISM: human
US-11-126-866-2

Query Match 73.4%; Score 3131.5; DB 6; Length 614;
Best Local Similarity 99.7%; Pred. No. 2.4e-265;
Matches 605; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 217 MTFLISYWGEGIQGKIRKIDCFCHVPPFLOQEEARLGAQLQQLQOQSOELQEVIGETER 276
DB |||||
DB 1 MTFLISYWGEGIQGKIRKIDCFCHVPPFLOQEEARLGAQLQQLQOQSOELQEVIGETER 60
QY 277 FLSQVLGRVQLQLPPGQVQVHKMKAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQEA 336
DB |||||
DB 61 FLSQVLGRVQLQLPPGQVQVHKMKAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQEA 120
QY 337 RDSSMEEGVSAVAHRIPCRDMPTLIRNRTFTASFGIVDRYGVGRYQEVNPAPYITITF 396
DB |||||
DB 121 RDSSMEEGVSAVAHRIPCRDMPTLIRNRTFTASFGIVDRYGVGRYQEVNPAPYITITF 180
QY 397 PFLPAMFGDVGHGLLMFLPALAMVLAENRPAKAAQNEIWTQFFRGRYLLLMGLFSIY 456
DB |||||
DB 181 PFLPAMFGDVGHGLLMFLPALAMVLAENRPAKAAQNEIWTQFFRGRYLLLMGLFSIY 240
QY 457 TGFYINECFSRATSIIPSGMSVAAMANQSGWSDAFLAQTMLTLDPNVTGVLGPPYPGI 516
DB |||||
DB 241 TGFYINECFSRATSIIPSGMSVAAMANQSGWSDAFLAQTMLTLDPNVTGVLGPPYPGI 300
QY 517 DPIMSLAANHLFSFNSFKMKMSVILGVVHMAFGVVLGVGNVHVFQGRHRLLETLPELTF 576

Db 301 DPTWLAANHLSPNSFKMMSVILGVVHAFGVVGVNFHFGQRHLLLETLPELTF 360
QY 577 LLGLFGYLVFLVIYKWLVCWAARAAS-PSILIHFINMFLFSHSPSNRLLYPRQEVQATL 635
Db 361 LLGLFGYLVFLVIYKWLVCWAARAASAPSILIHFINMFLFSHSPSNRLLYPRQEVQATL 420
QY 636 VVLALAMVPIILLGTPLHLHRRHRRRRPADQENKAGLLDLPDASVNGWSSDDEKA 695
Db 421 VVLALAMVPIILLGTPLHLHRRHRRRRPADQENKAGLLDLPDASVNGWSSDDEKA 480
QY 696 GGLDDEEAEALVPSEVLHMQAIIHTIEFCLGCVSNTASYLRILWALSALAHQOLSEVLWAWM 755
Db 481 GGLDDEEAEALVPSEVLHMQAIIHTIEFCLGCVSNTASYLRILWALSALAHQOLSEVLWAWM 540
QY 756 RIGLGLRGVGAHVLPVPIFAAFVAVMTVAILLVMEGLSAFLHALRLHWHVEFQNKFSYGT 815
Db 541 RIGLGLRGVGAHVLPVPIFAAFVAVMTVAILLVMEGLSAFLHALRLHWHVEFQNKFSYGT 600
QY 816 GYKLSPP 822
Db 601 GYKLSPP 607

RESULT 4

US-11-126-841A-2

; Sequence 2, Application US/11126841A

; Publication No. US20050271659A1

; GENERAL INFORMATION:

; APPLICANT: UTKU, et al., NALAN

; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS TO

; FILE REFERENCE: 1472/71099-ZB/JPW/AG

; CURRENT APPLICATION NUMBER: US/11/126,841A

; CURRENT FILING DATE: 2005-05-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 2

; LENGTH: 614

; TYPE: PRT

; ORGANISM: human

US-11-126-841A-2

Query Match 73.4%; Score 3131.5; DB 6; Length 614;
Best Local Similarity 99.7%; Pred. No. 2.4e-265;
Matches 605; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 217 MTELISYWGEOIGQIKIRKIDCFCHVFPFLOQEEARLQALQOLQOOSQELQEVLGSTER 276
Db 1 MTELISYWGEOIGQIKIRKIDCFCHVFPFLOQEEARLQALQOLQOOSQELQEVLGSTER 60
QY 277 FLSQVLGRVLQQLPPGQOVQVHKMAVYALNQCSTVTHKCLIAEAWCSVRDLPALQEAL 336
Db 61 FLSQVLGRVLQQLPPGQOVQVHKMAVYALNQCSTVTHKCLIAEAWCSVRDLPALQEAL 120
QY 337 RDSMEEGVSVAHRIPCRDMPTLIRTNRTASFGQIVDYGVRGYQEVNPPYTIITF 396
Db 121 RDSMEEGVSVAHRIPCRDMPTLIRTNRTASFGQIVDYGVRGYQEVNPPYTIITF 180
QY 397 PFLFAMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIWQTFFRGRYLLLLMGLFSIY 456
Db 181 PFLFAMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIWQTFFRGRYLLLLMGLFSIY 240
QY 457 TGFYINCEFSRATSIFFPSGWSVAAMANQSGWSDAFLAQHTMTLTDNPVTCVFLGPPYFPGI 516
Db 241 TGFYINCEFSRATSIFFPSGWSVAAMANQSGWSDAFLAQHTMTLTDNPVTCVFLGPPYFPGI 300
QY 517 DPTWLAANHLSPNSFKMMSVILGVVHAFGVVGVNFHFGQRHLLLETLPELTF 576
Db 301 DPTWLAANHLSPNSFKMMSVILGVVHAFGVVGVNFHFGQRHLLLETLPELTF 360
QY 577 LLGLFGYLVFLVIYKWLVCWAARAAS-PSILIHFINMFLFSHSPSNRLLYPRQEVQATL 635
Db 361 LLGLFGYLVFLVIYKWLVCWAARAASAPSILIHFINMFLFSHSPSNRLLYPRQEVQATL 420
QY 577 LLGLFGYLVFLVIYKWLVCWAARAAS-PSILIHFINMFLFSHSPSNRLLYPRQEVQATL 635

Db 361 LLGLFGYLVFLVIYKWLVCWAARAASAPSILIHFINMFLFSHSPSNRLLYPRQEVQATL 420
QY 636 VVLALAMVPIILLGTPLHLHRRHRRRRPADQENKAGLLDLPDASVNGWSSDDEKA 695
Db 421 VVLALAMVPIILLGTPLHLHRRHRRRRPADQENKAGLLDLPDASVNGWSSDDEKA 480
QY 696 GGLDDEEAEALVPSEVLHMQAIIHTIEFCLGCVSNTASYLRILWALSALAHQOLSEVLWAWM 755
Db 481 GGLDDEEAEALVPSEVLHMQAIIHTIEFCLGCVSNTASYLRILWALSALAHQOLSEVLWAWM 540
QY 756 RIGLGLRGVGAHVLPVPIFAAFVAVMTVAILLVMEGLSAFLHALRLHWHVEFQNKFSYGT 815
Db 541 RIGLGLRGVGAHVLPVPIFAAFVAVMTVAILLVMEGLSAFLHALRLHWHVEFQNKFSYGT 600
QY 816 GYKLSPP 822
Db 601 GYKLSPP 607

RESULT 5

US-10-145-012-13

; Sequence 13, Application US/10145012

; Publication No. US20030124614A1

; GENERAL INFORMATION:

; APPLICANT: UTKU et al.

; TITLE OF INVENTION: T-CELL MEMBRANE PROTEIN (TIRC7), PEPTIDES AND ANTIBODIES DERIVE

; FILE REFERENCE: 4400-0105P

; CURRENT APPLICATION NUMBER: US/10/145,012

; CURRENT FILING DATE: 2002-05-13

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 614

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-145-012-13

Query Match 73.3%; Score 3127.5; DB 4; Length 614;
Best Local Similarity 99.5%; Pred. No. 5.3e-265;
Matches 604; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 217 MTELISYWGEOIGQIKIRKIDCFCHVFPFLOQEEARLQALQOLQOOSQELQEVLGSTER 276
Db 1 MTELISYWGEOIGQIKIRKIDCFCHVFPFLOQEEARLQALQOLQOOSQELQEVLGSTER 60
QY 277 FLSQVLGRVLQQLPPGQOVQVHKMAVYALNQCSTVTHKCLIAEAWCSVRDLPALQEAL 336
Db 61 FLSQVLGRVLQQLPPGQOVQVHKMAVYALNQCSTVTHKCLIAEAWCSVRDLPALQEAL 120
QY 337 RDSMEEGVSVAHRIPCRDMPTLIRTNRTASFGQIVDYGVRGYQEVNPPYTIITF 396
Db 121 QDSMEEGVSVAHRIPCRDMPTLIRTNRTASFGQIVDYGVRGYQEVNPPYTIITF 180
QY 397 PFLFAMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIWQTFFRGRYLLLLMGLFSIY 456
Db 181 PFLFAMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIWQTFFRGRYLLLLMGLFSIY 240
QY 457 TGFYINCEFSRATSIFFPSGWSVAAMANQSGWSDAFLAQHTMTLTDNPVTCVFLGPPYFPGI 516
Db 241 TGFYINCEFSRATSIFFPSGWSVAAMANQSGWSDAFLAQHTMTLTDNPVTCVFLGPPYFPGI 300
QY 517 DPTWLAANHLSPNSFKMMSVILGVVHAFGVVGVNFHFGQRHLLLETLPELTF 576
Db 301 DPTWLAANHLSPNSFKMMSVILGVVHAFGVVGVNFHFGQRHLLLETLPELTF 360
QY 577 LLGLFGYLVFLVIYKWLVCWAARAAS-PSILIHFINMFLFSHSPSNRLLYPRQEVQATL 635
Db 361 LLGLFGYLVFLVIYKWLVCWAARAASAPSILIHFINMFLFSHSPSNRLLYPRQEVQATL 420
QY 636 VVLALAMVPIILLGTPLHLHRRHRRRRPADQENKAGLLDLPDASVNGWSSDDEKA 695
Db 421 VVLALAMVPIILLGTPLHLHRRHRRRRPADQENKAGLLDLPDASVNGWSSDDEKA 480

QY 696 GGLDDEEAEELVPSEVLHQAHTHTIEFCLGCVSNTASYLRLWALSALAHQAQLSEVLWAMVM 755
DB 481 GGLDDEEAEELVPSEVLHQAHTHTIEFCLGCVSNTASYLRLWALSALAHQAQLSEVLWAMVM 540
QY 756 RIGLGLGREVGVAADVLPFAFAVMTVAIILLVMEGLSAFLHALRLHWVEFQNKFYSGT 815
DB 541 RIGLGLGREVGVAADVLPFAFAVMTVAIILLVMEGLSAFLHALRLHWVEFQNKFYSGT 600
QY 816 GYKLSPP 822
DB 601 GYKLSPP 607

RESULT 6

US-10-489-725-5
; Sequence 5, Application US/10489725
; Publication NO. US20050048067A1
; GENERAL INFORMATION:
; APPLICANT: Utku, Nalan
; TITLE OF INVENTION: Peptides capable of modulating immune response
; FILE REFERENCE: GE19A46/P-WO
; CURRENT APPLICATION NUMBER: US/10/489,725
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/322,896
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/322,895
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-725-5

Query Match 73.3%; Score 3127.5; DB 5; Length 614;
Best Local Similarity 99.5%; Pred. No. 5.3e-265;
Matches 604; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 217 MTFLLSYNGEIQGQIRKIDCFHCHVFPFLQOEEARLALQLOOQSOQLQEVLETGER 276
DB 1 MTFLLSYNGEIQGQIRKIDCFHCHVFPFLQOEEARLALQLOOQSOQLQEVLETGER 60
QY 277 FLSQVLGRVLQLPPGQVQVHKMAVYLALNOCSTVTHKCLIAEAWCSVRDLPALQAL 336
DB 61 FLSQVLGRVLQLPPGQVQVHKMAVYLALNOCSTVTHKCLIAEAWCSVRDLPALQAL 120
QY 337 RDSMEEGVSVAHRIPCRDMPTLIRTNRTASFGQIVDYGVRGYQEVNPAPTYITTF 396
DB 121 QDSMEEGVSVAHRIPCRDMPTLIRTNRTASFGQIVDYGVRGYQEVNPAPTYITTF 180
QY 397 PFLFAMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIMQTFFRGYLLLLMGLFSY 456
DB 181 PFLFAMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIMQTFFRGYLLLLMGLFSY 240
QY 457 TGFYNCEFSRATSIFFPSGWSVAAMNOSGSDAFLAQTMLTLDPNVTGVLGYPYFGI 516
DB 241 TGFYNCEFSRATSIFFPSGWSVAAMNOSGSDAFLAQTMLTLDPNVTGVLGYPYFGI 300
QY 517 DPIWLAANHLISFLNSFKMKMSVILGVVHMAFGVVLGVFNHVFQGRHRLLETLPETLF 576
DB 301 DPIWLAANHLISFLNSFKMKMSVILGVVHMAFGVVLGVFNHVFQGRHRLLETLPETLF 360
QY 577 LLGLPGYLVFLVIYKWLCAWAAAS-PSILHFINMFLFSPSNRLLYPRQEVVQATL 635
DB 361 LLGLPGYLVFLVIYKWLCAWAAASPSILHFINMFLFSPSNRLLYPRQEVVQATL 420
QY 636 VVALAMVPIILLGTPLHLHRRRLRRRRPADROENKAGLLDLPDASVNGWSSDEEKA 695
DB 421 VVALAMVPIILLGTPLHLHRRRLRRRRPADROENKAGLLDLPDASVNGWSSDEEKA 480
QY 696 GGLDDEEAEELVPSEVLHQAHTHTIEFCLGCVSNTASYLRLWALSALAHQAQLSEVLWAMVM 755

DB 481 GGLDDEEAEELVPSEVLHQAHTHTIEFCLGCVSNTASYLRLWALSALAHQAQLSEVLWAMVM 540
QY 756 RIGLGLGREVGVAADVLPFAFAVMTVAIILLVMEGLSAFLHALRLHWVEFQNKFYSGT 815
DB 541 RIGLGLGREVGVAADVLPFAFAVMTVAIILLVMEGLSAFLHALRLHWVEFQNKFYSGT 600
QY 816 GYKLSPP 822
DB 601 GYKLSPP 607

RESULT 7

US-11-126-866-13
; Sequence 13, Application US/11126866
; Publication NO. US20050220789A1
; GENERAL INFORMATION:
; APPLICANT: UTKU, et al., NALAN
; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS 1
; FILE REFERENCE: 1472/71099-ZA/JPW/AG
; CURRENT APPLICATION NUMBER: US/11/126,866
; CURRENT FILING DATE: 2005-05-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-126-866-13

Query Match 73.3%; Score 3127.5; DB 6; Length 614;
Best Local Similarity 99.5%; Pred. No. 5.3e-265;
Matches 604; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 217 MTFLLSYNGEIQGQIRKIDCFHCHVFPFLQOEEARLALQLOOQSOQLQEVLETGER 276
DB 1 MTFLLSYNGEIQGQIRKIDCFHCHVFPFLQOEEARLALQLOOQSOQLQEVLETGER 60
QY 277 FLSQVLGRVLQLPPGQVQVHKMAVYLALNOCSTVTHKCLIAEAWCSVRDLPALQAL 336
DB 61 FLSQVLGRVLQLPPGQVQVHKMAVYLALNOCSTVTHKCLIAEAWCSVRDLPALQAL 120
QY 337 RDSMEEGVSVAHRIPCRDMPTLIRTNRTASFGQIVDYGVRGYQEVNPAPTYITTF 396
DB 121 QDSMEEGVSVAHRIPCRDMPTLIRTNRTASFGQIVDYGVRGYQEVNPAPTYITTF 180
QY 397 PFLFAMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIMQTFFRGYLLLLMGLFSY 456
DB 181 PFLFAMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIMQTFFRGYLLLLMGLFSY 240
QY 457 TGFYNCEFSRATSIFFPSGWSVAAMNOSGSDAFLAQTMLTLDPNVTGVLGYPYFGI 516
DB 241 TGFYNCEFSRATSIFFPSGWSVAAMNOSGSDAFLAQTMLTLDPNVTGVLGYPYFGI 300
QY 517 DPIWLAANHLISFLNSFKMKMSVILGVVHMAFGVVLGVFNHVFQGRHRLLETLPETLF 576
DB 301 DPIWLAANHLISFLNSFKMKMSVILGVVHMAFGVVLGVFNHVFQGRHRLLETLPETLF 360
QY 577 LLGLPGYLVFLVIYKWLCAWAAAS-PSILHFINMFLFSPSNRLLYPRQEVVQATL 635
DB 361 LLGLPGYLVFLVIYKWLCAWAAASPSILHFINMFLFSPSNRLLYPRQEVVQATL 420
QY 636 VVALAMVPIILLGTPLHLHRRRLRRRRPADROENKAGLLDLPDASVNGWSSDEEKA 695
DB 421 VVALAMVPIILLGTPLHLHRRRLRRRRPADROENKAGLLDLPDASVNGWSSDEEKA 480
QY 696 GGLDDEEAEELVPSEVLHQAHTHTIEFCLGCVSNTASYLRLWALSALAHQAQLSEVLWAMVM 755
DB 481 GGLDDEEAEELVPSEVLHQAHTHTIEFCLGCVSNTASYLRLWALSALAHQAQLSEVLWAMVM 540

QY 756 RIGLGLREVGVAHVLPPIFAAFVAVMTVAILLVMEGLSAPFLHALRLHWVEFQNKFSYGT 815
Db 541 RIGLGLREVGVAHVLPPIFAAFVAVMTVAILLVMEGLSAPFLHALRLHWVEFQNKFSYGT 600
QY 816 GYKLSPPF 822
Db 601 GYKLSPPF 607
RESULT 8
US-11-126-841A-13
; Sequence 13, Application US/11126841A
; Publication No. US20050271659A1
; GENERAL INFORMATION:
; APPLICANT: UTRO, et al., NALAN
; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS TO
; FILE REFERENCE: 1472/71099-ZB/JPW/AG
; CURRENT APPLICATION NUMBER: US/11/126,841A
; CURRENT FILING DATE: 2005-05-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-126-841A-13
Query Match 73.3%; Score 3127.5; DB 6; Length 614;
Best Local Similarity 99.3%; Pred. No. 5.3e-265;
Matches 604; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 217 MTLISYWGEGIQGKIRKIDCFCHVFPFLOQEEARLQALQOQSQBELQVIGETER 276
Db 1 MTLISYWGEGIQGKIRKIDCFCHVFPFLOQEEARLQALQOQSQBELQVIGETER 60
QY 277 FLISQVLRVQLLPPGQVQVHKMAVYALNQCSTVTHKCLIAEAWCSVRDLPALQAL 336
Db 61 FLISQVLRVQLLPPGQVQVHKMAVYALNQCSTVTHKCLIAEAWCSVRDLPALQAL 120
QY 337 ROSSMEEGSAVAHRIPCRDMPTLIRTNFTASFGQIVDGRYGVRYQVNPAPYIITF 396
Db 121 QSSMEEGSAVAHRIPCRDMPTLIRTNFTASFGQIVDGRYGVRYQVNPAPYIITF 180
QY 397 PFLFVAVFQVGHGLMFLFALAWLAENRPVAKAONEIWQFFRGYRLLLMGLFSIY 456
Db 181 PFLFVAVFQVGHGLMFLFALAWLAENRPVAKAONEIWQFFRGYRLLLMGLFSIY 240
QY 457 TGIYNECFSRATSIIPSGWSVAAMANQSGWSDAFLAQHTMTLTDPNVTGVFLGYPFGI 516
Db 241 TGIYNECFSRATSIIPSGWSVAAMANQSGWSDAFLAQHTMTLTDPNVTGVFLGYPFGI 300
QY 517 DPTWLSAANHLSTNSFKKMSVILGVVHMAFGVILGVFNHVFQGRHLLLTLPETLF 576
Db 301 DPTWLSAANHLSTNSFKKMSVILGVVHMAFGVILGVFNHVFQGRHLLLTLPETLF 360
QY 577 LGLFGYLVFLVIYKVLVWAAAS-PSILHIFINMFLSHSPSNRLLYPROEVVQATL 635
Db 361 LGLFGYLVFLVIYKVLVWAAASAPSLIHLINMFLSHSPSNRLLYPROEVVQATL 420
QY 636 VVALAMVPILLGTPHLHLHRRRLRRPADRQENKAGLLDLPDASVNGWSSDEEKA 695
Db 421 VVALAMVPILLGTPHLHLHRRRLRRPADRQENKAGLLDLPDASVNGWSSDEEKA 480
QY 696 GGLDDEEAEELVSEVLMHQAHTIEFCIGCVNTASYLRLWALSALHAQLSEVLWAVM 755
Db 481 GGLDDEEAEELVSEVLMHQAHTIEFCIGCVNTASYLRLWALSALHAQLSEVLWAVM 540
QY 756 RIGLGLREVGVAHVLPPIFAAFVAVMTVAILLVMEGLSAPFLHALRLHWVEFQNKFSYGT 815
Db 541 RIGLGLREVGVAHVLPPIFAAFVAVMTVAILLVMEGLSAPFLHALRLHWVEFQNKFSYGT 600

QY 816 GYKLSPPF 822
Db 601 GYKLSPPF 607
RESULT 9
US-10-264-049-2656
; Sequence 2656, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAI33PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2656
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (77)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (318)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (598)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-2656
Query Match 68.4%; Score 2917.5; DB 4; Length 643;
Best Local Similarity 99.3%; Pred. No. 1.5e-246;
Matches 559; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 67 FLOEYVRRAGLVLPKGRLLPAPPDRDLRIQETERLAQELDRVGNQALRAQLHQLQ 126
Db 35 FLOEYVRRAGLVLPKGRLLPAPPDRDLRIQETERLAQELDRVGNQALRAQLHQLQ 94
QY 127 LHAVALROGHEPQOLAAHTDASERTPLLOAPGGPHQDLRVNFAVAVEPHKAPALERLL 186
Db 95 LHAVALROGHEPQOLAAHTDASERTPLLOAPGGPHQDLRVNFAVAVEPHKAPALERLL 154
QY 187 WRACRGLFIASPRELEQPLEHPVTGEPATMTFLISYWGEOIGQKIRKIDCFCHVFPF 246
Db 155 WRACRGLFIASPRELEQPLEHPVTGEPATMTFLISYWGEOIGQKIRKIDCFCHVFPF 214
QY 247 LQOEERLQALQOQSQSQELQVIGETERFLSQVLRVQLLPPGQVQVHKMAVYAL 306
Db 215 LQOEERLQALQOQSQSQELQVIGETERFLSQVLRVQLLPPGQVQVHKMAVYAL 274
QY 307 NQCSVSTTHKCLIAEAWCSVRDLPALQALROSSMEEGSAVAHRIPCRDMPTLIRTNR 366
Db 275 NQCSVSTTHKCLIAEAWCSVRDLPALQALROSSMEEGSAVAHRIPCRDMPTLIRTNR 334
QY 367 FTASFQGIYDVRGVGRYQVNPAPYIITFPFLFVAVFQVGHGLMFLFALAWLAENR 426
Db 335 FTASFQGIYDVRGVGRYQVNPAPYIITFPFLFVAVFQVGHGLMFLFALAWLAENR 394
QY 427 PAVKAAQNEIWQFFRGYRLLLMGLFSIYTGFIYNECFSRATSIIPSGWSVAAMANQSG 486
Db 395 PAVKAAQNEIWQFFRGYRLLLMGLFSIYTGFIYNECFSRATSIIPSGWSVAAMANQSG 454
QY 487 WSDAFLAQHTMTLTDPNVTGVFLGYPFGIDPISLAANHLSTNSFKKMSVILGVVHM 546

Db 455 WSDAPLAQHTMLTLDNVTGVFLGPYPFGIDPISLAANHLSFNSFKMKSIVLGVHM 514
QY 547 AGCVVLGVNHHVFGQRHLLLETPELTFLGLFGYLVFLVIYKWLVCWAARAAS-PSI 605
Db 515 AGVVLGVNHHVFGQRHLLLETPELTFLGLFGYLVFLVIYKWLVCWAARAASAPSI 574
QY 606 LIHFINMFLFSHSPSNRLLYPRQ 628
Db 575 LIHFINMFLFSHSPSNRLLYPRQ 597
RESULT 10
US-10-495-446-32
; Sequence 32, Application US/10495446
; Publication No. US20040214191A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN RAS INTERACTING PROTEIN
; FILE REFERENCE: PB0190
; CURRENT APPLICATION NUMBER: US/10/495,446
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: PCT/US02/35128
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/332,756
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Aemica Sequence Listing Engine
; SEQ ID NO 32
; LENGTH: 818
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-495-446-32

Query Match 48.4%; Score 2066; DB 4; Length 818;
Best Local Similarity 51.1%; Pred. No. 1.le-171;
Matches 426; Conservative 128; Mismatches 225; Indels 54; Gaps 15;
QY 26 VSRIGELGLVPRDLNASVSFAFRFVVDVWRCCELEKTFITFLOEVRAGLVLPPKGR 85
Db 1 LSALEGKLVQPRDLNQNVSSQRFVGVKRCCELEILVLYVQETRADIPLEGEAS 60
QY 86 LPAPPRLRLRIQEBTERLAQRLDVRGNQQAALRAQL-----HQLQLHAAVLKQGEH- 137
Db 61 PPAPPLKXVLEMQEQLQKLELVRELVTKNKKLRLNLELVETHTMLRVTKTFLKRVF 120
QY 138 ----POLAAHTDASERTPLQAGGPHQDLRVNPFVAGBPHKAPALERLLWLRACRGF 193
Db 121 EPTYEFPALENDSLDYS-CMQLGA-----KLGFVSLIQQGRVEAFERMLWRACKY 174
QY 194 LIASPRELEQPLEHPVTGEPATMMTFLISYMGEOIGQIKITDCFCHVFPFLQGEAR 253
Db 175 TLVTVAELDECLDEPTEGIVKMYVFLISFWGEQGHKVKKICDCHYCHYIPYNTAER 234
QY 254 LGALQLOQSQSLEQLGETERFLSQVLGRVQLQLPPQGVQVHKMKAVYALNOCVSST 313
Db 235 RBIOGLNTRIQLDLYTLVHKTEDYRLQVLCKAESVCSRVVQVRMKKAIYHMLNWCSPDV 294
QY 314 THKCLIAEAWCSVRDLPALQALRDSSMEEG--VSAVAHRIPCRMDPPTLINTNPTASF 371
Db 295 TNKCLIAEWCPEVDLPGLRLRAEGSRESGATIPSMNTIPTKETPTLINTNPTSGF 354
QY 372 QGIVDRYGVGRYOENVNAPYTIITPPFLFVNFMDVGHGLMLFALPALAENPAVKA 431
Db 355 QNIVDAYGVGSVREYNPALFTIITPPFLFVNFMDVGHGLMLFALPALAENPNRUSQ 414
QY 432 AQNETWQTFRGRYLLMLGLFSIYTGFIYNECFSRATSIFFPSGWSAAMANQSG----- 486
Db 415 SQ-EILRMFFDGRYILLMLGLFSVVTGLIYNDSCFSKSNVLFSGNVSAMYSSSHSPBEQ 473
QY 487 -----WSDAFLAQHTMLTLDNVTGVFLGPYPFGIDPISLAANHLSFNSFKMKSIVL 541
Db 474 RQWLWMDSTIRHSRTLQLDNPIGVFGPYFGIDPISLAANHLSFNSFKMKSIVL 533

QY 542 GVVHMAFGVVLGVNHHVFGQRHLLLETPELTFLGLFGYLVFLVIYKWLVCWAARA- 600
Db 534 GIFHMTFGVVLGVNHHVFGQRHLLLETPELTFLGLFGYLVFLVIYKWLVCWAARA- 593
QY 601 ASPSILIHFINMFLFSHSPSNRLLYPRQEVQATLVVLAALAMVPITLLGLTPLHLLHRHR 660
Db 594 EAPSLIEFINMFLFSHSPSNRLLYPRQEVQATLVVLAALAMVPITLLGLTPLHLLHRHR 652
QY 661 R-----LRRRPADQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEVLVPS 709
Db 653 RNCFGMSRSRGYTLVRK--DSEEE--VSLIGNODIE--EGNSRME--GCREVTCEBFNF 704
QY 710 EVLMHQAHTHTIEFCIGCVSNATSYLRMLWALSIAHAQLSEVLWAMVNRIGLGLGREVGAA 769
Db 705 EILMTQAHISIEYICIGCISNTASYLRMLWALSIAHAQLSDVLWAMLMRVGLRVDVTTGV-- 762
QY 770 VVLVPIFAAFVMTVAILLVMEGLSAFLHALHLHWVEFQNKFYSGTGKLSPF 822
Db 763 LLLLPVMAFFAVLTITPILLVMEGLSAFLHAIHLHWVEFQNKFYSGTGKLSPF 815

RESULT 11
US-10-874-706-20
; Sequence 20, Application US/10874706
; Publication No. US20050048610A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: YANG, Junming
; APPLICANT: YUE, Henry
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: HUMAN TRANSPORT PROTEINS
; FILE REFERENCE: PF-0709 PCT
; CURRENT APPLICATION NUMBER: US/10/874,706
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: US/10/009,328
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/139,923; 60/148,177; 60/149,357; 60/162,287
; PRIOR FILING DATE: 1999-06-17; 1999-08-10; 1999-08-18; 1999-10-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 841
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: Incyte ID No: 2762348CD1
US-10-874-706-20

Query Match 45.0%; Score 1918.5; DB 5; Length 841;
Best Local Similarity 49.7%; Pred. No. 1e-158;
Matches 417; Conservative 123; Mismatches 272; Indels 27; Gaps 15;
QY 1 MGSFRSEVALVQLFLPTAAAYTCVSRIGELGLVEFPRDLNASVAFQRRFVVDVWRCSE 60
Db 1 MASVRSSEMCLSQLFLQVAAAYCCVAGELGLVQFKDLNMNVNSFORKFVNEVRCS 60
QY 61 LEKTFITFLOEVRAGLVLPPKGLPAPPDRDLRIQEBTERLAQRLDVRGNQQAALR- 119
Db 61 LERILRLEDEMONEIVVQLLEKSP--TLPREMITITLVLEKLEGELEQANQQAALQK 119
QY 120 --AQLHQQLHAAVLNRQGHFPQAAAAHTDASERTPLQAGGPP--HQDLRVNPFVAGVPE 176

Db 120 SFLELTELKYLKKTQDFPFTETNADDPFTEDTSGILLELKAVPAYMTGKLGFIAGCDPT 179
Qy 177 HKAPA-LERLLWRACRGFLIASPRELEBPHEPVTGEPATWMTFLISYWGEOIQOKIRKI 235
Db 180 GKMASFERLLMRVCRGNVYLKFSMDAPLEDPTKEEIQKHIFIIFYQGBQLKQIKKI 239
Qy 236 TDCFCHVFPFLOQEEARLGAQLQLOQSOQLQELVIGETERFLSQVLGRVQLLPPQOVQ 295
Db 240 CDGFRATVYCPPEPAVERREMLSVNRLEDLITVITQTESHRQLRLQEEAANWHMLIK 299
Qy 296 VHKMKAYVALNQCSTVTHKCLIAEAWCSVRDLPALQEAALRDSMBEGVSAVA--HRI 352
Db 300 VQMKAVYHILNMCNIDVTQCVIAEITWFPVADATRIKRAL-EOGMELSGSSMAPIMTV 358
Qy 353 PCRDMPPTLIRTRFTASFGQIVDRYGVGRYQEVNPAPIYITPPFLFAMVFGVGHLL 412
Db 359 QSKTAPTRNTRKNTKFTAGFQNIVDAYGVGSYREINPAPYITITPPFLFAMVFGDCHGT 418
Qy 413 MFLFALAWLAENRPAVKAAQNEIWOTFERGRYLLLMGLFSIYTGFIYNECSRATSI 472
Db 419 MLLAALMILNERLLSOKTDNEIWNTPFHGRYDILLMGIFSIYTGFIYNDGFSKLNIF 478
Qy 473 PSCWSVAAMQNSGWSDAFLAQHTMLTLDPNVTGVFLG-PYPFGIDPIWLSLAANHLSTLN 531
Db 479 GSSWSQPMFRNGTWNTHVMEESIYLQDPAIPGVYFGNYPYFGIDPIWNLASNKLTFLN 538
Qy 532 SFQKMSVILGVVHMAFGVVLGVFNHVFQGRHRLLETPELTFLGLFGYLVFLVIYK 591
Db 539 SYRKMSVILGIVQMVFGVLSLNFHNYFRRTNLIQFIPEMIFILCLFGYLVFMIIFK 598
Qy 592 WLC--VWAARASPSILIHFINFLFSH-PSNRLYPREVVOATLVLALAMVPTLL 648
Db 599 WCCFDVHVSQA-PSILIHFINFLFNYSDSSNAPLYKHQOEVQSFVVMALISVPMWLL 657
Qy 649 GTP--LHLHRRLRRPADROENKAGLLDLPDASVNGWSDEEKAGGLDDEBAEL 706
Db 658 IKFPILRASHKXSOQLASRIQEDATENIEGSSSP--SSRSQRTSADTHGALDDHGE-EP 715
Qy 707 VPSEVLHQAIHTIEFCLGCVSNTASYLRWLWALSLAHQALSEVLWAMVMRIGL---GLGR 763
Db 716 NFGDVFVHQAIHTIEYCLGCVSNTASYLRWLWALSLAHQALSEVLWAMVMRIGL---GLGR 775
Qy 764 EUGVAAVLPVIAFAFAMVTVAILLVMEGLSAPLHRLHWHVRFONKFYSGTGKLSPP 822
Db 776 IVGVFI-----IFAVFAVLTVAILLMEGLSAPLHRLHWHVRFONKFYSGTGKLSPP 829

RESULT 12

US-10-783-519-3
; Sequence 3, Application US/10783519
; Publication No. US2005064448A1
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; TITLE OF INVENTION: Octoclast Proton Pump Subunit
; FILE REFERENCE: 1564.1006-001
; CURRENT APPLICATION NUMBER: US/10783,519
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/618,304
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 08/605,378
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 847

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
; NAME/KEY: VARIANT
; LOCATION: (1)...(847)

; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-783-519-3

Query Match 42.2%; Score 1801.5; DB 5; Length 847;
Best Local Similarity 46.8%; Pred. No. 1.9e-148;
Matches 391; Conservative 45; Mismatches 384; Indels 15; Gaps 6;

Qy 1 MGSMPRESEVALVOLFLPTAAAYTCVSRISLGLVLFVDFRDNLASVASFORRRVVDVWRCCE 60
Db 1 MGXLFSEEXXLLQFLXXAAAYCVSKXELGXXVFRDLNXXVXXFQRFVFXVRRCEE 60
Qy 61 LEXTFTFLQEVRRAGLVLPKGRLPAPPRDLRLIQEETERLAQLRDLVRGNOQALRA 120
Db 61 MDXILFXFXEIRAXXXXXXXXPPAPRDMXXXXXXEXXEXXELXEIXXNQXALX 120
Qy 121 QLHQQLHAAVLRQGHFPLQAAAHDTGASBRTPLL-QAPGGPHODLRVNFVAGAVEPHKA 179
Db 121 XFXXLXXXXXILRXXXXXXXDXDXEXXLLXXXXXXGXKXKXFXVAGIXXXXX 180
Qy 180 PALERLLWRACRGFLIASPRELEBPHEPVTGEPATWMTFLISYWGEOIQOKIRKIDCF 239
Db 181 PXFERMLWRXCRGXXXXXXEXEXPLEXPVTGDXXXXXXFXIXFXGQXXXXXVXKIXEF 240
Qy 240 HCVFPLQOEEARLGAQLQLOQSOQLQELVIGETERFLSQVLGRVQLLPPQOVVHKM 299
Db 241 XXXXYPXXXXXXRXXXXXXXDXDXEXXLLXXXXXXVLTXXXXXXXIXVXKM 300
Qy 300 KAVYVALNQCSTVTHKCLIAEAWCSVRDLPALQEAALRDSMBEG--VSAVAHRIPCRDM 357
Db 301 KAIYXXLNCXIXXTXKCLIAEAWCXVXDLXQXQXALRXXXXXXGXVXXIXXXXXXX 360
Qy 358 PPTLIRNRTASFGQIVDRYGVGRYQEVNPAPIYITPPFLFAMVFGDVGHLMLFLFA 417
Db 361 PPTXXXTNKTXFXQXIVD-YGIXYXEINPAPYITITPPFLFAMVFGDVGHLMLFLFA 419
Qy 418 LAMVLAENRPAVKAAQNEIWOTFERGRYLLLMGLFSIYTGFIYNECSRATSIFFSGWS 477
Db 420 XXVWLXEXRXXXXXXNEXFXXFXGRYXXLLMGXFSIYTGFIYNDGFSXXXXXIFXSKWS 479
Qy 478 VAAMANQSGWSDAFLAQHTMLTLDPNVTGVFLGYPYFGIDPIWLSLAANHLSTLN 537
Db 480 VXXMXXXXXXWEXXLLXXXXXXLXLPXVXGVXFXGYPYFGIDPIWXXAXXNLXFLN 539
Qy 538 SVILGVVHMAFGVVLGVFNHVFQGRHRLLETPELTFLGLFGYLVFLVIYKWLVCWA 597
Db 540 SVILGIITHXFGVXKXFXFNHXXFXXXXXXXFXXXPEXFXMXLFGYLVXLIYKXXXXY 599
Qy 598 A--RAASPSLIIHFINFLFSHSPS-NRLIYPROEVVOATLVLALAMVPTLLGTLPHL 654
Db 600 AXXXXXXPSLIIHFINFLFSXXXXXXNMLYXXQXXIQXXLVXVXALXXVPMXLLXXPLX 659
Qy 655 LHRHRR-----LRLRRPADRQENKAGLLDLPDASVNGWSDEEKAGGLDDEBAEL 706
Db 660 XXXXRXXXXXXXXXXXXXRXXXXXXXFXXXXXXXXXXXXXEXXXXXXEXXDF 719
Qy 707 VPSEVLHQAIHTIEFCLGCVSNTASYLRWLWALSLAHQALSEVLWAMVMRIGLGLREV 766
Db 720 XXXDXMKHQAIHTIEYCLGCVSNTASYLRWLWALSLAHQALSEVLWAMVMRIGLGLREV 779
Qy 767 VAAVLPVIAFAFAMVTVAILLVMEGLSAPLHRLHWHVRFONKFYSGTGKLSPP 821
Db 780 XXXXFXFXIIFAAFAVXLTVAILLMEGLSAPLHRLHWHVRFONKFYSGTGKLSPP 834

RESULT 13

US-10-714-995-14
; Sequence 14, Application US/10714995
; Publication No. US20060039941A1
; GENERAL INFORMATION:
; APPLICANT: Stam, Lynn
; APPLICANT: Kamdar, Kim
; APPLICANT: Spana, Eric
; APPLICANT: Bachman, Jane

FOR THE BOARD OF DIRECTORS OF THE COMPANY

[illegible]

RESULT 15

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US-11-097-143-41499
; Sequence 41499, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41499
; LENGTH: 834
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-41499

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Query Match	39.9%	Score 1701;	DB 6;	Length 834;
Best Local Similarity	42.2%;	Pred. No. 1.3e-139;		
Matches	365;	Conservative 147;	Mismatches 268;	Indels 84; Gaps 18;
Qy	1	MGSMFSEEEVALVQLFLPTAAATVCSRLGELGLVFRDLNANVSFAQRFFVVDVWRCEE	60	
Db	1	MGDMFSEEWALCOMFIQPEAAITVSEIGETCGVQFRDLNVNNAFORKFVTEVRRCDE	60	
Qy	61	LEKTFTFLQBEVRRAGLVPPPPKGRLP-APPPRDLRLIQ-----EETE-----RLAQ-----	106	
Db	61	LERKIRVIETIKKQGVLPDIODDIPRAPNPREDIIDLEAHLKTESEMIELAQNEVNMK	120	
Qy	107	-----ELRDVGNQOALRAQLHQLQHLAAVLROQHEPOLAAAHTDGASERTPLQAPG	159	
Db	121	SNYLELTTELKVLNTQGFSDQEVNLNLDSS-NRAGGDNDAQAHRG-----	166	
Qy	160	GPHQDLRVNVAGAVPHKAPALERLLWRACRGFLTASPRELEOPLHPVTGEPATWMTF	219	
Db	167	-----RLGFVAGVIVNRVFAFERMLWIRSGNVFLKRSDDLDEPLNDPATGHPYKTVF	220	
Qy	220	LISYWGEEIQGKIRKIDTDFCHVFPFLQOEEARLQALQOQSOELOEVLGETERFLS	279	
Db	221	VAFFQGEQLKNRIKKVCTGFHASLYPCPSHNEREBWNRVTRLEDLKLVLSTQEDHRS	280	
Qy	280	QVLGRVLQLLPPQOVQVHKMKAVYIALNOCSTVSTHKCLIAEAWCSVRDLPALQEAALRS	339	
Db	281	RLVATVSKNLPWSIMVYKMKAIYHTLNFNMDVTKKCLIGECVPTNDLPVVQKALS DG	340	
Qy	340	SMEEG-VSAVAHRIPCRDMPTPLIRTNFTASFGQIVDRYGVRYQEVNPAPYTIITPP	397	
Db	341	SAAVGSTIFSFLNVIDTNEQPTPTFNRTNKTGTFQNLIDAYGVASRECNPAIYTCITPP	400	
Qy	398	FLFAVMFGDVGHGLLMFLFALAMVLAENRPVAKAAQNEIWQTFFRGRYILLMLGLFSIYT	457	
Db	401	FLFAVMFGDLGHGLILVLFGAMVLCERKLARIRNGGEIWNIFFGGRYILLMLGLFAMYT	460	
Qy	458	GFTYNECFSEATSI FSGSHSVAAMANQSGWSADFLAQHTMLTLDPNVTGVFGPPYFGID	517	
Db	461	GLVYNDVFSKSNMLFGSRWF-----NNYNTTTLTNPNLQLPPNSSAV--GVYPPFGMD	511	
Qy	518	PIWSLAANHLSPLNSFKMKMSVILGVVHMAFGVLGVFNHVFQGRHRLLETLPBLTFL	577	
Db	512	PVQLADNKIIFLNSFKMLSIIFGLVHWVFGVMSVNFTHKRYASTFLEFVPQLFL	571	
Qy	578	LGFLGYLVFLVIYKIVCVWAARAA-----SPSILIHFINMFLFHSHP-----SNRLLYT	625	
Db	572	LLLFGYVFMWMPFKWS-YNARTSFQETPGCAPSVLIMFINMFLFKNTEPPKGCNEFMF	630	
Qy	626	PROEVQATLVVLALAMVPIILLGTPHLHRRRLRRRDRADROBENK-AGLLDLPDAS	684	
Db	631	ESQFOIQAQFVIALCCIPMMLLKGPLYI-----KPTRKNKAHANHGOLTGNIELAEGE	685	
Qy	685	V----NGWSSDEEKAGGLDDEEAELVPSVLMHQAIHTIEFCIGCVSNITASLRLWALS	741	
Db	686	TPLPDPTGSGNEENAGAGHGDDEPM--SEIYIHQAIHTIEYVLSTISHTASVLRWLWALS	743	
Qy	742	AHAQLSEVLWAMVRIGL---GLGREVGVAAVVLVPFAAFAMVTVAIILVMMEGLSAFLH	798	
Db	744	AHAQLSEVLWQMWVLSGLKMSGVGGAIG-----LFTIFGAWCLFTLAILVLMMEGLSAFLH	798	
Qy	799	ALRLHWVEFQNFYSGTYKLSGPF	822	
Db	799	TLRLHWVEFQNFYSGTYKLSGPF	822	

Search completed: June 29, 2006, 13:13:04
Job time : 184 secs

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OM protein - protein search, using sw model

Run on: June 29, 2006, 13:10:14 ; Search time 20 Seconds
(without alignments) 970.769 Million cell

Title: US-10-783-519-2
Perfect score: 4266
Sequence: 1 MGSMSRSEEEVALVQLFLPTA.....HWVEFQNKFYSGTGKYLSPF 822

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103426 seqs, 23619683 residues

Total number of hits satisfying chosen parameters: 103426

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB pep.*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB pep.*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	4235.5	99.3	830	6	US-10-511-937-2474	Sequence 2474, App	
2	1325.5	31.1	820	6	US-10-449-902-53048	Sequence 53048, A	
3	1202	28.2	818	6	US-10-449-902-53444	Sequence 53444, A	
4	1195	28.0	818	6	US-10-449-902-47207	Sequence 47207, A	
5	1113	26.1	923	6	US-10-449-902-41603	Sequence 41603, A	
6	897	21.0	489	6	US-10-449-902-52773	Sequence 52773, A	
7	627.5	14.1	357	6	US-10-449-902-29928	Sequence 29928, A	
8	600	14.1	314	6	US-10-953-349-18079	Sequence 18079, A	
9	521	12.2	273	6	US-10-953-349-18080	Sequence 18080, A	
10	511	12.0	271	6	US-10-953-349-18081	Sequence 18081, A	
11	361	8.5	306	6	US-10-953-349-30245	Sequence 30245, A	
12	361	8.5	317	6	US-10-953-349-30244	Sequence 30244, A	
13	361	8.5	358	6	US-10-953-349-30243	Sequence 30243, A	
14	152	3.6	43	6	US-10-449-902-29221	Sequence 29221, A	
15	129	3.0	1966	6	US-10-829-000-5	Sequence 5, Appli	
16	129	3.0	1966	6	US-10-829-000-6	Sequence 6, Appli	
17	124.5	2.9	1977	6	US-10-829-000-7	Sequence 7, Appli	
18	112	2.6	333	6	US-10-953-349-33859	Sequence 33859, A	
19	112	2.6	378	6	US-10-953-349-33858	Sequence 33858, A	
20	112	2.6	442	6	US-10-953-349-33857	Sequence 33857, A	
21	106.5	2.5	553	7	US-11-233-089-36	Sequence 36, Appl	
22	101.5	2.4	526	6	US-10-449-902-34698	Sequence 34698, A	
23	101.5	2.4	526	6	US-10-449-902-52054	Sequence 52054, A	
24	101	2.4	1181	7	US-11-241-596-255	Sequence 255, App	
25	101	2.4	1181	7	US-11-241-596-256	Sequence 256, App	

ALIGNMENTS

RESULT 1

US-10-511-937-2474
; Sequence 2474, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2474
; LENGTH: 830
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2474

Query Match	99.3%;	Score 4235.5;	DB 6;	Length 830;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 820; Conservative	0;	Mismatches	2;	Indels 1; Gaps 1;
Qy	1	MGSMPFSEEEVALVOLFLPTAAATCTVSRLGELGLVFEFRDINASVSFAQRRFVVDVWRCEE	60	
Db	1	MGSMPFSEEEVALVOLFLPTAAATCTVSRLGELGLVFEFRDINASVSFAQRRFVVDVWRCEE	60	
Qy	61	LEKTFPLQBEVRRAGVLVLPFPKGRLPAPPPPDRLRLRQEETERLAQELRDVRGNQQALRA	120	
Db	61	LEKTFPLQBEVRRAGVLVLPFPKGRLPAPPPPDRLRLRQEETERLAQELRDVRGNQQALRA	120	
Qy	121	QLHQLQLHAVALRQGHQPQLAAAHTDGASERTPLLOAPGGPHQDLRVNFVAGVEPHKAP	180	
Db	121	QLHQLQLHAVALRQGHQPQLAAAHTDGASERTPLLOAPGGPHQDLRVNFVAGVEPHKAP	180	

Db 514 GLIKVRDPYFPGVDSWGRSGELPFLNLSKMKMSILMGVTQWNLGVLVSYPDAKPHGNA 573
Qy 564 HRLLETPELFLGLGVLVFLVYKWLVCWAAASPSILIHFINFLSHSPSRL 623
Db 574 LDIRVQFIPRMIFLNSFLGALLILIKW-----CRGSOADLYHVMYMF-----DPSGNL 625
Qy 624 ----LYPROEVQATLVVLALAMVPILLGLTPLLHLHRRHRLRRRPPADQENKAGLLD 679
Db 626 GENQLFWQKEQLILLALLMAIIVAPWMLFPKPFILKLNRPQ-----CHTYRFLGTSE 680
Qy 680 L-PDASVNGSSDEKAGGLDEBEAEALVPSSEVLHQAIHTIEFCLGCVSNTASYLRLWA 738
Db 681 MDPD-----SEPDARSRHDDFNF-----SEVFHQMIHSIEFVLGAVSNTASYLRLWA 729
Qy 739 LSLAHLAQSLSEVLWAMVMRIGLGLGREGVGAUVLPIFAAFVMTVAILLVMEGLSAPLH 798
Db 730 LSLAHLSELSVTFYKLLVLAWGDNLV-VKLVLGV-----IFSFATAPILLGMSLSAPLH 784
Qy 799 ALRLHWVEPQNFYSGTYKLSPP 822
Db 785 ALRLHWVEPMNFYHGDGYKFRPF 808

RESULT 5

US-10-449-902-41603
; Sequence 41603, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41603
; LENGTH: 923
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41603

Query Match 26.1%; Score 1113; DB 6; Length 923;
Best Local Similarity 31.3%; Pred. No. 1.5e-82;
Matches 304; Conservative 143; Mismatches 307; Indels 218; Gaps 33;
Qy 3 SMFRESEVALVOLFLPTAAAYTCVSRGLBGLVFEFDLNA-----SVSAFORRVV 53
Db 10 SLFRSRPMYSVITAMTDIAYDTIRELGNFLGHVVDLNAAGKASVNDKNLAGYKKR--- 66
Qy 54 DWRCCELEKTFYLOEVRAGLVLPKPKGLPAPPPDLRIOEETERLAQE---LRD 110
Db 67 -VQDCIMYERKLHDESOIK-----EYNIPAPPP---LREHEERHHTKONAVLPD 113
Qy 111 VRGNOQALRAQLHQ-LQLHAALVR-----OQHEPQ-----L 140
Db 114 IRAHLEPLEERLRSVQVQADITRAISELTERVWYKTCRNQVGRVEAHDDKHEVPYSA 173
Qy 141 AAHTDGA-----SER---TFLQAPGPGHODLRV 167
Db 174 AAAAVFGAILVBLGTTAAGLPAALAPPKQKNDVLCGERDVGTPPGTGGG---DSKL 230
Qy 168 N-----FV-----AGAVEPKAPALERLLWACRGLIA 196
Db 231 NQLGVSLISADHARSAGGAAAKVLPKFRITLTVGLPTDKSSFFQRLYRISGNALT 290
Qy 197 SFRELEQPLEHPVTGEPATWMTF-LISYNGEQIGQKIRKITDCFHCHVFPFLQBEARLG 255

Db 291 HTFDIPVDPVAGSELVKNKSVFSLIVVSELLERIKTKVQCFQATIVRMDPTQAAIDE 350
Qy 256 ALQOIQOQSQELQ-----EVLGETERFLSQVLGRVLQLLP--PGQVQVHKMKAVYALNQC 309
Db 351 ALHRTEAQIDEQMLKVNTLRDIEQALRQLAGDPQVNSPLREWQVLLRCEKAVCDTMMKC 410
Qy 310 SVSTTHKCLIA-EANCSVRDLPALQEAR-----DSSMEEGVSAVAHRIPCRD--MPPTL 361
Db 411 HFLYLT---MVAPEGCPVEEVDNLKIAVKRAVPPGDKIPERPAVEVAPEKPIRDGPPPT 467
Qy 362 INTNFTASFOGIVDRYGVGRYQEVNPAFYTIITFPFLFVAVMFGDVGHGLLFLPALAMV 421
Db 468 FKLNFSTISFOGIVNTYGVPRYQEVNPGFLTIVTFPFLFGVMYGDIGHTFTTILSLMI 527
Qy 422 LAENR-PAVKAA--ONEIWQTFFRGRLYLLMLGLFSIYTFYINCEFSRATSIFFSGMSV 478
Db 528 IPEDRLTRLKESGNMNEIFRMCFCGRYLLVCMGMGIYCGTLYNDCMSIPVSLYAPTWEY 587
Qy 479 AAMANQSGNSDAFLAQHTMLTLDPNVTGVFLGPPGIDPIWLSLAANHLSPLNSFKMKMS 538
Db 588 EGTADPA-----TRIGAV-----YPYGVDPAWYHTKNQLTFFNGMKMKTS 628
Qy 539 VILGVVHMAFGVVLGVFNHVFHQRHLLLETLPELTLLGLFGLVFLVIVKMLCVAA 598
Db 629 VILGVQWTFGLIINGLLNHHIHRDOISIWLEFLPQLLPMCTGFWYCIILIIKNCWDSQ 688
Qy 599 RAASPSILIH-FINMPL-FSHSPSNRLLYPRQEVVQATLVVLALAMVPILLGLTPLLH- 655
Db 689 TSQEPNLIQTMITMFLGLGGVKEGAQLVAGQSTVQAILLIIFAGSIPVMLLAKPCILAY 748
Qy 656 -----HRHRRRLRRRADRQENKAGLLDLPDASVNGSSDEKAGGLDDEBEAEALVP 708
Db 749 CSKDDHGHGHAKPQAAQPA-----AAAAAG-----DVEAKGFD--EKGEVIP 787
Qy 709 SEV-----LMHQAIHTIEFCLGCVSNTASYLRLWLSLAHOLSEVL 750
Db 788 AEAPAGAGAAHEEBEHTFGDYMIHQSIHTIEFVLGTVTNTASYLRLWLSLAHSELDYF 847
Qy 751 WAMVMRIGLGLGREGVGAUVLPIFAAFVMTVAILLVMEGLSAPLHRLHWVEFQNK 810
Db 848 WTKLI-LEYGMYKNSAFFSMVAV---AVMFMVTAGVLLSMDVLECFHLALRLHWVEFQNK 903
Qy 811 FVSGTYGKLSPP 822
Db 904 FFHADGYAFKPF 915

RESULT 6

US-10-449-902-52773
; Sequence 52773, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52773
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-52773


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RESULT 9
US-10-953-349-18080
; Sequence 18080, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18080
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18080

Query Match      12.2%; Score 521; DB 6; Length 273;
Best Local Similarity 43.7%; Pred. No. 4.6e-35;
Matches 129; Conservative 36; Mismatches 92; Indels 38; Gaps 8;

QY 535 MMSVILGVVHMAFGVVLGVFNHVFQQRHRLLELTPELTFLGLFGYLVFLVIYKWL 594
Db 1 MMSVILGVVHMAFGVVLGVFNHVFQQRHRLLELTPELTFLGLFGYLVFLVIYKWL 58
QY 595 VMAAASPSILIH-FINMFLFSHSPNRL-----LYPRQEVVQATLVVLALAMVPILLG 649
Db 59 ----ATGSQADLYHILYMF-----SPTDDLGENQLFAGQKNLQVLLVLLAVISVPMLLP 111
QY 650 TPLHLHRRHRRRRPADRQENKAGLLDLPDASVNGWSSDE--EKAGGLDDEEAEIV 707
Db 112 KPFLKKQHEAR-----HGVSAYPL-----QSTDESQVSNHDSHGHEEPE 154
QY 708 PSEVLHQAHTTIEFCIGCVSNNTASYLRMLWALSLAHQAQLSEVLMAMVMRIGLGLGREVG 767
Db 155 PSEVPVQLIHTIEFVLGAVSNNTASYLRMLWALSLAHSELSSVFEKVLMMAMWYNNVIL 214
QY 768 AAVLVPIFAAPAVMTVAILLVMEGLSAFLHRLHWHVEFQNKFGYGTGYKLSPP 822
Db 215 IVGLVIFIFA-----TVGVLLVMTLSAFLHRLHWHVEFQNKFGYGTGYKHPFP 264

RESULT 10
US-10-953-349-18081
; Sequence 18081, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18081
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18081

Query Match      12.0%; Score 511; DB 6; Length 271;
Best Local Similarity 43.3%; Pred. No. 3e-34;
Matches 127; Conservative 36; Mismatches 92; Indels 38; Gaps 8;

QY 537 MSVILGVVHMAFGVVLGVFNHVFQQRHRLLELTPELTFLGLFGYLVFLVIYKWL 596
Db 1 MSVILGVVHMAFGVVLGVFNHVFQQRHRLLELTPELTFLGLFGYLVFLVIYKWL 56
QY 597 AARAASPSILIH-FINMFLFSHSPNRL-----LYPRQEVVQATLVVLALAMVPILLGTP 651
```

```
Db 57 --ATGSQADLYHILYMF-----SPTDDLGENQLFAGQKNLQVLLVLLAVISVPMLLP 111
QY 652 LHLHRRHRRRRPADRQENKAGLLDLPDASVNGWSSDE--EKAGGLDDEEAEIVPS 709
Db 112 FILKKQHEAR-----HGVSAYPL-----QSTDESQVSNHDSHGHEEFP 154
QY 710 EVLHQAHTTIEFCIGCVSNNTASYLRMLWALSLAHQAQLSEVLMAMVMRIGLGLGREVG 769
Db 155 EVFVQLIHTIEFVLGAVSNNTASYLRMLWALSLAHSELSSVFEKVLMMAMWYNNVIL 214
QY 770 VVLVPIFAAPAVMTVAILLVMEGLSAFLHRLHWHVEFQNKFGYGTGYKLSPP 822
Db 215 GLIVFIFA-----TVGVLLVMTLSAFLHRLHWHVEFQNKFGYGTGYKHPFP 262
```

```
RESULT 11
US-10-953-349-30245
; Sequence 30245, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30245
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30245

Query Match      8.5%; Score 361; DB 6; Length 306;
Best Local Similarity 29.9%; Pred. No. 5.8e-22;
Matches 87; Conservative 63; Mismatches 101; Indels 40; Gaps 5;

QY 4 MFRSEVALVQLFPTAAAYTCVSRGELGVLGFRDLNASVAFORFVVDVWRCCELEK 63
Db 3 LMRSEAMQLQVITPTSAHLAVSHLGLDGLIQFDNLNADKSPFORTYAAQIKRCAEMAR 62
QY 64 TFTFQEBVRBAGLVLPKGRLPAPPRDLRLRQESETERLAQELRDYRGNQQAQLH 123
Db 63 KLRFFKEQMSKAGILVSPMQS---TETPLDQDDMEVKLGELEAEUTEVNADEKLQRAHN 119
QY 124 QLQLHAAVLRQHE-----PQLAAHTDGAERTPLIQAPEGPHQDL----- 165
Db 120 ELLEYSTVLQKAGEFFYSQAQRSAQAHRQMEANQSGETSLESPLLE-----QDMLTDAS 173
QY 166 ---RVNFMVAGAVEPHKAPALERLLWRACRGPLIASFRELEQPLEHPVTGEPATWMTPLIS 222
Db 174 KQVKLGSLGLVPKPKAMAFERILFRATRGNNILLRQESVDEPVTDPQSGEKYKNTFVVF 233
QY 223 YWGEIGQKIRKTTDCPHCHVFPEFLQEEARLQALQQLQQQSQELQEVLGE 273
Db 234 YSGERAKAKILKICDAFRANKRYP-----PEDLAKQTHVTQEVSGK 274

RESULT 12
US-10-953-349-30244
; Sequence 30244, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
```


Db 495 RVCRR-----RLRRANR-----VLRARCBRAVKNACYWAVLLVFLNTLTIASHHQ 542
QY 412 LMFPLALAMVLAENPAVKAONEIWTFFRGYLLLLMGLF-SYTGFIYN--BCFSRA 468
Db 543 PWWL-----TQIOEYANKVLLCLFTVEMLLKLYGLGPSAYVSSFFNRDFCFVVC 591
QY 469 TSIF-----PSGWSVAAMANQSGMSDAFLAHTMLTLDPNVTGVLGYPFGID 517
Db 592 GGILETTLVEVGAMPGLGISVLRV-----LLRI-----FKVT 625
QY 518 PIWSLAANHL-SFLNSFKMKMSVIL-----GVVHMAFGVVL--GVFNHVFQGRH--RL 567
Db 626 RHWASLSNLVASLNSMKSISLILLFLFIIFSILGMQLFGGKFN---PDQTHKRST 682
QY 568 LETLPE--LTFLGLFGYLVFLVYKMLCVWAARAASPSIL--IHPINMFLFSHSPSNRL 623
Db 683 FDTFFQALLTVFQILTGEDWNVYDGINMAYGG-PFFPGMLVCIYFIILFIC---GNYI 737
QY 624 LYPRQEVVQATLVVLALAM-----VPILLGTPLHLLHRHR 660
Db 738 LLN-----VFLAIVDNLASGDAGTAKDKGKSKNEKLPQENEGLVFGVEKEEEE 788
QY 661 RLRRPADRQERNKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLHQAIHTI 720
Db 789 GARREGADMEEBE-----EEEEEEEEEGAGGV--ELLQEVVPKVKVPIPEGSA 839
QY 721 EFLCGCVNTASYLRNLWALSIAHQL--SEVLWAMVNRIGLGLGREVGVA-----VVLV 773
Db 840 FFCL-----SQTNPLRKGCHTLIHHVFTNLILVFIILSSVSLAEDPIRAHSFRNHILGY 895
QY 774 PIFAAPAVMTVAILLVMEGLSAFLH 798
Db 896 FDYAFTSIFTVEILLXMTVEGAFLH 920

Search completed: June 29, 2006, 13:13:30
Job time : 23 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2006, 13:13:20 ; Search time 194 Seconds
(without alignments)
1937.278 Million cell updates/sec

Title: US-10-783-519-2.

Perfect score: 822

Sequence: 1 MGSMFRSEVALVQLFLPTRA.....HWVEFQNKFGYGYKLSPLF 822

Scoring table:

Capop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2589342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_8.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*
- 10: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	822	100.0	822	2 AAW41943	AAW41943 Human OC-
2	822	100.0	822	5 ABB81811	Abb81811 Human OC-
3	822	100.0	822	8 ADR44119	Adr44119 Human 116
4	822	100.0	822	9 ADY92606	Ady92606 Human 116
5	545	66.3	830	8 ADI28834	Adi28834 Human mod
6	545	66.3	830	8 ADP12465	Adp12465 Protein e
7	545	66.3	830	8 ABM81281	Abm81281 Tumour-as
8	501	60.9	787	8 ADH22516	Adh22516 Human tra
9	445	54.1	787	8 ABM84820	Abm84820 Human dia
10	385	46.8	614	2 AAW98112	Aaw98112 T-cell me
11	385	46.8	614	8 ABM81282	Abm81282 Tumour-as
12	325	39.5	614	2 AAW98113	Aaw98113 T-cell me
13	325	39.5	614	6 ABR43098	AbR43098 Human T-c
14	291	35.4	643	5 ABP41524	Abp41524 Human ova
15	124	15.1	124	7 ADD27652	Add27652 Human adi
16	112	13.6	203	7 ADK27225	Add27225 Human adi
17	34	4.1	60	5 ADK35292	Adk35292 Novel hum
18	33	4.0	33	8 ADR44126	Adr44126 Human OC-
19	33	4.0	33	9 ADY92613	Ady92613 Human 116
20	32	3.9	32	8 ADR44121	Adr44121 Human OC-
21	32	3.9	32	9 ADY92608	Ady92608 Human 116
22	30	3.6	30	8 ADR44124	Adr44124 Human OC-
23	30	3.6	30	9 ADY92611	Ady92611 Human 116

ALIGNMENTS

RESULT 1

AAW41943

ID AAW41943 standard; protein; 822 AA.

XX AAW41943;

AC AAW41943;

DT 02-JUL-1998 (first entry)

XX Human OC-116 kDa protein.

DE Human OC-116 kDa protein.

XX Osteoclast; human; OC-116 kDa; screening; cell surface marker; probe.

XX Homo sapiens.

XX WO9803651-AL.

XX 29-JAN-1998.

XX 10-JUL-1997; 97WO-US012569.

XX 19-JUL-1996; 96US-00684932.

XX (FORS-) FORSYTH DENTAL INFIRMARY FOR CHILDREN.

XX Stashenko P, Li Y, Wucherpfennig AL;

XX WPI; 1998-120776/11.

XX N-PSDB; AAV04529.

XX Osteoclast specific or related DNA sequence - useful as probe to screen

XX genomic DNA or cDNA library, or as osteoclast cell surface marker.

XX Example 8; Page 61-64; 75pp; English.

XX The present sequence represents the human OC-116 kDa protein sequence

XX which is used in an example of the present invention, which describes

XX isolated osteoclast specific or related DNA sequences. The present

XX invention also describes; a DNA construct capable of replicating and

XX optionally expressing, in a host cell, osteoclast specific or related

XX DNA, comprising an osteoclast specific or related DNA sequence and

XX sequences necessary for transforming or transfecting a host cell, and for

XX replicating and optionally expressing an osteoclast specific or related

XX DNA sequence in a host cell; and a cell stably transformed or transfected

XX with the DNA construct. The osteoclast specific or related DNA sequence

XX can be used as a probe to screen a genomic DNA or cDNA library for

XX osteoclast specific or related DNA sequences, or as a osteoclast cell

24 29 3.5 29 6 ABR43100 ABr43100 Human T-c
25 27 3.3 830 8 ADH09947 Adh09947 Human hos
26 27 3.3 831 5 ABB08457 Abb08457 Human tum
27 27 3.3 831 8 ADH09948 Adh09948 Human hos
28 27 3.3 831 8 ADH09952 Adh09952 Human hos
29 27 3.3 831 8 ADH09953 Adh09953 Human hos
30 27 3.3 831 8 ADI28837 Adi28837 Human mod
31 26 3.2 26 8 ADR44122 ADr44122 Human OC-
32 26 3.2 26 9 ADY92609 Ady92609 Human 116
33 24 2.9 24 6 ABR43102 ABr43102 Human T-c
34 24 2.9 24 6 AAE37759 Aae37759 TIRC7 pep
35 24 2.9 24 6 AAE37809 Aae37809 TIRC7 pep
36 24 2.9 513 6 ADA54643 Ada54643 Human pro
37 24 2.9 558 4 ABG09380 Abg09380 Novel hum
38 24 2.9 821 7 ADC87337 Adc87337 Human GPC
39 24 2.9 840 5 ABP69796 Abp69796 Human pol
40 24 2.9 840 8 ADH09949 Adh09949 Human hos
41 24 2.9 840 8 ADI28836 Adi28836 Human mod
42 24 2.9 841 4 AAB60100 Aab60100 Human tra
43 24 2.9 847 8 ADR44120 ADr44120 Human OC-
44 24 2.9 847 9 ADY92607 Ady92607 116 kD os
45 23 2.8 23 8 ADR44125 ADr44125 Human OC-

```
CC surface marker
XX
SQ Sequence 822 AA;

Query Match 100.0%; Score: 822; DB 2; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSFRSEVALVQLPFLPTAAAYTCVSRIGELGLVEFRDLNASVSFAQRRFVVDVWRCSE 60
DB 1 MGSFRSEVALVQLPFLPTAAAYTCVSRIGELGLVEFRDLNASVSFAQRRFVVDVWRCSE 60

QY 61 LEKTTFTLQEEVRRAGLVLPKPGRLPAPPDRLRIQETERLAQELRDVRGNQOALRA 120
DB 61 LEKTTFTLQEEVRRAGLVLPKPGRLPAPPDRLRIQETERLAQELRDVRGNQOALRA 120

QY 121 QLHQLQHAALVLRQGHPEPOLAAHTDGASERTPLLAQPGPHQDLRVNPFVAGAVEPHKAP 180
DB 121 QLHQLQHAALVLRQGHPEPOLAAHTDGASERTPLLAQPGPHQDLRVNPFVAGAVEPHKAP 180

QY 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATMTFLISYWGEOIQGKIRKIDTDPH 240
DB 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATMTFLISYWGEOIQGKIRKIDTDPH 240

QY 241 CHVFPFLQOEERARLQALQOQOQSELOELVETSERFLSQVLGRVLQLLPQGVQVHKMK 300
DB 241 CHVFPFLQOEERARLQALQOQOQSELOELVETSERFLSQVLGRVLQLLPQGVQVHKMK 300

QY 301 AVYLAALNQCSTTHKCLIAEAWCSVRDLPAQELALRDSMEEGVSAVAHRIPCRDMPPT 360
DB 301 AVYLAALNQCSTTHKCLIAEAWCSVRDLPAQELALRDSMEEGVSAVAHRIPCRDMPPT 360

QY 361 LIIRNRPFTASFOGIVDRYGVGRYQEVNPAFYIIITFPFLFAVMFGDVGHLLMFLPALAM 420
DB 361 LIIRNRPFTASFOGIVDRYGVGRYQEVNPAFYIIITFPFLFAVMFGDVGHLLMFLPALAM 420

Query Match 100.0%; Score 822; DB 5; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSFRSEVALVQLPFLPTAAAYTCVSRIGELGLVEFRDLNASVSFAQRRFVVDVWRCSE 60
DB 1 MGSFRSEVALVQLPFLPTAAAYTCVSRIGELGLVEFRDLNASVSFAQRRFVVDVWRCSE 60

QY 61 LEKTTFTLQEEVRRAGLVLPKPGRLPAPPDRLRIQETERLAQELRDVRGNQOALRA 120
DB 61 LEKTTFTLQEEVRRAGLVLPKPGRLPAPPDRLRIQETERLAQELRDVRGNQOALRA 120

QY 121 QLHQLQHAALVLRQGHPEPOLAAHTDGASERTPLLAQPGPHQDLRVNPFVAGAVEPHKAP 180
DB 121 QLHQLQHAALVLRQGHPEPOLAAHTDGASERTPLLAQPGPHQDLRVNPFVAGAVEPHKAP 180

QY 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATMTFLISYWGEOIQGKIRKIDTDPH 240
DB 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATMTFLISYWGEOIQGKIRKIDTDPH 240

QY 241 CHVFPFLQOEERARLQALQOQOQSELOELVETSERFLSQVLGRVLQLLPQGVQVHKMK 300
DB 241 CHVFPFLQOEERARLQALQOQOQSELOELVETSERFLSQVLGRVLQLLPQGVQVHKMK 300

QY 301 AVYLAALNQCSTTHKCLIAEAWCSVRDLPAQELALRDSMEEGVSAVAHRIPCRDMPPT 360
DB 301 AVYLAALNQCSTTHKCLIAEAWCSVRDLPAQELALRDSMEEGVSAVAHRIPCRDMPPT 360

QY 361 LIIRNRPFTASFOGIVDRYGVGRYQEVNPAFYIIITFPFLFAVMFGDVGHLLMFLPALAM 420
DB 361 LIIRNRPFTASFOGIVDRYGVGRYQEVNPAFYIIITFPFLFAVMFGDVGHLLMFLPALAM 420

The invention relates to novel human osteoclast-specific or -related cDNA sequences. The sequence represents human osteoclast 116KDa (OC-116KDa). The sequences may have a use in gene therapy. The sequences of the invention are useful in the production of gene products useful in the therapeutic treatment or diagnosis of disorders involving aberrant bone resorption, for generating peptides which are useful for producing antibodies for identifying osteoclast-specific or -related peptides or gene products

Example 8; Fig 3; 34pp; English.

Novel isolated osteoclast-specific or -related DNA sequence, useful for producing gene products useful in the therapeutic treatment or diagnosis of disorders involving aberrant bone resorption.

(FORES-) FORSYTH DENTAL INFIRMARY FOR CHILDREN.

Stashenko P, Li Y, Wuchertpfennig AL;
WPI; 2002-536031/57.
N-PSDB; ABN86735.

Human OC-116KDa.
Human; osteoclast; gene therapy; aberrant bone resorption; OC-116KDa.
Homo sapiens.
US6403304-B1.
11-JUN-2002.
19-JUL-1996; 96US-00684932.
06-APR-1993; 93US-00045270.
23-FEB-1995; 95US-00392678.
20-JUL-1995; 95US-0001292P.
22-FEB-1996; 96US-00605378.
(FORS-) FORSYTH DENTAL INFIRMARY FOR CHILDREN.
Stashenko P, Li Y, Wuchertpfennig AL;
WPI; 2002-536031/57.
N-PSDB; ABN86735.
Novel isolated osteoclast-specific or -related DNA sequence, useful for producing gene products useful in the therapeutic treatment or diagnosis of disorders involving aberrant bone resorption.
Example 8; Fig 3; 34pp; English.
The invention relates to novel human osteoclast-specific or -related cDNA sequences. The sequence represents human osteoclast 116KDa (OC-116KDa). The sequences may have a use in gene therapy. The sequences of the invention are useful in the production of gene products useful in the therapeutic treatment or diagnosis of disorders involving aberrant bone resorption, for generating peptides which are useful for producing antibodies for identifying osteoclast-specific or -related peptides or gene products
Sequence 822 AA;

Query Match 100.0%; Score 822; DB 5; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSFRSEVALVQLPFLPTAAAYTCVSRIGELGLVEFRDLNASVSFAQRRFVVDVWRCSE 60
DB 1 MGSFRSEVALVQLPFLPTAAAYTCVSRIGELGLVEFRDLNASVSFAQRRFVVDVWRCSE 60

QY 61 LEKTTFTLQEEVRRAGLVLPKPGRLPAPPDRLRIQETERLAQELRDVRGNQOALRA 120
DB 61 LEKTTFTLQEEVRRAGLVLPKPGRLPAPPDRLRIQETERLAQELRDVRGNQOALRA 120

QY 121 QLHQLQHAALVLRQGHPEPOLAAHTDGASERTPLLAQPGPHQDLRVNPFVAGAVEPHKAP 180
DB 121 QLHQLQHAALVLRQGHPEPOLAAHTDGASERTPLLAQPGPHQDLRVNPFVAGAVEPHKAP 180

QY 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATMTFLISYWGEOIQGKIRKIDTDPH 240
DB 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATMTFLISYWGEOIQGKIRKIDTDPH 240

QY 241 CHVFPFLQOEERARLQALQOQOQSELOELVETSERFLSQVLGRVLQLLPQGVQVHKMK 300
DB 241 CHVFPFLQOEERARLQALQOQOQSELOELVETSERFLSQVLGRVLQLLPQGVQVHKMK 300

QY 301 AVYLAALNQCSTTHKCLIAEAWCSVRDLPAQELALRDSMEEGVSAVAHRIPCRDMPPT 360
DB 301 AVYLAALNQCSTTHKCLIAEAWCSVRDLPAQELALRDSMEEGVSAVAHRIPCRDMPPT 360

QY 361 LIIRNRPFTASFOGIVDRYGVGRYQEVNPAFYIIITFPFLFAVMFGDVGHLLMFLPALAM 420
DB 361 LIIRNRPFTASFOGIVDRYGVGRYQEVNPAFYIIITFPFLFAVMFGDVGHLLMFLPALAM 420

RESULT 2
ABB81811
ID ABB81811 standard; protein; 822 AA.
XX
AC ABB81811;
XX
DT 16-SEP-2002 (first entry)
XX
```

QY 421 VLAENRPAKAAQNEIWTQTFRGRYLLMLGLPSIYTGFIYNECFSRATSIFFSGWSVAA 480
DB 421 VLAENRPAKAAQNEIWTQTFRGRYLLMLGLPSIYTGFIYNECFSRATSIFFSGWSVAA 480
QY 481 MANQSGWSDAFLAQHTMTLDPNVTGVFLGYPFGIDPIWISLAANHLSPNSFKMKSIVI 540
DB 481 MANQSGWSDAFLAQHTMTLDPNVTGVFLGYPFGIDPIWISLAANHLSPNSFKMKSIVI 540
QY 541 LGVVMHAFGVVLGVFNHVFQGRHRLLETLPELTFLGLFGYLVFLVIYKWLVCWAAARA 600
DB 541 LGVVMHAFGVVLGVFNHVFQGRHRLLETLPELTFLGLFGYLVFLVIYKWLVCWAAARA 600
QY 601 ASPSILIHFINMFLFSHSPNRLLYPROEVVQATLVVLALAMVPIILLGTPLHLHRRR 660
DB 601 ASPSILIHFINMFLFSHSPNRLLYPROEVVQATLVVLALAMVPIILLGTPLHLHRRR 660
QY 661 RLRRRPAQREKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLHQAIHTI 720
DB 661 RLRRRPAQREKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLHQAIHTI 720
QY 721 EFCIGCVSNTASYLRWLWALSLAHQAQSEVLWAMVMRIGLGLGREGVGAAVLVPIFAAFA 780
DB 721 EFCIGCVSNTASYLRWLWALSLAHQAQSEVLWAMVMRIGLGLGREGVGAAVLVPIFAAFA 780
QY 781 VMTVAILLVMEGLSAFLHRLHWHVEFQNKFSYGTGYKLSPP 822
DB 781 VMTVAILLVMEGLSAFLHRLHWHVEFQNKFSYGTGYKLSPP 822

RESULT 3

ADR44119
ID ADR44119 standard; protein; 822 AA.

XX ADR44119;

XX 04-NOV-2004 (first entry)

XX Human 116-kDa osteoclast proton pump subunit (OC-116 kDa) protein.

XX Human; OC-116 kD; 116-kDa osteoclast proton pump subunit; therapy;
KW bone degradation; osteoporosis; osteoarthritis.

XX Homo sapiens.

Key	Location/Qualifiers
FT Domain	319..422
FT Domain	/note = Transmembrane domain
FT Domain	438..463
FT Domain	/note = Transmembrane domain
FT Domain	537..558
FT Domain	/note = Transmembrane domain
FT Domain	571..600
FT Domain	/note = Transmembrane domain
FT Domain	632..653
FT Domain	/note = Transmembrane domain
FT Domain	764..796
FT Domain	/note = Transmembrane domain

XX US6777537-B1.

XX 17-AUG-2004.

XX 18-JUL-2000; 2000US-00618304.

XX 22-FEB-1996; 96US-00605378.

XX (FORS-) FORSYTH DENTAL INFIRMARY FOR CHILDREN.

XX Stashenko P, Li Y;

XX WPI; 2004-591304/57.

XX N-PSDB; ADR44118.

XX

PT New isolated human 116-kDa osteoclast (OC-116 kDa) proton pump subunit
PT polypeptide, useful for preventing and/or treating diseases with bone
PT degradation, such as osteoporosis and osteoarthritis.

XX Claim 2; SEQ ID NO 2; 16pp; English.

XX The present invention relates to a human 116-kDa osteoclast proton pump
XX subunit (OC-116 kDa) polypeptide and its encoding polynucleotide. The
XX invention is useful for the prevention and treatment of diseases or
XX conditions associated with aberrant expression or activity of the OC-116
XX kDa protein and bone degradation, such as osteoporosis and
XX osteoarthritis. The present sequence is human OC-116 kDa protein.

XX Sequence 822 AA;

Query Match 100.0%; Score 822; DB 8; Length 822;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSMPRSEEEVALVQLFLPTAAAYTCVSRIGELGVFRDLNANASVAFQRRFVVDVNRCEE 60

DB 1 MGSMPRSEEEVALVQLFLPTAAAYTCVSRIGELGVFRDLNANASVAFQRRFVVDVNRCEE 60

QY 61 LEKTFEFLQEEVRRAGLVLPKGRLPAPPDRLRIQETERLAQELRDVNRGQOALRA 120

DB 61 LEKTFEFLQEEVRRAGLVLPKGRLPAPPDRLRIQETERLAQELRDVNRGQOALRA 120

QY 121 QLHQLQHAALVLRQGHQEPQLAAHTDGASERTPLQAPGGPHQDLRVNFVAGAVEPHKAP 180

DB 121 QLHQLQHAALVLRQGHQEPQLAAHTDGASERTPLQAPGGPHQDLRVNFVAGAVEPHKAP 180

QY 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGSGOIGKIRKIKTDCPH 240

DB 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGSGOIGKIRKIKTDCPH 240

QY 241 CHVFPEFLQEEARLQALQQLQQSQSELQEVLGETERFLSQVLGRVLQQLPPGQVQVHKMK 300

DB 241 CHVFPEFLQEEARLQALQQLQQSQSELQEVLGETERFLSQVLGRVLQQLPPGQVQVHKMK 300

QY 301 AVYALALNQCSVSTTHKCLIAEAWCSVRDLPALQEARLDSMEERGSAVAHRIFCRDMPT 360

DB 301 AVYALALNQCSVSTTHKCLIAEAWCSVRDLPALQEARLDSMEERGSAVAHRIFCRDMPT 360

QY 361 LIRTNRTASFOGIVDRYGVRYQEVNPAPTYITTPPFLFVAVMGDVGHLMLFLFALAM 420

DB 361 LIRTNRTASFOGIVDRYGVRYQEVNPAPTYITTPPFLFVAVMGDVGHLMLFLFALAM 420

QY 421 VLAENRPAKAAQNEIWTQTFRGRYLLMLGLPSIYTGFIYNECFSRATSIFFSGWSVAA 480

DB 421 VLAENRPAKAAQNEIWTQTFRGRYLLMLGLPSIYTGFIYNECFSRATSIFFSGWSVAA 480

QY 481 MANQSGWSDAFLAQHTMTLDPNVTGVFLGYPFGIDPIWISLAANHLSPNSFKMKSIVI 540

DB 481 MANQSGWSDAFLAQHTMTLDPNVTGVFLGYPFGIDPIWISLAANHLSPNSFKMKSIVI 540

QY 541 LGVVMHAFGVVLGVFNHVFQGRHRLLETLPELTFLGLFGYLVFLVIYKWLVCWAAARA 600

DB 541 LGVVMHAFGVVLGVFNHVFQGRHRLLETLPELTFLGLFGYLVFLVIYKWLVCWAAARA 600

QY 601 ASPSILIHFINMFLFSHSPNRLLYPROEVVQATLVVLALAMVPIILLGTPLHLHRRR 660

DB 601 ASPSILIHFINMFLFSHSPNRLLYPROEVVQATLVVLALAMVPIILLGTPLHLHRRR 660

QY 661 RLRRRPAQREKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLHQAIHTI 720

DB 661 RLRRRPAQREKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLHQAIHTI 720

QY 721 EFCIGCVSNTASYLRWLWALSLAHQAQSEVLWAMVMRIGLGLGREGVGAAVLVPIFAAFA 780

DB 721 EFCIGCVSNTASYLRWLWALSLAHQAQSEVLWAMVMRIGLGLGREGVGAAVLVPIFAAFA 780

QY 781 VMTVAILLVMEGLSAFLHRLHWHVEFQNKFSYGTGYKLSPP 822

DB 781 VMTVAILLVMEGLSAFLHRLHWHVEFQNKFSYGTGYKLSPP 822

Db 781 VMTVAILLVMEGLSAFLHALRLHWVEFQNKFYSGTGKLSPP 822

RESULT 4

ADY92606

ID ADY92606 standard; protein; 822 AA.

XX

AC ADY92606;

XX

DT 02-JUN-2005 (first entry)

XX

DE Human 116 kD osteoclast proton pump OC-116 subunit protein.

XX

XX cloning; osteopathic; antiarthritic; gene therapy;

KW osteoclast proton pump; bone disease; osteoporosis; osteoarthritis.

XX

OS Homo sapiens.

XX

XX US2005064448-A1.

XX

XX 24-MAR-2005.

XX

XX 20-FEB-2004; 2004US-00783519.

XX

XX 22-FEB-1996; 96US-00605378.

XX

XX 18-JUL-2000; 2000US-00618304.

XX

XX (STAS/) STASHENKO P.

XX

XX (LIYY/) LI Y.

XX

XX Stashenko P, Li Y;

XX

XX WPI; 2005-241271/25.

XX

XX N-PSDB; ADY92605.

XX

XX New isolated genes and encoded human 116-kDa osteoclast proton pump

PT subunit polypeptides useful for treating bone mass disorders associated

PT with aberrant rate of bone degradation (e.g. osteoporosis or

PT osteoarthritis).

XX

XX Claim 18; SEQ ID NO 2; 17pp; English.

XX

XX The invention relates to an isolated gene encoding a polypeptide which is

CC a human 116-kD osteoclast proton pump subunit. The composition and

CC methods are useful for treating bone mass disorders characterized by

CC aberrant rate of bone degradation (e.g. osteoporosis or osteoarthritis).

CC The protein may also be used as cell surface markers for osteoclasts.

CC This sequence corresponds to the novel OC-116 proton pump subunit. The

CC encoding cDNA was isolated by differential screening of a human

CC osteoclastoma cDNA library.

XX

SQ Sequence 822 AA;

XX

Query Match 100.0%; Score 822; DB 9; Length 822;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSFRSEVALVOLFLPTAAATCVSRIGELGLVEFRDLNASVSAPQRRFVVDVWRCCE 60

Db 1 MGSFRSEVALVOLFLPTAAATCVSRIGELGLVEFRDLNASVSAPQRRFVVDVWRCCE 60

QY 61 LEKTTFTLQEEVRRAGLVLPKGRLPAPPDRLRLIQETELRLAQELRDVRGNOQLRA 120

Db 61 LEKTTFTLQEEVRRAGLVLPKGRLPAPPDRLRLIQETELRLAQELRDVRGNOQLRA 120

QY 121 QLHQQLHAAVLRQGHPEPOLAAHTDGASERTPLQAQPGPHQDLRVNFVAGAVEPHKAP 180

Db 121 QLHQQLHAAVLRQGHPEPOLAAHTDGASERTPLQAQPGPHQDLRVNFVAGAVEPHKAP 180

QY 181 ALERLLWRACRGLFLASPRELQPLEHPVTGEPATWMTFLISYWGEOIGQKIRKIDCPH 240

Db 181 ALERLLWRACRGLFLASPRELQPLEHPVTGEPATWMTFLISYWGEOIGQKIRKIDCPH 240

QY 241 CHVFFPFLQOEERLALGALQLOOQSOBLOEVLGETERFLSQVLGRVLQLLPPGQOVVHKMK 300
Db 241 CHVFFPFLQOEERLALGALQLOOQSOBLOEVLGETERFLSQVLGRVLQLLPPGQOVVHKMK 300
QY 301 AVYLALNQCSTVTHKCLIAEAWCSVRDLPALQELRDSSMEEGVSAAVHRIPCRDMPPT 360
Db 301 AVYLALNQCSTVTHKCLIAEAWCSVRDLPALQELRDSSMEEGVSAAVHRIPCRDMPPT 360
QY 361 LIRTNRTASFOGIVDRYGVGRYQEVNPAPYTIITPPFLFAVMFGDVGHLLMFLALAM 420
Db 361 LIRTNRTASFOGIVDRYGVGRYQEVNPAPYTIITPPFLFAVMFGDVGHLLMFLALAM 420
QY 421 VLAENRPVAKAAQNEIWOTFFRGRVILLMLGLFSIYTGFIYNECFSRATSIFFSGNSVAA 480
Db 421 VLAENRPVAKAAQNEIWOTFFRGRVILLMLGLFSIYTGFIYNECFSRATSIFFSGNSVAA 480
QY 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGPPYFGIDPIWSLAANHLSPNSFKMQMSVI 540
Db 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGPPYFGIDPIWSLAANHLSPNSFKMQMSVI 540
QY 541 LGVVMHAFGVILGVNHNHFGQHRLLLTETLDELTLFGLFGYLVFLVIYKMLCVMAARA 600
Db 541 LGVVMHAFGVILGVNHNHFGQHRLLLTETLDELTLFGLFGYLVFLVIYKMLCVMAARA 600
QY 601 ASPSILLIHFINMFLFSHSPSNRLLYPRQEVQATLVVLALAMVPILLTGPLHLHRHR 660
Db 601 ASPSILLIHFINMFLFSHSPSNRLLYPRQEVQATLVVLALAMVPILLTGPLHLHRHR 660
QY 661 RLRRRPADQREENKAGLLDLPDASVNGWSSDEKAGGLDDEEAEELVPSEVLHQAIHTI 720
Db 661 RLRRRPADQREENKAGLLDLPDASVNGWSSDEKAGGLDDEEAEELVPSEVLHQAIHTI 720
QY 721 EFCLGCVSNTASYLRMLWLSLAHQSLSEVLWAMVMRIGLGLGREGVGAANVLVPIFAAFA 780
Db 721 EFCLGCVSNTASYLRMLWLSLAHQSLSEVLWAMVMRIGLGLGREGVGAANVLVPIFAAFA 780
QY 781 VMTVAILLVMEGLSAFLHALRLHWVEFQNKFYSGTGKLSPP 822
Db 781 VMTVAILLVMEGLSAFLHALRLHWVEFQNKFYSGTGKLSPP 822

RESULT 5

AD128834

ID AD128834 standard; protein; 830 AA.

XX

AC AD128834;

XX

DT 22-APR-2004 (first entry)

XX

XX Human modifier of p53 (MP53) TCIRG-1.

XX

XX Human; MP53; modifier of p53; p53; cytostatic; gene therapy;

XX

XX T-cell immune regulator 1; TCIRG-1.

XX

XX Homo sapiens.

XX

XX WO2004004766-A1.

XX

XX 15-JAN-2004.

XX

XX 09-JUL-2003; 2003WO-US021378.

XX

XX 10-JUL-2002; 2002US-0394992P.

XX

XX 07-AUG-2002; 2002US-0401604P.

XX

XX 16-SEP-2002; 2002US-0410988P.

XX

XX 25-NOV-2002; 2002US-0428837P.

XX

XX (EXEL-) EXELIXIS INC.

XX

XX Costa MA, Maxwell ME, Lackner MR, Hung T, O'Brien CL, Jin Y;

XX

XX Nicoll M, Hai B, Zhang H, Lickteig K, Amundeen CD;

XX

XX WPI; 2004-142922/14.

DR N-PSDB; ADI28820.
 DR GENBANK; 19924145.
 XX
 PT Identifying a candidate p53 pathway modulating agent for treating e.g.,
 PT cancer, comprises contacting an assay system comprising a MP53
 PT polypeptide or nucleic acid with a test agent and detecting a test agent-
 PT biased activity.
 XX
 XX Example 2; SEQ ID NO 25; 139pp; English.
 CC In the present invention, genetic screens were designed to identify
 CC modifiers of the p53 pathway in *Caenorhabditis elegans*, where a
 CC homozygous p53 deletion mutant was used. Various specific genes were
 CC silenced by RNA inhibition. Genes causing altered phenotypes in the worms
 CC were identified as modifiers of the p53 pathway. Human orthologs, denoted
 CC modifiers of p52 (MP53), of these modifiers were identified. These
 CC include the present sequence, characterised as T-cell immune regulator 1,
 CC ATPase, H+ transporting, or lysosomal V0 protein a isoform 3. MP53
 CC nucleic acids and polypeptides are attractive drug targets for the
 CC treatment of pathologies associated with a defective p53 signalling
 CC pathway, such as cancer. Methods for modulating MP53-function and/or the
 CC p53 pathway in a mammalian cell involve contacting the cell with an agent
 CC that specifically binds a MP53 polypeptide or nucleic acid. The agent may
 CC be a small molecular modulator, a nucleic acid modulator or an antibody.
 XX
 XX Sequence 830 AA;
 SQ
 Query Match 66.3%; Score 545; DB 8; Length 830;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 765; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 57 RCELEKTFPQEEVRRAGLVLPKGRPLPAPPPRDLRIQETETERLAQELRDVRNQ 116
 DB 57 RCELEKTFPQEEVRRAGLVLPKGRPLPAPPPRDLRIQETETERLAQELRDVRNQ 116
 QY 117 ALRAQLHQLHAQVLRQGHQEPOLAAHTDGAERTTLLQAPCGPHQDLRVNFAGAVEP 176
 DB 117 ALRAQLHQLHAQVLRQGHQEPOLAAHTDGAERTTLLQAPCGPHQDLRVNFAGAVEP 176
 QY 177 HKPALERLLWRACRGLFIASFRELEQLEHPVTGEPATWTFILSYGQIQGKIRKIT 236
 DB 177 HKPALERLLWRACRGLFIASFRELEQLEHPVTGEPATWTFILSYGQIQGKIRKIT 236
 QY 237 DCFHCHVFPQEEARLQALQOQOSELQVGLGTERFLSQVLRVLIQLPPGQVQV 296
 DB 237 DCFHCHVFPQEEARLQALQOQOSELQVGLGTERFLSQVLRVLIQLPPGQVQV 296
 QY 297 HKMKNVYALNOCVSTTHKLTAEAWCSVRDLPAQELARDSSMEEGVSAVAHRIPCRD 356
 DB 297 HKMKNVYALNOCVSTTHKLTAEAWCSVRDLPAQELARDSSMEEGVSAVAHRIPCRD 356
 QY 357 MPPTLIRTNRTASFGQIVDRYGVGRYQEVNPAPIYITPPFLFAVMFGDVGHGLMFLP 416
 DB 357 MPPTLIRTNRTASFGQIVDRYGVGRYQEVNPAPIYITPPFLFAVMFGDVGHGLMFLP 416
 QY 417 ALAMVLAENRPAKAAQNEIQTFFRGYRLLMLGLFSIYGTIYNECFSRATSIFFSGW 476
 DB 417 ALAMVLAENRPAKAAQNEIQTFFRGYRLLMLGLFSIYGTIYNECFSRATSIFFSGW 476
 QY 477 SVAAANQSGWSDAFLAQHTMLTLDNVTGVFLGPPYGGIDPIWLSLAANHLSTNLSFKMK 536
 DB 477 SVAAANQSGWSDAFLAQHTMLTLDNVTGVFLGPPYGGIDPIWLSLAANHLSTNLSFKMK 536
 QY 537 MSVILGVVHMAFGVLGVFNHVFQGRHRLLETLPELTFLGLFGLVFLVIYKMLCVW 596
 DB 537 MSVILGVVHMAFGVLGVFNHVFQGRHRLLETLPELTFLGLFGLVFLVIYKMLCVW 596
 QY 597 AARAAS-PSLIHFINFLSHSPSNRLLYPRQEVQATLVIALAMVPIILLGTPLHLL 655
 DB 597 AARAASPSILIHFINFLSHSPSNRLLYPRQEVQATLVIALAMVPIILLGTPLHLL 656
 QY 656 HRHRRRLRRPADRQENKAGLLDLPASVNGWSSDEEKAGGLDDEEAEELVSEVLMHQ 715

DB 657 HRHRRRLRRPADRQENKAGLLDLPASVNGWSSDEEKAGGLDDEEAEELVSEVLMHQ 716
 QY 716 AIHTIEFCGCVNTASYLRWLSLAHAQSEVLWAMVMRIGLGLGREVGVAAVLVLP 775
 DB 717 AIHTIEFCGCVNTASYLRWLSLAHAQSEVLWAMVMRIGLGLGREVGVAAVLVLP 776
 QY 776 FAAPAVMTVAILLVMEGLSAPFLHALRLHWVEFQNKFYSGTGKLSPP 822
 DB 777 FAAPAVMTVAILLVMEGLSAPFLHALRLHWVEFQNKFYSGTGKLSPP 823

RESULT 6
 ADP12465
 ID ADP12465 standard; protein; 830 AA.
 XX
 AC ADP12465;
 DT 12-AUG-2004 (first entry)
 XX
 DE Protein encoded by mRNA of the invention #75.
 XX
 KW transplant rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX
 OS Homo sapiens.
 XX
 PN WO2004042346-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 PR 24-APR-2002; 2002US-00131831.
 PR 20-DEC-2002; 2002US-00325899.
 XX
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX
 PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 XX
 DR WPI; 2004-400724/37.
 XX
 PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX
 PS Claim 65; SEQ ID NO 2474; 1762pp; English.
 XX
 CC The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection,
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC protein that is encoded by the mRNA of the invention.

Query Match 66.3%; Score 545; DB 8; Length 830;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 765; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 57 RCELEKTFPQEEVRRAGLVLPKGRPLPAPPPRDLRIQETETERLAQELRDVRNQ 116
 DB 57 RCELEKTFPQEEVRRAGLVLPKGRPLPAPPPRDLRIQETETERLAQELRDVRNQ 116

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QY 117 ALRAQLHQLHAAVLROGHEPOLAAAHDTGASERTPLLAQPGGPHQDLRVNPFVAGAVEP 176
Db 117 ALRAQLHQLHAAVLROGHEPOLAAAHDTGASERTPLLAQPGGPHQDLRVNPFVAGAVEP 176
QY 177 HKPALERLLWRACRGFLIASPRELEQPLEHPVTGEPATWMTFLISYWGEGIQKIRKIT 236
Db 177 HKPALERLLWRACRGFLIASPRELEQPLEHPVTGEPATWMTFLISYWGEGIQKIRKIT 236
QY 237 DCFHCHVFPFLOQEEARLGAALQLOQSOQELQVGLGTERFSLQVLGRVQLLPPQGVQV 296
Db 237 DCFHCHVFPFLOQEEARLGAALQLOQSOQELQVGLGTERFSLQVLGRVQLLPPQGVQV 296
QY 297 HKMKAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDRSSMEEGVSAVAHRIPCRD 356
Db 297 HKMKAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDRSSMEEGVSAVAHRIPCRD 356
QY 357 MPPTLIRNRTFASFGQIVDRIYGVGRYQEVNPPAPYTIITFPFLFAMFGDVGHLMLFLF 416
Db 357 MPPTLIRNRTFASFGQIVDRIYGVGRYQEVNPPAPYTIITFPFLFAMFGDVGHLMLFLF 416
QY 417 ALAMVLAENRPAVKAAQNEIMQTFPRGRYLLMLGLFSIYTGFIYNECSRATSIIPPSGW 476
Db 417 ALAMVLAENRPAVKAAQNEIMQTFPRGRYLLMLGLFSIYTGFIYNECSRATSIIPPSGW 476
QY 477 SVAAANQSGWSDAFIAQHTMLTLDPNVTGVFLGYPFGIDPTWLSAANHLSFLNSFKMK 536
Db 477 SVAAANQSGWSDAFIAQHTMLTLDPNVTGVFLGYPFGIDPTWLSAANHLSFLNSFKMK 536
QY 537 MSVILGVVHMAQGVVLGVNHHVFGQRHLLLETLPFLGLGLFGLYVFLVIYKWLQVW 596
Db 537 MSVILGVVHMAQGVVLGVNHHVFGQRHLLLETLPFLGLGLFGLYVFLVIYKWLQVW 596
QY 597 AARAAAS-PSILTHFINMFLSPSNRLLYPROEVVQATLVLAAMVPIILLGTPLHL 655
Db 597 AARAAASPSILTHFINMFLSPSNRLLYPROEVVQATLVLAAMVPIILLGTPLHL 656
QY 656 HRRHRLRRPADROENKAGLLDLPDASVNGSSDEEKAGGLDDEEAEALVPSEVLHQ 715
Db 657 HRRHRLRRPADROENKAGLLDLPDASVNGSSDEEKAGGLDDEEAEALVPSEVLHQ 716
QY 716 ALHTIEFCLGCVSNTASYLRLLWALSALHAQLSEVLWAMVMRIGLGRGVGVAAVLVPI 775
Db 717 ALHTIEFCLGCVSNTASYLRLLWALSALHAQLSEVLWAMVMRIGLGRGVGVAAVLVPI 776
QY 776 PAAPAVMTVAILLVMEGLSAPLHALRLHWHVFNQKPYSGTKLSPF 822
Db 777 PAAPAVMTVAILLVMEGLSAPLHALRLHWHVFNQKPYSGTKLSPF 823

RESULT 7
ABM81281
ID ABM81281 standard; protein; 830 AA.
XX
AC ABM81281;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO82023, SEQ:3305.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
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PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
XX
DR WPI; 2004-347921/32.
XX
XX N-PSDB; ACN39267.
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX Claim 12; SEQ ID NO 3305; 7273pp; English.
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
XX Sequence 830 AA;
XX
Query Match 66.3%; Score 545; DB 8; Length 830;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 765; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 57 RCELEKTFTLQEEVRRAGLVLPKGRLLPAPPDRDLRLRQETRLAQELRDVRGNQ 116
Db 57 RCELEKTFTLQEEVRRAGLVLPKGRLLPAPPDRDLRLRQETRLAQELRDVRGNQ 116
QY 117 ALRAQLHQLHAAVLROGHEPOLAAAHDTGASERTPLLAQPGGPHQDLRVNPFVAGAVEP 176
Db 117 ALRAQLHQLHAAVLROGHEPOLAAAHDTGASERTPLLAQPGGPHQDLRVNPFVAGAVEP 176
QY 177 HKPALERLLWRACRGFLIASPRELEQPLEHPVTGEPATWMTFLISYWGEGIQKIRKIT 236
Db 177 HKPALERLLWRACRGFLIASPRELEQPLEHPVTGEPATWMTFLISYWGEGIQKIRKIT 236
QY 237 DCFHCHVFPFLOQEEARLGAALQLOQSOQELQVGLGTERFSLQVLGRVQLLPPQGVQV 296
Db 237 DCFHCHVFPFLOQEEARLGAALQLOQSOQELQVGLGTERFSLQVLGRVQLLPPQGVQV 296
QY 297 HKMKAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDRSSMEEGVSAVAHRIPCRD 356
Db 297 HKMKAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDRSSMEEGVSAVAHRIPCRD 356
QY 357 MPPTLIRNRTFASFGQIVDRIYGVGRYQEVNPPAPYTIITFPFLFAMFGDVGHLMLFLF 416
Db 357 MPPTLIRNRTFASFGQIVDRIYGVGRYQEVNPPAPYTIITFPFLFAMFGDVGHLMLFLF 416
QY 417 ALAMVLAENRPAVKAAQNEIMQTFPRGRYLLMLGLFSIYTGFIYNECSRATSIIPPSGW 476
Db 417 ALAMVLAENRPAVKAAQNEIMQTFPRGRYLLMLGLFSIYTGFIYNECSRATSIIPPSGW 476
```


QY 477 SVAAANQSGSDAFLAQTMLTLDPNVTGVLGPGYFGIDPIWSLAANHLSPFLNSPKMK 536
DB 477 SVAAANQSGSDAFLAQTMLTLDPNVTGVLGPGYFGIDPIWSLAANHLSPFLNSPKMK 536
QY 537 MSVILGVVHMAFGVVLGVFNHVFQGRHRLILLETLPETLFLGLFGYLVFLVIYKWLVCW 596
DB 537 MSVILGVVHMAFGVVLGVFNHVFQGRHRLILLETLPETLFLGLFGYLVFLVIYKWLVCW 596
QY 597 AARAAS-PSILIHFINFLPSHSPSNRLLYPRQEVQATLVVLALAMVPILLGTPLHL 655
DB 597 AARAASAPSILIHFINFLPSHSPSNRLLYPRQEVQATLVVLALAMVPILLGTPLHL 656
QY 656 HRHRRRLRRPADQENKAGLLDLPASVNGWSSDEKAGGLDDEEAEELVPSEVLMLHQ 715
DB 657 HRHRRRLRRPADQENKAGLLDLPASVNGWSSDEKAGGLDDEEAEELVPSEVLMLHQ 716
QY 716 AIHTIEFCGCVSNTASYLRWLWLSLAHAQLSEVLWAMVMRIGLIGLREGVGAVALVLP 775
DB 717 AIHTIEFCGCVSNTASYLRWLWLSLAHAQLSEVLWAMVMRIGLIGLREGVGAVALVLP 776
QY 776 FAAPAVMTVAILLVMEGLSAPFLHALRLHWVEFQNKFSYGTGYKLSPP 822
DB 777 FAAPAVMTVAILLVMEGLSAPFLHALRLHWVEFQNKFSYGTGYKLSPP 823

RESULT 8

ADH22516
ID ADH22516 standard; protein; 787 AA.
XX
AC ADH22516;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human transporter & ion channel (TRICH) protein SeqID14.
XX
KW human; transporters and ion channel; TRICH; cell proliferative;
KW arteriosclerosis; cancer; autoimmune/inflammatory; AIDS; asthma;
KW neurological; epilepsy; stroke; developmental; Cushing's syndrome;
KW hypothyroidism; infection; gene therapy; cytostatic; antiinflammatory;
KW immunosuppressive; antiaesthetic; anticonvulsant; nootropic;
KW neuroprotective; single nucleotide polymorphism; SNP.
XX
OS Homo sapiens.
XX
PN WO2003093444-A2.
XX
PD 13-NOV-2003.
XX
PF 02-MAY-2003; 2003WO-US014026.
XX
PR 03-MAY-2002; 2002US-0377435P.
PR 03-MAY-2002; 2002US-0377444P.
PR 05-JUN-2002; 2002US-0386497P.
PR 11-JUN-2002; 2002US-0388180P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Baughn MR, Becha SD, Bulloch SA, Chang H, Elliott VS;
PI Emerling BM, Griffin JA, Hafalia AJA, Ison CH, Jackson AA, Jiang X;
PI Jin P, Kable AB, Khare R, Lee SY, Lee S, Mason PM, Marquis JP;
PI Ramkumar J, Richardson TW, Swarnakar A, Tran UK, Chawla NK;
PI Wilson AD;
XX
DR WPI; 2004-022655/02.
DR N-PSDB; ADH22582.
XX
PT New human transporters and ion channels (TRICH), useful for diagnosing,
PT treating and preventing diseases or conditions associated with the
PT aberrant TRICH expression e.g. cancer, AIDS, arteriosclerosis, epilepsy,
PT or infections.
XX
PS Claim 1; SEQ ID NO 14; 448pp; English.
XX

CC This invention relates to novel isolated polynucleotides identified as
CC human transporters and ion channels (TRICH), and the encoded polypeptides
CC thereof. Specifically, it describes using these TRICH molecules, as well
CC as agonists, antagonists, antibodies, expression vectors and host cells,
CC in appropriate screening and toxicity assays to assess the effects of
CC exogenous compounds on TRICH expression. The present invention describes
CC TRICH compositions that are useful in the diagnosis, treatment and
CC prevention of various disorders such as cell proliferative (e.g.
CC arteriosclerosis, cancer), autoimmune/inflammatory (e.g. AIDS, asthma),
CC neurological (e.g. epilepsy, stroke) and developmental (e.g. Cushing's
CC syndrome hypothyroidism) and for infections. Accordingly, these TRICH
CC molecules can be used for gene therapy purposes and exhibit various
CC activities such as cytostatic, antiinflammatory, immunosuppressive,
CC antiaesthetic, anticonvulsant, nootropic and neuroprotective.
CC Furthermore, a microarray is useful in monitoring or measuring protein-
CC protein interactions, drug-target interactions and gene expression
CC profiles. This polypeptide sequence is a human TRICH protein of the
CC invention.
XX

SQ Sequence 787 AA;

Query Match 60.9%; Score 501; DB 8; Length 787;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 601; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGSFMRSEVALVOLFLPTAAAYTCVSRGELGLVEFRDLNASVAFQRFVVDVWRCCE 60
DB 1 MGSFMRSEVALVOLFLPTAAAYTCVSRGELGLVEFRDLNASVAFQRFVVDVWRCCE 60
QY 61 LEKTFTEQEEVRRAGLVLPKGRLPAPPDRDLRIQETTERLAQLRDRVGNQOALRA 120
DB 61 LEKTFTEQEEVRRAGLVLPKGRLPAPPDRDLRIQETTERLAQLRDRVGNQOALRA 120
QY 121 QLHLQLHAAVLRRQGHPEPQLAAATDCASERTPLQAPGPHQDLRVNFAVAGVEPHKAP 180
DB 121 QLHLQLHAAVLRRQGHPEPQLAAATDCASERTPLQAPGPHQDLRVNFAVAGVEPHKAP 180
QY 181 ALBRLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEOIGQKIRKITDCFH 240
DB 181 ALBRLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEOIGQKIRKITDCFH 240
QY 241 CHVFPFLOQEEARLQALQLOQSOELOEVLGETERFELSQVLGRVLOLLPQGVQVHKMK 300
DB 241 CHVFPFLOQEEARLQALQLOQSOELOEVLGETERFELSQVLGRVLOLLPQGVQVHKMK 300
QY 301 AVYALNQCSVSTTHKCLIAEAWCSVRDLPALQEARLDSMEEGVSAVAHRIPCRDMPPT 360
DB 301 AVYALNQCSVSTTHKCLIAEAWCSVRDLPALQEARLDSMEEGVSAVAHRIPCRDMPPT 360
QY 361 LIRTNRTASFOGIVDRYGVGRYOEVNPAPTYITITPPFLFAVMFGDVGHGLLMFLFALAM 420
DB 361 LIRTNRTASFOGIVDRYGVGRYOEVNPAPTYITITPPFLFAVMFGDVGHGLLMFLFALAM 420
QY 421 VLAENRPAVKAAQNEIWQTFRRGRYLLMLLSIYTGFIYNECFSRATSIIFPSGWSVAA 480
DB 421 VLAENRPAVKAAQNEIWQTFRRGRYLLMLLSIYTGFIYNECFSRATSIIFPSGWSVAA 480
QY 481 MANQSGWSDAFLAQTMLTLDPNVTGVLGPGYFGIDPIWSLAANHLSPFLNSPKMKSVI 540
DB 481 MANQSGWSDAFLAQTMLTLDPNVTGVLGPGYFGIDPIWSLAANHLSPFLNSPKMKSVI 540
QY 541 LGVHVHMAFGVVLGVFNHVFQGRHRLILLETLPETLFLGLFGYLVFLVIYKWLVCWAARA 600
DB 541 LGVHVHMAFGVVLGVFNHVFQGRHRLILLETLPETLFLGLFGYLVFLVIYKWLVCWAARA 600
QY 601 AS 602
DB 601 AS 602

RESULT 9

ABM84820
ID ABM84820 standard; protein; 787 AA.

XX AC ABM84820;
XX DT 18-NOV-2004 (first entry)
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:5069.
XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX OS Homo sapiens.
XX PN WO2004023973-A2.
XX PD 25-MAR-2004.
XX PF 12-SEP-2003; 2003WO-US0282227.
XX PR 12-SEP-2002; 2002US-0410259F.
XX PR 12-SEP-2002; 2002US-0410260F.
XX PA (INCY-) INCYTE CORP.
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patry S, Shi X, Suarez CJ;
XX WPI; 2004-329368/30.
XX DR N-PSDB; ACN43472.
XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX PT in diagnosing a condition, disease or disorder associated with human
XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX PT in gene mapping.
XX PS Claim 27; Page; 190pp; English.
XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
XX CC selected from one of the 2722 sequences defined in the specification. A
XX CC polynucleotide of the invention may have a use in gene therapy. The human
XX CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
XX CC used to diagnose a particular condition, disease or disorder associated
XX CC with human molecules, e.g. cell proliferative disorders,
XX CC autoimmune/inflammatory disorder, developmental disorder, endocrine
XX CC disorder, neurological disorders, gastrointestinal disorders, or
XX CC infections caused by virus, bacteria, fungi or parasite. The dithp
XX CC molecules may also be used in genetic mapping, in identifying individuals
XX CC from minute biological samples, in detecting single nucleotide
XX CC polymorphisms, as molecular weight markers, and for somatic or germline
XX CC gene therapy. The present sequence represents a dithp protein of the
XX CC invention. Note: The sequence data for this patent is not represented in
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX SQ Sequence 787 AA;
Query Match 54.1%; Score 445; DB 8; Length 787;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 545; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 57 RCELEKFTFLQEEVRRAGLVLPKPKGLPAPPPRDLRLIQEETERLAQELRDVRGNQ 116
DB 57 RCELEKFTFLQEEVRRAGLVLPKPKGLPAPPPRDLRLIQEETERLAQELRDVRGNQ 116
QY 117 ALRAQLHQLHAAVLROGHEPQLAAAHDTGASERTLLQAPGGPHODLRVNFVAGVPEP 176
DB 117 ALRAQLHQLHAAVLROGHEPQLAAAHDTGASERTLLQAPGGPHODLRVNFVAGVPEP 176
QY 177 HKAPALERLLWRACRGLFIASPRELEQPLEHPVTGEPATWMTFLISYWGEGIQGKIRKIT 236

DB 177 HKAPALERLLWRACRGLFIASPRELEQPLEHPVTGEPATWMTFLISYWGEGIQGKIRKIT 236
QY 237 DCFHCHVFPFLQEEARLQALQLOOQSOQELQEVIGETERFLSQVLGRVLQQLPPGQVQV 296
DB 237 DCFHCHVFPFLQEEARLQALQLOOQSOQELQEVIGETERFLSQVLGRVLQQLPPGQVQV 296
QY 297 HOKKAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQEBALRDSSMBEGVSAVAHRIPCRD 356
DB 297 HOKKAVYLALNQCSTVTHKCLIAEAWCSVRDLPALQEBALRDSSMBEGVSAVAHRIPCRD 356
QY 357 MPPTLIRTNRTASFGQIVDRYGVGRYQSVNPAPVTIITFPFLFAVMFGDVGHLLMELF 416
DB 357 MPPTLIRTNRTASFGQIVDRYGVGRYQSVNPAPVTIITFPFLFAVMFGDVGHLLMELF 416
QY 417 ALAMVLAENRPAVKAQNSIWTFFRGYLLLLMGLFSIYTGFIYNECFSRATSIIPPSGW 476
DB 417 ALAMVLAENRPAVKAQNSIWTFFRGYLLLLMGLFSIYTGFIYNECFSRATSIIPPSGW 476
QY 477 SVAMANOSGWSDAFLAQTMTLTLDPNVTGVFLGYPFGIDDIWSLAANHLSFLNSFKMK 536
DB 477 SVAMANOSGWSDAFLAQTMTLTLDPNVTGVFLGYPFGIDDIWSLAANHLSFLNSFKMK 536
QY 537 MSVILGVVHMAFGVVLGVFNHVFQGRHLLLETLPELTFLGLFGYLVFLVIYKWLQVW 596
DB 537 MSVILGVVHMAFGVVLGVFNHVFQGRHLLLETLPELTFLGLFGYLVFLVIYKWLQVW 596
QY 597 AARAAS 602
DB 597 AARAAS 602
RESULT 10
AAW98112
ID AAW98112 standard; protein; 614 AA.
XX AC AAW98112;
XX DT 21-JUN-1999 (first entry)
XX DE T-cell membrane protein TIRC7.
XX KW TIRC7; T-cell immune response cDNA 7; T-cell membrane protein; human;
XX KW immunosuppressive; organ transplantation; graft rejection;
XX KW transplant rejection; autoimmune disease; allergy; infection; tumour;
XX KW cancer; rheumatoid arthritis; lupus erythematosus; multiple sclerosis;
XX KW encephalitis; vasculitis; diabetes mellitus; pancreatitis; gastritis;
XX KW thyroiditis; asthma; lepraematosis; therapy.
XX OS Homo sapiens.
XX FH Location/Qualifiers
XX FT Protein 1..601
XX FT /note= "separately claimed in Claim 1"
XX FT Domain 173..209
XX FT /note= "transmembrane domain"
XX FT Domain 229..246
XX FT /note= "transmembrane domain"
XX FT Domain 319..346
XX FT /note= "transmembrane domain"
XX FT Domain 356..400
XX FT /note= "transmembrane domain"
XX FT Domain 413..437
XX FT /note= "transmembrane domain"
XX FT Domain 513..532
XX FT /note= "transmembrane domain"
XX FT Domain 544..585
XX FT /note= "transmembrane domain"
XX PN WO9911782-A1.
XX PD 11-MAR-1999.
XX

PF 28-AUG-1998; 98WO-EF005462.
XX
PR 29-AUG-1997; 97DE-01038710.
PR 12-FEB-1998; 98DE-02002653.
XX
PA (BCHM) BRIGHAM & WOMENS HOSPITAL.
PA (UTKU/) UTKU N.
XX
XX Utku N, Gullans SR, Milford EL;
PI WPI; 1999-205186/17.
XX N-PSDB; AAX24912.
DR
DR
PT A novel T-cell transmembrane protein (TIRC7) - useful for modulating
PT immune responses, for use in organ transplantations and treatment of
PT infectious disease.
XX
XX Claim 1(i); Page 84-86; 97pp; English.
XX
XX The present sequence is TIRC7, a novel T-cell transmembrane protein that
CC exhibits a central role in T-cell activation in vitro and in vivo. TIRC7
CC mRNA is transiently up-regulated in the early phase of T-cell activation
CC via a calcineurin-dependent pathway. TIRC7 cDNA (see AAX24912) was
CC identified following a screen for genes that are differentially expressed
CC in alloactivated human T cells. A second TIRC7 protein (see AAW98113) is
CC identical except for one amino acid substitution (Arg121 to Gln),
CC suggesting 2 alleles of the TIRC7 gene. The invention provides vectors,
CC host cells, antibodies, TIRC7 peptides, polypeptides and polynucleotides
CC that are useful in diagnostic compositions for identifying T-cell
CC activating or co-stimulating compounds, or for identifying inhibitors of
CC T-cell activation and stimulation. TIRC7 peptides or polypeptides,
CC vectors and antibodies are useful in the preparation of pharmaceutical
CC compositions for treatment of acute and chronic diseases involving T-cell
CC activation and Th1 and Th2 immune response, for the treatment of acute
CC and chronic rejection of allo- and xeno organ transplants and bone marrow
CC transplantation, for the treatment of rheumatoid arthritis, lupus
CC erythematosus, multiple sclerosis, encephalitis, vasculitis, diabetes
CC mellitus, pancreatitis, gastritis, thyroiditis, for the treatment of
CC malign disorders of T, B or NK cells, for the treatment of asthma,
CC lepramatosi, Helicobacter pylori associated gastritis, or for the
XX treatment of skin, adrenal or lung tumors (claimed)
XX
XX Sequence 614 AA;
SQ
Query Match 46.8%; Score 385; DB 2; Length 614;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 605; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 217 MTFLLSYWGEIQGKIRKIDCFCHVFPFLOQEEARLQALQOQSQBLQVLGETER 276
DB 1 MTFLLSYWGEIQGKIRKIDCFCHVFPFLOQEEARLQALQOQSQBLQVLGETER 60
QY 277 FLSQVLGRVLQPLPGQVQVHKVAVYALNQCSTVTHKCLIAEAWCSVRDLPALQAL 336
DB 61 FLSQVLGRVLQPLPGQVQVHKVAVYALNQCSTVTHKCLIAEAWCSVRDLPALQAL 120
QY 337 RDSMEEGVSAAVHRIPCRDMPPTLIRNTRFTASFGQIVDYGVRGYQVNPAPYTIITF 396
DB 121 RDSMEEGVSAAVHRIPCRDMPPTLIRNTRFTASFGQIVDYGVRGYQVNPAPYTIITF 180
QY 397 PFLFVAVFQVGVHGLMLFALAMVLAENRPAVKAQNEIWQTFRRGRYLLLMGLFSIY 456
DB 181 PFLFVAVFQVGVHGLMLFALAMVLAENRPAVKAQNEIWQTFRRGRYLLLMGLFSIY 240
QY 457 TGIYNECSRATSIIPSGWSVAAANQSGWSDAFLAQHTMLTLDNVTGVFLGPPYPGI 516
DB 241 TGIYNECSRATSIIPSGWSVAAANQSGWSDAFLAQHTMLTLDNVTGVFLGPPYPGI 300
QY 517 DPTWSLAANHLFLNSFKMKQSVILGVVHMAFGVLFVFNHFGQRHRLLLTLPDLTF 576
DB 301 DPTWSLAANHLFLNSFKMKQSVILGVVHMAFGVLFVFNHFGQRHRLLLTLPDLTF 360
QY 577 LLGLFGYLVFLYKWLVCVMAAAS-PSLIHFINNLFSPSNRLLYPROEVVQATL 635

DB 361 LLGLFGYLVFLYKWLVCVMAAASAPSLIHFINNLFSPSNRLLYPROEVVQATL 420
QY 636 VVLALAMVPILLGCTPLHLLHRRRLRRPADRQENKAGLLDLPDASVNGWSSDDEKA 695
DB 421 VVLALAMVPILLGCTPLHLLHRRRLRRPADRQENKAGLLDLPDASVNGWSSDDEKA 480
QY 696 GGLDDEEAELVPSEVLMHQAIHTIEFCLGCVSNTASYLRLWALSALAHQQLSEVLMAMVM 755
DB 481 GGLDDEEAELVPSEVLMHQAIHTIEFCLGCVSNTASYLRLWALSALAHQQLSEVLMAMVM 540
QY 756 RIGLGIGREVGVAAVLVLPFAFAVMTVAILLVMEGLSAFLHALRLHWFQNKFSYSGT 815
DB 541 RIGLGIGREVGVAAVLVLPFAFAVMTVAILLVMEGLSAFLHALRLHWFQNKFSYSGT 600
QY 816 GYKLSPPF 822
DB 601 GYKLSPPF 607
RESULT 11
ABM81282
ID ABM81282 standard; protein; 614 AA.
XX
AC ABM81282;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO24831, SEQ:3307.
XX
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
OS Homo sapiens.
XX
XX WO2004030615-A2.
XX
XX 15-APR-2004.
XX
XX 29-SEP-2003; 2003WO-US028547.
XX
XX 02-OCT-2002; 2002US-0414971P.
XX
XX (GETH) GENENTECH INC.
XX
XX Wu TD, Zhang Z, Zhou Y;
XX
XX WPI: 2004-347921/32.
XX N-PSDB; ACN39268.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 3307; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,

CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention

XX SQ Sequence 614 AA;

Query Match 46.8%; Score 385; DB 8; Length 614;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 605; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 217 MTFLLSYMGEGIQGKIRKIKITDFCHCHVFPFLOQEEARLQALQOQSQSELQVIGETER 276

Db 1 MTFLLSYMGEGIQGKIRKIKITDFCHCHVFPFLOQEEARLQALQOQSQSELQVIGETER 60

QY 277 FLSQVLGRVLQLLPQGVQVHKAVYALNQCSTTHKCLIAEAWCSVRDLPALQEL 336

Db 61 FLSQVLGRVLQLLPQGVQVHKAVYALNQCSTTHKCLIAEAWCSVRDLPALQEL 120

QY 337 RDSMEEGVSAVAHRIPCRDMPPTLIRTNRTASFGIYDVRGVGRQVNPAPYTIIF 396

Db 121 RDSMEEGVSAVAHRIPCRDMPPTLIRTNRTASFGIYDVRGVGRQVNPAPYTIIF 180

QY 397 PFLFVMPGDVGHLMLFALAMVLAENRPAKAAQNEIWQTFGRYLLLLMGLFSY 456

Db 181 PFLFVMPGDVGHLMLFALAMVLAENRPAKAAQNEIWQTFGRYLLLLMGLFSY 240

QY 457 TGFYNECSRATSIFFPSGWSVAAMNQSWSDAFLAQTMLTLDNVTGVFLGYPFGI 516

Db 241 TGFYNECSRATSIFFPSGWSVAAMNQSWSDAFLAQTMLTLDNVTGVFLGYPFGI 300

QY 517 DPIMSLAANHLFLSFKMKSIVILGVHMAFGVILGVFNHVFHGORHRLLETPELTF 576

Db 301 DPIMSLAANHLFLSFKMKSIVILGVHMAFGVILGVFNHVFHGORHRLLETPELTF 360

QY 577 LIGLFGYLVFLVIYKWCWAAARAAS-PSILIHFINMFLFSPNSNRLLYPRQEVVQATL 635

Db 361 LIGLFGYLVFLVIYKWCWAAARAASPSILIHFINMFLFSPNSNRLLYPRQEVVQATL 420

QY 636 VVALAMVPILLLGTPHLHLHRRRLRRPRADQENKAGLLDLPDASVNGWSSDEKA 695

Db 421 VVALAMVPILLLGTPHLHLHRRRLRRPRADQENKAGLLDLPDASVNGWSSDEKA 480

QY 696 GGLDDEEAELVPSVLMHQAHTIEFCLGCVSNTASYLRLWALSIAHAQLSEVLWAMVM 755

Db 481 GGLDDEEAELVPSVLMHQAHTIEFCLGCVSNTASYLRLWALSIAHAQLSEVLWAMVM 540

QY 756 RIGLGLGREVGVAAVLVPIFAFVMTVAILLVMGLSAFLHALRLHWVEFQNFYSGT 815

Db 541 RIGLGLGREVGVAAVLVPIFAFVMTVAILLVMGLSAFLHALRLHWVEFQNFYSGT 600

QY 816 GYKLSPF 822

Db 601 GYKLSPF 607

RESULT 12

ID AAW98113 standard; protein; 614 AA.

XX AC AAW98113;

XX DT 21-JUN-1999 (first entry)

XX DE T-cell membrane protein TIRC7.

XX KW TIRC7; T-cell immune response cDNA 7; T-cell membrane protein; human;

KW immunosuppressive; organ transplantation; graft rejection.

KW transplant rejection; autoimmune disease; allergy; infection; tumour;
KW cancer; rheumatoid arthritis; lupus erythematosus; multiple sclerosis;
KW encephalitis; vasculitis; diabetes mellitus; pancreatitis; gastritis;
KW thyroiditis; asthma; lepramatosi; therapy.

XX Homo sapiens.

PH Key Location/Qualifiers

FT 1. .601 /note= "separately claimed in Claim 1"

FT Domain 173. .209 /note= "transmembrane domain"

FT Domain 229. .246 /note= "transmembrane domain"

FT Domain 319. .346 /note= "transmembrane domain"

FT Domain 356. .400 /note= "transmembrane domain"

FT Domain 413. .437 /note= "transmembrane domain"

FT Domain 513. .532 /note= "transmembrane domain"

FT Domain 544. .585 /note= "transmembrane domain"

XX WO9911782-A1.

PN 11-MAR-1999.

XX 28-AUG-1998; 98WO-EP005462.

XX 29-AUG-1997; 97DB-01038710.

XX 12-FEB-1998; 98DE-02002653.

XX (BGM) BRIGHAM & WOMENS HOSPITAL.

XX (UTKU/) UTKU N.

XX Utku N, Gullans SR, Milford EL;

XX WPI; 1999-205186/17.

XX N-PSDB; AAX24913.

CC A novel T-cell transmembrane protein (TIRC7) - useful for modulating
CC immune responses, for use in organ transplantations and treatment of
CC infectious disease.

PS Claim 1(i); Page 93-95; 97pp; English.

CC The present sequence is TIRC7, a novel T-cell transmembrane protein that
CC exhibits a central role in T-cell activation in vitro and in vivo. TIRC7
CC mRNA is transiently up-regulated in the early phase of T-cell activation
CC via a calcineurin-dependent pathway. TIRC7 cDNA (see AAX24912) was
CC identified following a screen for genes that are differentially expressed
CC in alloactivated human T cells. A second TIRC7 protein (see AAW98112) is
CC identical except for one amino acid substitution (Gln121 to Arg),
CC suggesting 2 alleles of the TIRC7 gene. The invention provides vectors,
CC host cells, antibodies, TIRC7 peptides, polypeptides and polynucleotides
CC that are useful in diagnostic compositions for identifying T-cell
CC activating or co-stimulating compounds, or for identifying inhibitors of
CC T-cell activation and stimulation. TIRC7 peptides or polypeptides,
CC vectors and antibodies are useful in the preparation of pharmaceutical
CC compositions for treatment of acute and chronic diseases involving T-cell
CC activation and Th1 and Th2 immune response, for the treatment of acute
CC and chronic rejection of allo- and xeno organ transplants and bone marrow
CC transplantation, for the treatment of rheumatoid arthritis, lupus
CC erythematosus, multiple sclerosis, encephalitis, vasculitis, diabetes
CC mellitus, pancreatitis, gastritis, thyroiditis, for the treatment of
CC malign disorders of T, B or NK cells, for the treatment of asthma,
CC lepramatosi, Helicobacter pylori associated gastritis, or for the
CC treatment of skin, adrenal or lung tumors (claimed)

XX Sequence 614 AA;

Query Match 39.5%; Score 325; DB 2; Length 614;
Best Local Similarity 99.8%; Pred. No. 3.5e-309;
Matches 445; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 378 YGGRYQEVNPAPYTIITFPFLFAVMFGDVGHGLLMFLFALAMVLAENRPAVKAQNEIW 437
DB 162 YGGRYQEVNPAPYTIITFPFLFAVMFGDVGHGLLMFLFALAMVLAENRPAVKAQNEIW 221

QY 438 QTFRGRYLLMLGLFSIYTGFIYNECFSRATSIFFPSGWSVAAMANOSGWSDAFLAHTM 497
DB 222 QTFRGRYLLMLGLFSIYTGFIYNECFSRATSIFFPSGWSVAAMANOSGWSDAFLAHTM 281

QY 498 LTLDPNVTGVFLGYPGIDPIWLSAANHLNFLNSFKMKMSVILGVVHMAFGVVLGVFNH 557
DB 282 LTLDPNVTGVFLGYPGIDPIWLSAANHLNFLNSFKMKMSVILGVVHMAFGVVLGVFNH 341

QY 558 VHFQGRHLLLETPELTFLGLFGYLVFLVIYKWLVCWAARAAS-PSILIHFINMFLFS 616
DB 342 VHFQGRHLLLETPELTFLGLFGYLVFLVIYKWLVCWAARAASPSILIHFINMFLFS 401

QY 617 HPSNRLLYPRQEVVQATLVVLAAMVPIILLGTPLHLHRRRRLRRPADROEENKAG 676
DB 402 HPSNRLLYPRQEVVQATLVVLAAMVPIILLGTPLHLHRRRRLRRPADROEENKAG 461

QY 677 LLDLPDASVNGSSDEEKAGLDDEEAEALVPSEVLHMQAIHTIEFCIGCVSNTASYLRL 736
DB 462 LLDLPDASVNGSSDEEKAGLDDEEAEALVPSEVLHMQAIHTIEFCIGCVSNTASYLRL 521

QY 737 WALSLAHAQLSEVLWAMVMRIGLGLREVGVAAVVLVPIFAAFVAVMTVAILLVMEGLSAP 796
DB 522 WALSLAHAQLSEVLWAMVMRIGLGLREVGVAAVVLVPIFAAFVAVMTVAILLVMEGLSAP 581

QY 797 LHALLHWWBFQNKFSYGTGYKLSPP 822
DB 582 LHALLHWWBFQNKFSYGTGYKLSPP 607

RESULT 13

ABR43098
ID ABR43098 standard; protein; 614 AA.

XX
AC ABR43098;

XX
DT 03-JUL-2003 (first entry)

XX
DE Human T-cell immune response cDNA 7 (TIRC7) protein SEQ ID NO:5.

XX
KW Human; human leukocyte antigen; HLA; T-cell immune response cDNA 7;
KW TIRC7; immune response; immune disease; immunosuppressive; antiallergic;
KW antimicrobial; antibacterial; cytostatic; vulnerable.

XX
OS Homo sapiens.

XX
PN WO2003025000-A2.

XX
PD 27-MAR-2003.

XX
PF 17-SEP-2002; 2002WO-EP010440.

XX
PR 17-SEP-2001; 2001US-0322895P.

XX
PR 17-SEP-2001; 2001US-0322896P.

XX
PA (UTKU/) UTKU N.

XX
PI Utku N;

XX
WI 2003-381482/36.

XX
PT Peptide useful for the preparation of a pharmaceutical composition for
PT inhibition of an immune response comprises fragment of the amino acid
XX sequence.

XX
PS Claim 5; Fig 4A; 40pp; English.

XX

CC The present invention describes a peptide (P1) comprising a fragment of
CC the amino acid sequence from human leukocyte associated antigen (HLA)
CC class II alpha 2 chain (see ABR43094) or T cell immune response cDNA7
CC (TIRC7) protein (see ABR43098). Also described is a composition
CC comprising at least one (P1). (P1) has immunosuppressive, antiallergic,
CC antimicrobial, antibacterial, cytostatic and vulnerary activities, and
CC can be used as an inhibitor of the proliferation of peripheral blood
CC mononuclear cells (PBMCs), and as an immune response modulator. (P1) can
CC be used for the preparation of a pharmaceutical composition for the
CC inhibition of an immune response. (P1) can also be used for treating
CC graft versus host disease, autoimmune diseases, allergic diseases,
CC infectious diseases, sepsis and tumours. (P1) can be used for the
CC improvement of wound healing, and for inducing or maintaining immune
CC unresponsiveness. The present sequence represents the human TIRC7
CC protein, which is used in the exemplification of the present invention

XX
SQ Sequence 614 AA;

Query Match 39.5%; Score 325; DB 6; Length 614;
Best Local Similarity 99.8%; Pred. No. 3.5e-309;
Matches 445; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 378 YGGRYQEVNPAPYTIITFPFLFAVMFGDVGHGLLMFLFALAMVLAENRPAVKAQNEIW 437
DB 162 YGGRYQEVNPAPYTIITFPFLFAVMFGDVGHGLLMFLFALAMVLAENRPAVKAQNEIW 221

QY 438 QTFRGRYLLMLGLFSIYTGFIYNECFSRATSIFFPSGWSVAAMANOSGWSDAFLAHTM 497
DB 222 QTFRGRYLLMLGLFSIYTGFIYNECFSRATSIFFPSGWSVAAMANOSGWSDAFLAHTM 281

QY 498 LTLDPNVTGVFLGYPGIDPIWLSAANHLNFLNSFKMKMSVILGVVHMAFGVVLGVFNH 557
DB 282 LTLDPNVTGVFLGYPGIDPIWLSAANHLNFLNSFKMKMSVILGVVHMAFGVVLGVFNH 341

QY 558 VHFQGRHLLLETPELTFLGLFGYLVFLVIYKWLVCWAARAAS-PSILIHFINMFLFS 616
DB 342 VHFQGRHLLLETPELTFLGLFGYLVFLVIYKWLVCWAARAASPSILIHFINMFLFS 401

QY 617 HPSNRLLYPRQEVVQATLVVLAAMVPIILLGTPLHLHRRRRLRRPADROEENKAG 676
DB 402 HPSNRLLYPRQEVVQATLVVLAAMVPIILLGTPLHLHRRRRLRRPADROEENKAG 461

QY 677 LLDLPDASVNGSSDEEKAGLDDEEAEALVPSEVLHMQAIHTIEFCIGCVSNTASYLRL 736
DB 462 LLDLPDASVNGSSDEEKAGLDDEEAEALVPSEVLHMQAIHTIEFCIGCVSNTASYLRL 521

QY 737 WALSLAHAQLSEVLWAMVMRIGLGLREVGVAAVVLVPIFAAFVAVMTVAILLVMEGLSAP 796
DB 522 WALSLAHAQLSEVLWAMVMRIGLGLREVGVAAVVLVPIFAAFVAVMTVAILLVMEGLSAP 581

QY 797 LHALLHWWBFQNKFSYGTGYKLSPP 822
DB 582 LHALLHWWBFQNKFSYGTGYKLSPP 607

RESULT 14

ABP41524

ID ABP41524 standard; protein; 643 AA.

XX
AC ABP41524;

XX
DT 22-AUG-2002 (first entry)

XX
DE Human ovarian antigen HTAES83, SEQ ID NO:2656.

XX
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;

KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; chromosome 11q13.4-13.5.
 XX
 OS Homo sapiens.
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US019569.
 XX
 PR 07-JUN-2000; 2000US-0209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX WPI; 2002-147878/19.
 XX N-PSDB; ABQ54601.
 DR
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 PS Claim 11; SEQ ID NO 2656; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 643 AA;
 SQ
 Query Match 35.4%; Score 291; DB 5; Length 643;
 Best Local Similarity 99.6%; Pred. No. 8.3e-276;
 Matches 491; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 110 DVRGNQALRAQLHQLHAAVLRLQGHPEQLAAHTDGAERTPLLPAGGPHQDLRVNF 169
 DB 78 DVRGNQALRAQLHQLHAAVLRLQGHPEQLAAHTDGAERTPLLPAGGPHQDLRVNF 137
 QY 170 VAGAVEPHKAPALERLLWRACRGFLIASPRELEQPLEHPVTGEPATMTTFLISYGEQIG 229
 DB 138 VAGAVEPHKAPALERLLWRACRGFLIASPRELEQPLEHPVTGEPATMTTFLISYGEQIG 197
 QY 230 QKIRKITDCFHCHVFFPFLQOEERLALQLOOQQSQELQEVLTETERFSLQVLGRVLQL 289

Db 198 QKIRKITDCFHCHVFFPFLQOEERLALQLOOQQSQELQEVLTETERFSLQVLGRVLQL 257
 QY 290 PFGQVQVHKMAVYLALNQCSVSTTHKCLIAEAWCSVRDLPALQEARLDSSMEEGVSAVA 349
 Db 258 PFGQVQVHKMAVYLALNQCSVSTTHKCLIAEAWCSVRDLPALQEARLDSSMEEGVSAVA 317
 QY 350 HRIPCRDMPPTLIRNRTFASFGQIVDRYGVGRYQEVNRPAPYTIITFPFLFAVMFGDVGH 409
 Db 318 XRIPCRDMPPTLIRNRTFASFGQIVDAYGVGRYQEVNRPAPYTIITFPFLFAVMFGDVGH 377
 QY 410 GLLMFLFALAMVLAENRPAVKAQNEIWOTFFRGYLLLLMGLFSIYTGFIYNECSRAT 469
 Db 378 GLLMFLFALAMVLAENRPAVKAQNEIWOTFFRGYLLLLMGLFSIYTGFIYNECSRAT 437
 QY 470 SIFPSGWSVAAMANQSGMSDAFLAQHTMLTLDPNVTGVFLGYPFGIDPIWLSLAANHLSF 529
 Db 438 SIFPSGWSVAAMANQSGMSDAFLAQHTMLTLDPNVTGVFLGYPFGIDPIWLSLAANHLSF 497
 QY 530 LNSFKMKMSVILGVVHMAFGVVLGVFNHVFQGRHLLLETLPELTFLGLGFLYLVFLVI 589
 Db 498 LNSFKMKMSVILGVVHMAFGVVLGVFNHVFQGRHLLLETLPELTFLGLGFLYLVFLVI 557
 QY 590 YKWLVCVMAARAAS 602
 Db 558 YKWLVCVMAARAAS 570
 RESULT 15
 ADD27652
 ID ADD27652 standard; protein; 124 AA.
 XX
 AC ADD27652;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human adipocyte Selected Interacting Domain (SID) prey protein #1109.
 XX
 KW Adipocyte; protein-protein interaction; protein complex;
 KW bait-prey complex; Selected Interacting Domain; SID; drug screening;
 KW drug discovery; metabolic disease; obesity; lipodystrophy;
 KW diabetes mellitus; type 2; non-insulin dependent; NIDDM;
 KW adipogenesis modulation; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200290544-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 03-MAY-2002; 2002WO-EP006333.
 XX
 PR 04-MAY-2001; 2001US-0288885P.
 XX
 PA (HYBR-) HYBRIGENICS.
 PA (LYNX-) LYNX THERAPEUTICS INC.
 XX
 PI Legrain P, Whiteside S, Mao J, Khrebtukova I, Luo S;
 DR WPI; 2003-111975/10.
 DR N-PSDB; ADD27651.
 XX
 PT New complex of bait and prey between two polypeptides or polynucleotides
 PT encoding the two polypeptides of adipocytes, useful for selecting a
 PT modulating compound that inhibits or activates protein-protein
 PT interactions.
 XX
 PS Claim 6; SEQ ID NO 1109; 232pp; English.
 XX
 CC The invention relates to a bait-prey complex between two adipocyte
 CC polypeptides, or between two polynucleotides encoding adipocyte
 CC polypeptides. The invention also relates to selected interacting Domain
 CC (SID) polypeptides which interact with selected bait polypeptides;

CC polynucleotides encoding SID polypeptides; vectors comprising SID
CC polynucleotides; recombinant host cells comprising an adipocyte
CC polynucleotide or a SID-encoding vector; a method of selecting for a
CC compound which modulates interactions between adipocyte polypeptides;
CC adipocyte modulator compounds identified using the method; a
CC pharmaceutical composition comprising an adipocyte modulator, or a SID-
CC encoding vector or host cell; and a protein chip comprising adipocyte
CC bait polypeptides. The bait-prey complexes of the invention are useful
CC for selecting a compound that inhibits or activates protein-protein
CC interactions between adipocyte polypeptides. The modulatory compounds
CC identified can be used in the treatment of metabolic diseases such as
CC obesity, lipodystrophy and type 2 diabetes mellitus, and in the
CC modulation of adipogenesis. The present sequence represents a
CC specifically claimed adipocyte SID prey polypeptide of the invention.
XX
SQ Sequence 124 AA;

Query Match 15.1%; Score 124; DB 7; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.3e-112;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 606 LIHFNNFLFSHSPSNLLYPQREVQVQATLVVLALAMVPILLGTPHLHLHRRRLRR 665
Db 1 LIHFNNFLFSHSPSNLLYPQREVQVQATLVVLALAMVPILLGTPHLHLHRRRLRR 60

QY 666 PADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEIIVPSEVLHQAIHTIEFCLG 725
Db 61 PADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEIIVPSEVLHQAIHTIEFCLG 120

QY 726 CVSN 729
Db 121 CVSN 124

Search completed: June 29, 2006, 13:16:50
Job time : 197 secs

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OM protein - protein search, using sw model

Run on: June 29, 2006, 13:17:09 ; Search time 46 Seconds
(without alignments)
1719.352 Million cell updates/sec

Title: US-10-783-519-2
Perfect score: 822
Sequence: 1 MGSMPRSEVALVQLFLPTA.....HWVEFQNKFSYGTGYKLSPF 822

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 80:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	3.3	163	2 T46449	hypothetical prote
2	27	3.3	838	2 A54163	vacuolar ATPase (E
3	24	2.9	838	2 B38656	vacuolar proton pu
4	22	2.7	873	2 T16282	hypothetical prote
5	22	2.7	1236	2 T19492	hypothetical prote
6	20	2.4	775	2 T46719	probable vacuolar
7	20	2.4	843	2 T06068	probable proton pu
8	20	2.4	855	2 JH0287	immune regulatory
9	19	2.3	935	2 S15795	vacuolar proton pu
10	18	2.2	840	1 A42970	H+-exporting ATPas
11	18	2.2	865	2 T18565	probable H+-export
12	18	2.2	890	2 S54554	H+-exporting ATPas
13	17	2.1	780	2 H84685	probable vacuolar
14	17	2.1	831	2 H84600	probable vacuolar
15	14	1.7	805	2 T37787	probable vacuolar
16	8	1.0	86	2 B82006	hypothetical prote
17	8	1.0	169	2 G71944	hypothetical prote
18	8	1.0	171	2 E64655	hypothetical prote
19	8	1.0	177	2 F87441	hypothetical prote
20	8	1.0	187	2 S23595	hypothetical prote
21	8	1.0	192	2 S54407	embryonic fibrobla
22	8	1.0	202	2 E87046	probable lipoprote
23	8	1.0	210	2 T41025	hypothetical prote
24	8	1.0	248	2 G83694	hypothetical prote
25	8	1.0	249	2 A70786	probable Cobs - My
26	8	1.0	255	2 G69533	hypothetical prote
27	8	1.0	263	2 T23473	hypothetical prote
28	8	1.0	324	2 T08729	RING zinc finger p
29	8	1.0	342	2 AF2177	glucokinase [impor

30 8 1.0 382 2 D84766 hypothetical prote
31 8 1.0 389 2 AD0271 conserved hypothet
32 8 1.0 442 2 D84224 heme synthase [imp
33 8 1.0 447 2 AF3313 osmolarity sensor
34 8 1.0 606 2 F71330 probable DNA repai
35 8 1.0 693 2 AF2357 hypothetical prote
36 8 1.0 758 2 A83121 probable two-compo
37 8 1.0 930 2 E96600 protein F14J16.20
38 7 0.9 36 1 JU0352 4.6K protein - Chl
39 7 0.9 93 2 I84714 H2-1A-beta-2 anti
40 7 0.9 93 2 I54421 MHC RT1.B-beta2 -
41 7 0.9 106 2 S66735 probable membrane
42 7 0.9 116 1 C64423 conserved hypothet
43 7 0.9 116 1 E69393 probable erp prot
44 7 0.9 118 2 H70378 hypothetical prote
45 7 0.9 134 2 A59055 phospholipase A2 (

ALIGNMENTS

RESULT 1

T46449
hypothetical protein DKFPZ434H202.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46449
R;Ansoerge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23028
A;Accession: T46449
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-163 <AAA>
A;Cross-references: UNIPROT:Q93050; UNIPARC:UPI000016ACB4; EMBL:AL137683
A;Experimental source: adult testis; Clone DKFPZ434H202
C;Genetics:
A;Note: DKFPZ434H202.1
C;Superfamily: vacuolar ATP synthase 95K chain

Query Match 3.3%; Score 27; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 790 MEGLSAFLHALRLHWVEFQNKFSYGTG 816
DB / 119 MEGLSAFLHALRLHWVEFQNKFSYGTG 145
|||||

RESULT 2

A54163
vacuolar ATPase (EC 3.6.1.1-) 116k chain long form - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A54163
R;Peng, S.B.; Crider, B.P.; Xie, X.S.; Stone, D.K.
J. Biol. Chem. 269, 17262-17266, 1994
A;Title: Alternative mRNA splicing generates tissue-specific isoforms of 116-kDa polype
A;Reference number: A54163; MUID:94274722; PMID:8006034
A;Accession: A54163
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-838 <PEN>
A;Cross-references: UNIPROT:Q29466; UNIPARC:UPI0000138CEA; GB:L31770; NID:G469231; PTDN

Query Match 3.3%; Score 27; DB 2; Length 838;
Best Local Similarity 100.0%; Pred. No. 4.2e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 790 MEGLSAFLHALRLHWVEFQNKFSYGTG 816
|||||

Db 794 MBGLSAFLHALRLHWVFQNKFGTGTG 820

RESULT 3
B38656
vacuolar proton pump 116K chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 09-Jul-2004
C:Accession: B38656
R:Perin, M.S.; Fried, V.A.; Stone, D.K.; Xie, X.S.; Suedhof, T.C.
J. Biol. Chem. 266, 3877-3881, 1991
A:Title: Structure of the 116-kDa polypeptide of the clathrin-coated vesicle/synaptic vesicle
A:Reference number: A38656; MUID:91139686; PMID:1704894
A:Accession: B38656
A>Status: preliminary
A:Accession: T19492
A:Molecule type: mRNA
A:Residues: 1-838 <PER>
A:Cross-references: UNIPROT:P25286; UNIPARC:UPI0000138CED; GB:M58758; NID:G206429; PIDN:
C:Superfamily: vacuolar ATP synthase 95K chain
C:Keywords: alternative splicing; transmembrane protein

Query Match 2.9%; Score 24; DB 2; Length 838;
Best Local Similarity 100.0%; Pred. No. 4.3e-15; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0

QY 728 SNTASYLRWLWLSLAHAQLSEVLW 751
|||||
Db 734 SNTASYLRWLWLSLAHAQLSEVLW 757

RESULT 4
T16282
hypothetical protein F35H10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16282
R:Woesner, J.
Submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F35H10.
A:Reference number: Z18490
A:Accession: T16282
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-873 <WOE>
A:Cross-references: UNIPROT:Q20072; UNIPARC:UPI000008163D; EMBL:U40934; NID:G1072149; PI
C:Genetics:
A:Gene: CESP:F35H10.4
A:Introns: 39/3; 709/3; 785/1; 843/2
C:Superfamily: vacuolar ATP synthase 95K chain

Query Match 2.7%; Score 22; DB 2; Length 873;
Best Local Similarity 100.0%; Pred. No. 4.5e-13; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0

QY 730 TASYLRWLWLSLAHAQLSEVLW 751
|||||
Db 770 TASYLRWLWLSLAHAQLSEVLW 791

RESULT 5
T19492
hypothetical protein C26H9A.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19492
R:Smyle, R.
Submitted to the EMBL Data Library, September 1997
A:Reference number: Z19131
A:Accession: T19492
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1236 <WIL>
A:Cross-references: UNIPROT:Q9XTS8; UNIPARC:UPI000017B7C6; EMBL:Z99169; PIDN:CAB16306.1;

A:Experimental source: clone C26H9A
C:Genetics:
A:Gene: CESP:C26H9A.1
A:Map position: 4
A:Introns: 50/2; 107/2; 119/3; 151/1; 209/2; 327/3; 432/3; 451/3; 482/2; 524/3; 552/2;
Query Match 2.7%; Score 22; DB 2; Length 1236;
Best Local Similarity 100.0%; Pred. No. 6.1e-13; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0

QY 385 EVNPAPYTIITPPFLFAVMFGD 406
|||||
Db 700 EVNPAPYTIITPPFLFAVMFGD 721

RESULT 6
T46719
probable vacuolar ATPase (EC 3.6.1.-) proton pump chain 116K [imported] - Leishmania m.
C:Species: Leishmania major
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46719
R:Voickaert, G.; Ivens, A.C.; Lawson, D.; Quail, M.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, December 1999
A:Reference number: Z23137
A:Accession: T46719
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-775 <VOL>
A:Cross-references: UNIPROT:Q9UI50; UNIPARC:UPI000007C98D; EMBL:AL121861; PIDN:CAB58384
A:Experimental source: strain Friedlin
C:Genetics:
A:Note: L4326.08
C:Superfamily: vacuolar ATP synthase 95K chain
C:Keywords: hydrolase

Query Match 2.4%; Score 20; DB 2; Length 775;
Best Local Similarity 100.0%; Pred. No. 4.1e-11; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0

QY 724 LGCVSNTASYLRWLWLSLAH 743
|||||
Db 670 LGCVSNTASYLRWLWLSLAH 689

RESULT 7
T06068
Probable proton pump F19H22.180 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06068
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
Submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15184
A:Accession: T06068
A:Molecule type: DNA
A:Residues: 1-843 <BEV>
A:Cross-references: UNIPROT:Q9SVI5; UNIPARC:UPI00000AAT64; EMBL:AL035679; GSPDB:GN00062
A:Experimental source: cultivar Columbia; BAC clone F19H22
C:Genetics:
A:Gene: ATSP:F19H22.180
A:Map position: 4
A:Introns: 51/3; 66/3; 107/3; 143/3; 179/3; 237/3; 283/3; 319/3; 355/3; 405/2; 456/3; 5
C:Superfamily: vacuolar ATP synthase 95K chain

Query Match 2.4%; Score 20; DB 2; Length 843;
Best Local Similarity 100.0%; Pred. No. 4.4e-11; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0

QY 793 LSAPFLHALRLHWVFQNKFY 812
|||||
Db 804 LSAPFLHALRLHWVFQNKFY 823

RESULT 8

JH0287
immune regulatory protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
A;Accession: JH0287
R;Lee, C.K.; Ghoshal, K.; Beaman, K.D.
Mol Immunol. 27, 1137-1144, 1990
A;Title: Cloning of a cDNA for a T cell produced molecule with a putative immune regulator
A;Reference number: JH0287; MUID:91061805; PMID:2247090
A;Accession: JH0287
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-855 <LEE>
A;Cross-references: UNIPROT:P15920; UNIPARC:UPI0000161PAB; GB:X55184; NID:G52754; PIDN:C
C;Superfamily: vacuolar ATP synthase 95K chain

Query Match 2.4%; Score 20; DB 2; Length 855;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 728 SNTASYLRRLWALSIAHAQLS 747
|||||
DB 748 SNTASYLRRLWALSIAHAQLS 767

RESULT 9

S15795
vacuolar proton pump homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
A;Accession: S15795
R;Craxton, M.; Anscough, R.; Coulson, A.; Dear, S.; Du, Z.; Durbin, R.; Green, P.; Hall
Staden, R.; Sulston, J.; Thierry-Mieg, J.; Thomas, K.; Waterston, R.; Wilson, R.
submitted to the EMBL Data Library, May 1991
A;Reference number: S15786
A;Accession: S15795
A;Molecule type: DNA
A;Residues: 1-935 <CRA>
A;Cross-references: UNIPROT:P30628; UNIPARC:UPI0000175EED; EMBL:Z11115; NID:G6953; PID:G
C;Genetics:
A;Introns: 51/3; 110/3; 153/3; 194/2; 264/2; 682/3; 723/3; 770/3; 844/1; 901/2
C;Superfamily: vacuolar ATP synthase 95K chain
C;Keywords: transmembrane protein

Query Match 2.3%; Score 19; DB 2; Length 935;
Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 790 MEGLSAPFLHALRLHWVEFQ 808
|||||
DB 887 MEGLSAPFLHALRLHWVEFQ 905

RESULT 10

A42970
H+-exporting ATPase (EC 3.6.3.6) 95K chain, vacuolar - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O5430c; protein YOR270C
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A;Accession: A42970; S67167; S67172; S72041
R;Manolson, M.F.; Proteau, D.; Preston, R.A.; Stenbit, A.; Roberts, B.T.; Hoyt, M.A.; P
J. Biol. Chem. 267, 14294-14303, 1992
A;Title: The VPH1 gene encodes a 95-kDa integral membrane polypeptide required for in vi
A;Reference number: A42970; MUID:92332542; PMID:1385813
A;Accession: A42970
A;Molecule type: DNA
A;Residues: 1-840 <MAN>
A;Cross-references: UNIPROT:P32563; UNIPARC:UPI0000053075; GB:M89778; NID:G173172; PIDN:
A;Experimental source: strain X2180-1b; vacuolar acidification-defective mutants
A;Note: sequence extracted from NCBI backbone (NCBIN:108529, NCBI:P.108530)
R;Jauniaux, J.C.; Poirey, R.
submitted to the Protein Sequence Database, July 1996

A;Reference number: S67143
A;Accession: S67167
A;Molecule type: DNA
A;Residues: 1-840 <JAU>
A;Cross-references: UNIPARC:UPI0000053075; EMBL:Z75178; NID:G1420605; PIDN:CAA99494.1;
A;Experimental source: strain S288C
R;Cheret, G.; Sor, F.
submitted to the Protein Sequence Database, July 1996

A;Reference number: S67169
A;Accession: S67172
A;Molecule type: DNA
A;Residues: 1-840 <CHE>
A;Cross-references: UNIPARC:UPI0000053075; EMBL:Z75178; NID:G1420605; PIDN:CAA99494.1;
A;Experimental source: strain S288C
R;Cheret, G.; Bernardi, A.; Sor, F.
Yeast 12, 1059-1064, 1996

A;Title: DNA sequence analysis of the VPH1-SNF2 region on chromosome XV of Saccharomyces
A;Reference number: S72039; MUID:97051594; PMID:8896271
A;Accession: S72041
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-840 <CHW>
A;Cross-references: UNIPARC:UPI0000053075; EMBL:X89633; NID:G1279694; PIDN:CAA61776.1;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995

C;Genetics:
A;Gene: SGD:VPH1; MIPS:YOR270C
A;Cross-references: MIPS:YOR270C; SGD:S0005796
A;Map position: 15R
C;Function:
A;Description: hydrogen ion transport; hydrolase; required for assembly and activity of
C;Superfamily: vacuolar ATP synthase 95K chain
C;Keywords: ATP; glycoprotein; hydrogen ion transport; hydrolase; membrane-associated
F;407-441/Domain: transmembrane #status predicted <TM1>
F;457-478/Domain: transmembrane #status predicted <TM2>
F;539-558/Domain: transmembrane #status predicted <TM3>
F;565-591/Domain: transmembrane #status predicted <TM4>
F;635-656/Domain: transmembrane #status predicted <TM5>
F;733-795/Domain: transmembrane #status predicted <TM6>

Query Match 2.2%; Score 18; DB 1; Length 840;
Best Local Similarity 100.0%; Pred. No. 4.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 TASYLRRLWALSIAHAQLS 747
|||||
DB 730 TASYLRRLWALSIAHAQLS 747

RESULT 11

T18565
probable H+-exporting ATPase (EC 3.6.3.6) vacuolar [similarity] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A;Accession: T18565; T19177
R;Mortimore, B.
submitted to the EMBL Data Library, December 1998
A;Reference number: Z18977
A;Accession: T18565
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-865 <WIL>
A;Cross-references: UNIPROT:Q17660; UNIPARC:UPI000007E97E; EMBL:AL031269; PIDN:CAA20334
A;Experimental source: clone VW02B12L
R;Coles, L.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z19084
A;Accession: T19177
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-865 <WI2>
A;Cross-references: UNIPARC:UPI000007E97E; EMBL:Z50872; PIDN:CAA90758.1; GSPDB:GN000020;
A;Experimental source: clone C05D12
C;Genetics:

A:Gene: CESP:VW02B12L.1
 A:Map position: 2
 A:Introns: 66/1; 181/2; 576/2; 648/3; 775/1
 C:Superfamily: vacuolar ATP synthase 95K chain
 C:Keywords: hydrolase

Query Match 2.2%; Score 18; DB 2; Length 865;
 Best Local Similarity 100.0%; Pred. No. 4.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 TASYLRLWALSLSHAQLS 747
 DB 760 TASYLRLWALSLSHAQLS 777

RESULT 12

S54554 H+-exporting ATPase (EC 3.6.3.6) chain STV1 - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YM9796.07; protein YMR054W
 C:Species: Saccharomyces cerevisiae
 C:Date: 08-Jul-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004

C:Accession: S54554; A54081
 R:Devlin, K.; Churcher, C.M.

submitted to the EMBL Data Library, May 1995

A:Reference number: S54548

A:Accession: S54554

A:Molecule type: DNA

A:Residues: 1-890 <DEV>

A:Cross-references: UNIPROT:P37296; UNIPARC:UPI000013615B; EMBL:Z49703; NID:G817880; PID:R:Manolson, M.F.; Wu, B.; Proteau, D.; Tallon, L.A.; Roberts, B.T.; Hoyt, M.A.; Jones, J. Biol. Chem. 269, 14064-14074, 1994

A:Title: STV1 gene encodes functional homologue of 95-kDa yeast vacuolar H(+)-ATPase subunit
 A:Reference number: A54081; MUID:94245725; PMID:7514599

A:Accession: A54081

A:Molecule type: DNA

A:Residues: 1-804; 'E', 806-890 <MAN>

A:Cross-references: UNIPARC:UPI00001689CE; GB:U06465; NID:G460159; PID:AAA20596.1; PID: C:Genetics:

A:Gene: SGD:STV1

A:Cross-references: SGD:S0004658; MIPS:YMR054W

A:Map position: 138

C:Function:

A:Description: hydrogen ion transport; hydrolase

C:Superfamily: vacuolar ATP synthase 95K chain

C:Keywords: ATP; hydrogen ion transport; hydrolase; transmembrane protein; yeast vacuole

F:451-487/Domain: transmembrane #status predicted <TM1>

F:509-525/Domain: transmembrane #status predicted <TM2>

F:585-600/Domain: transmembrane #status predicted <TM3>

F:614-637/Domain: transmembrane #status predicted <TM4>

F:681-696/Domain: transmembrane #status predicted <TM5>

F:833-851/Domain: transmembrane #status predicted <TM6>

Query Match 2.2%; Score 18; DB 2; Length 890;
 Best Local Similarity 100.0%; Pred. No. 4.7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 730 TASYLRLWALSLSHAQLS 747
 DB 790 TASYLRLWALSLSHAQLS 807

RESULT 13

H84685

probable vacuolar proton-ATPase subunit [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: H84685

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84685
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-780 <STO>

C:Cross-references: UNIPROT:Q9SK06; UNIPARC:UPI00000A9CB0; GB:AE002093; NID:G6598613;

C:Genetics:

A:Gene: At2g28520

A:Map position: 2

C:Superfamily: vacuolar ATP synthase 95K chain

Query Match 2.1%; Score 17; DB 2; Length 780;
 Best Local Similarity 100.0%; Pred. No. 4.2e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 VSNTASYLRLWALSLSAH 743
 DB 685 VSNTASYLRLWALSLSAH 701

RESULT 14

H84600

probable vacuolar proton-ATPase subunit [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: H84600

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84600

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-821 <STO>

A:Cross-references: UNIPROT:Q9SUT7; UNIPARC:UPI00000A1530; GB:AE002093; NID:G4567273;

C:Genetics:

A:Gene: At2g21410

A:Map position: 2

C:Superfamily: vacuolar ATP synthase 95K chain

Query Match 2.1%; Score 17; DB 2; Length 821;
 Best Local Similarity 100.0%; Pred. No. 4.4e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 VSNTASYLRLWALSLSAH 743
 DB 721 VSNTASYLRLWALSLSAH 737

RESULT 15

T37787

probable vacuolar atpase subunit - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T37787

R:Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, September 1995

A:Reference number: Z21746

A:Accession: T37787

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-805 <OLI>

A:Cross-references: UNIPROT:O13742; UNIPARC:UPI0000138CD1; EMBL:Z98529; PIDN:CAB11035

A:Experimental source: strain 972h-; cosmid c16E8

C:Genetics:

A:Gene: SPAC16E8.07c

A:Map position: 1

A:Introns: 14/3

C:Superfamily: vacuolar ATP synthase 95K chain

Query Match 1.7%; Score 14; DB 2; Length 805;
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 730 TASYRLWALSLAH 743

Db 708 TASYRLWALSLAH 721

Search completed: June 29, 2006, 13:22:56
Job time : 48 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2006, 13:13:44 ; Search time 308 Seconds
(without alignments)
2468.710 Million cell updates/sec

Title: US-10-783-519-2

Perfect score: 822

Sequence: 1 MGSFSESEVALQLFLPTA.....HWVEFQNKFSYGTGYKLSPF 822

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	601	73.1	830	1 VPP3_HUMAN	Q13488 h vacuolar
2	545	66.3	830	2 Q8WC55_HUMAN	Q8WC55 homo sapien
3	153	18.6	218	2 Q64F87_HUMAN	Q64F87 homo sapien
4	60	7.3	60	2 Q6QBN6_HUMAN	Q6QBN6 homo sapien
5	58	7.1	125	2 Q6QBN8_HUMAN	Q6QBN8 homo sapien
6	46	5.6	61	2 Q8TCH1_HUMAN	Q8TCH1 homo sapien
7	40	4.9	430	2 Q9CTA9_MOUSE	Q9CTA9 mus musculus
8	40	4.9	834	2 Q9JHF5_MOUSE	Q9JHF5 mus musculus
9	40	4.9	834	2 Q9JL12_MOUSE	Q9JL12 mus musculus
10	40	4.9	834	2 Q9LW06_MOUSE	Q9LW06 mus musculus
11	40	4.9	834	2 Q216B0_RAT	Q216B0 rattus norv
12	38	4.6	420	2 Q6P735_RAT	Q6P735 rattus norv
13	35	4.3	45	2 Q6QBN7_HUMAN	Q6QBN7 homo sapien
14	34	4.1	822	2 Q7ZVM7_BRAKE	Q7ZVM7 brachydanio
15	32	3.9	846	2 Q6PA83_XENLA	Q6PA83 xenopus lae
16	30	3.6	833	1 VPP4_MOUSE	Q920T6 mus musculus
17	30	3.6	837	2 Q918C8_CHICK	Q918C8 gallus gall
18	29	3.5	838	2 Q4RSZ3_TETNG	Q4RSZ3 tetraodon n
19	29	3.5	839	2 Q7TLN9_TORMA	Q7TLN9 torpedo mar
20	29	3.5	840	2 Q7TLN8_TORMA	Q7TLN8 torpedo mar
21	29	3.5	897	2 Q4SJ89_TETNG	Q4SJ89 tetraodon n
22	27	3.3	831	2 Q53ET5_HUMAN	Q53ET5 homo sapien
23	27	3.3	831	2 Q53X12_HUMAN	Q53X12 homo sapien
24	27	3.3	834	2 Q6NY92_BRAKE	Q6NY92 brachydanio
25	27	3.3	837	1 VPP1_HUMAN	Q93050 h vacuolar
26	27	3.3	837	1 VPP1_PONPY	Q5r422 pongo pygma
27	27	3.3	837	2 Q5R5X1_PONPY	Q5r5x1 pongo pygma
28	27	3.3	837	2 Q5R6N4_PONPY	Q5r6n4 pongo pygma
29	27	3.3	838	1 VPP1_BOVIN	Q29466 h vacuolar
30	27	3.3	838	2 Q5CZB6_HUMAN	Q5CZB6 homo sapien
31	26	3.2	95	2 Q6QBN5_HUMAN	Q6QBN5 homo sapien

32	26	3.2	852	2	Q4DY50_TRYCR	Q4dy50 trypanosoma
33	26	3.2	854	1	VPP2_BOVIN	Q37681 bos taurus
34	25	3.0	169	2	Q9JL11_MOUSE	Q9jll1 mus musculus
35	25	3.0	823	2	Q5CZ26_XENTR	Q5czz6 xenopus tro
36	25	3.0	827	2	Q4RZB2_TETNG	Q4rzb2 tetraodon n
37	25	3.0	835	2	Q4S964_TETNG	Q4s964 tetraodon n
38	24	2.9	113	2	Q4RBL1_TETNG	Q4rbl1 tetraodon n
39	24	2.9	161	2	Q5DI34_SCHJA	Q5di34 schistosoma
40	24	2.9	236	2	Q5C2K8_SCHJA	Q5c2k8 schistosoma
41	24	2.9	483	2	Q6AHY6_HUMAN	Q6ahy6 homo sapien
42	24	2.9	513	2	Q96N91_HUMAN	Q96n91 homo sapien
43	24	2.9	779	2	Q3TV98_MOUSE	Q3ty98 mus musculus
44	24	2.9	831	2	Q8AVM5_XENLA	Q8avm5 xenopus lae
45	24	2.9	832	2	Q3TXT5_MOUSE	Q3txt5 mus musculus

ALIGNMENTS

RESULT 1
VPP3_HUMAN
ID VPP3_HUMAN STANDARD; PRS; 830 AA.
AC Q13488; O75877;
DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2000, sequence version 2.
DT 07-FEB-2006, entry version 49.
DE Vacuolar proton translocating ATPase 116 kDa subunit a isoform 3 (V-ATPase 116-kDa isoform a3) (Osteoclastic proton pump 116 kDa subunit) (OC-116 kDa) (OC116) (T-cell immune regulator 1) (T cell immune response cDNA7 protein) (TIRC7)
GN Name=TCIRG1; Synonyms=ATP6N1C, ATP6V0A3;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RC TISSUE=Osteoclastoma;
RX MEDLINE=96158968; PubMed=8579597; DOI=10.1006/bbrc.1996.0145;
RA Li Y.-P., Chen W., Stashenko P.;
RT "Molecular cloning and characterization of a putative novel human osteoclast-specific 116-kDa vacuolar proton pump subunit.";
RL Biochem. Biophys. Res. Commun. 218:813-821(1996).
[2]
RN NUCLEOTIDE SEQUENCE (ISOFORM SHORT).
RA Utku N., Heinemann T., Bulwin C.-G., Beinke S., Beato F., Randall J., Busconi L., Delphire E., Robertson E.R., Kojima R., Volk H.D., Milford E.L., Gullans S.R.;
RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE (ISOFORM SHORT).
RX MEDLINE=99263502; PubMed=10329006; DOI=10.1006/geno.1999.5751;
RA Heinemann T., Bulwin G.C., Randall J., Schnieders B., Sandhoff K., Volk H.D., Milford E., Gullans S.R., Utku N.;
RT "Genomic organization of the gene coding for TIRC7, a novel membrane protein essential for T cell activation.";
RL Genomics 57:398-406(1999).
[4]
RN VARIANTS OPTB1 ARG-405 AND LEU-444.
RX PubMed=11532986; DOI=10.1093/hmg/10.17.1767;
RA Sobacchi C., Frattini A., Orchard P., Porras O., Texcan I., Andolina M., Babul-Hirji R., Baric I., Canham N., Chitayat D., Dupuis-Girod S., Ellis I., Etzioni A., Faeth A., Fisher A., Gerritsen B., Gulino V., Horwitz E., Klamroth V., Lanino E., Mirolo M., Musio A., Matthijs G., Nonomaya S., Notarangelo L.D., Ochs H.D., Superti Furga A., Valiaho J., van Hove J.L.K., Vihinen M., Vujic D., Vezzoni P., Villa A.;
RT "The mutational spectrum of human malignant autosomal recessive osteopetrosis.";
RL Hum. Mol. Genet. 10:1767-1773(2001).
[5]
RN VARIANT OPTB1 ARG-405.

RX PubMed=12552563; DOI=10.1002/humu.10165;
RA Scineca J.-C., Quincey D., Perrinello H., Romatet D., Grosgeorge J.,
RA Gaudray P., Philip N., Fischer A., Carle G.F.;
RT "Novel mutations in the TCIRG1 gene encoding the a3 subunit of the
RT vacuolar proton pump in patients affected by infantile malignant
RT osteopetrosis";
RL Hum. Mutat. 21:151-157(2003).
RN [6].
RP VARIANTS OPTB1 PRO-141; ARG-405; ASN-462 DEL; ASN-517 AND ARG-775.
RX PubMed=15300850; DOI=10.1002/humu.20076;
RA Susani L., Pangrazio A., Sobacchi C., Taranta A., Mortier G.,
RA Savarirayan R., Villa A., Orchard F., Vezzoni P., Albertini A.,
RA Frattini A., Pagani F.;
RT "TCIRG1-dependent recessive osteopetrosis: mutation analysis,
RT functional identification of the splicing defects, and in vitro rescue
RT by U1 snRNA";
RL Hum. Mutat. 24:225-235(2004).
CC -I- FUNCTION: Part of the proton channel of V-ATPases (By similarity).
CC Seems to be directly involved in T cell activation.
CC -I- SUBUNIT: The V-ATPase is an heteromultimeric enzyme composed of at
CC least thirteen different subunits. It has a membrane peripheral V1
CC sector for ATP hydrolysis and an integral V0 for proton
CC translocation. The V1 sector comprises subunits A-H, whereas V0
CC includes subunits a, d, c, c', and c''.
CC -I- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
CC similarity).
CC -I- ALTERNATIVE PRODUCTS:
CC Event=alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q13488-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q13488-2; Sequence=VSP_000345;
CC Notes=No experimental confirmation available;
CC -I- TISSUE SPECIFICITY: The long isoform is highly expressed in
CC osteoclasts. The short isoform is highly expressed in thymus.
CC -I- DISEASE: Defects in TCIRG1 are a cause of autosomal recessive
CC osteopetrosis (OPTB1) [MIM:259700]; also called autosomal
CC recessive Albers-Schonberg disease. Osteopetrosis is a rare
CC genetic disease characterized by abnormally dense bone, due to
CC defective resorption of immature bone. The defect is an
CC heterogeneous disorder of bone metabolism, which, if untreated, has
CC a fatal outcome. It occurs in two forms: a severe autosomal
CC recessive form, occurring in utero, infancy, or childhood, and a
CC benign autosomal dominant form, occurring in adolescence or
CC adulthood. However, mild and atypical forms have also been
CC reported. It is not known whether these latter cases represent
CC separate nosological entities or a mild form of the recessive
CC conditions. However, given the large number of genes and gene
CC mutations associated with this condition a large spectrum of
CC clinical manifestation is expected as seen in animal studies. The
CC features of OPTB1 are macrocephaly, progressive deafness and
CC blindness, hepatosplenomegaly, and severe anemia beginning in
CC early infancy or in fetal life. Deafness and blindness are
CC generally thought to represent effects of pressure on nerves.
CC -I- SIMILARITY: Belongs to the V-ATPase 116 kDa subunit family.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; U45285; AAA97878.1; -; mRNA.
CC EMBL; AF025374; AAC35742.1; -; mRNA.
CC EMBL; AF033033; AAD31081.2; -; Genomic DNA.
CC Ensembl; ENSG00000110719; Homo sapiens.
CC H-InvDB; HIX0009874; -;
CC HGNC; HGNC:11647; TCIRG1.
CC MIM; 259700; phenotype.
CC MIM; 604592; Gene.
CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.
CC DR GO; GO:0005886; C:plasma membrane; TAS.
CC DR GO; GO:0005215; P:transporter activity; TAS.
CC DR GO; GO:0006968; P:cellular defense response; TAS.
CC DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
CC DR GO; GO:0015992; P:proton transport; TAS.

DR InterPro: IPR002490; V_ATPase_sub116.
DR PANTHER: PTHR11629; V_ATPase_sub116; 1.
DR Pfam; PF01496; V_ATPase_1; 1.
KW Alternative splicing; Disease mutation; Glycoprotein;
KW Hydrogen ion transport; Ion transport; Membrane; Transmembrane;
KW Transport.
FT CHAIN 1 830 Vacuolar proton translocating ATPase 116
FT kDa subunit a isoform 3.
FT /FTID=PRO_0000119218.
FT Extracellular (Potential).
FT TOPO_DOM 1 397
FT TRANSMEM 398 418
FT TRANSMEM 445 465
FT TRANSMEM 504 524
FT TRANSMEM 538 558
FT TRANSMEM 576 596
FT TRANSMEM 636 656
FT TRANSMEM 771 791
FT CARBOHYD 41 41
FT CARBOHYD 483 483
FT CARBOHYD 503 503
FT VARSPLIC 1 216
FT Missing (in isoform Short).
FT /FTID=VSP_000345.
FT A -> P (in OPTB1).
FT VARIANT 141 141
FT /FTID=VAR_020988.
FT G -> R (in OPTB1).
FT VARIANT 405 405
FT /FTID=VAR_019569.
FT R -> L (in OPTB1).
FT VARIANT 444 444
FT /FTID=VAR_019570.
FT Missing (in OPTB1).
FT VARIANT 462 462
FT /FTID=VAR_020989.
FT D -> N (in OPTB1).
FT VARIANT 517 517
FT /FTID=VAR_020990.
FT P -> R (in OPTB1).
FT VARIANT 775 775
FT A -> R (in Ref. 1).
FT CONFLICT 377 377
FT CONFLICT 603 603
FT Missing (in Ref. 1).
SQ SEQUENCE 830 AA; 92998 MW; 62EAC5A9A22DC698B CRC64;

Query Match 73.1%; Score 601; DB 1; Length 830;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 821; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MGSMFSEVALVQLFLPTAAAYTCVSLGELGLVEFRDLNASVAFQRRFVVDVWRCEE 60
Db 1 MGSMFSEVALVQLFLPTAAAYTCVSLGELGLVEFRDLNASVAFQRRFVVDVWRCEE 60

QY 61 LEKTTFTLQEEVRRAGLVLPPLPKGRLPAPPRDLRLIQEETERLAQELRDVRGNQALRA 120
Db 61 LEKTTFTLQEEVRRAGLVLPPLPKGRLPAPPRDLRLIQEETERLAQELRDVRGNQALRA 120

QY 121 QLHQQLHAANVLROGHEPOLAAAHDTGASERTPLLOAGPGPHQDLRVNPFVAGAVEPHKAP 180
Db 121 QLHQQLHAANVLROGHEPOLAAAHDTGASERTPLLOAGPGPHQDLRVNPFVAGAVEPHKAP 180

QY 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEOIGQKIRKTTDCPH 240
Db 181 ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEOIGQKIRKTTDCPH 240

QY 241 CHVFPFLQEEARLQALQOQQSQELQEVLTETERFLSQVLGRVLQQLPPQGVQVHKMK 300
Db 241 CHVFPFLQEEARLQALQOQQSQELQEVLTETERFLSQVLGRVLQQLPPQGVQVHKMK 300

QY 301 AVYLALNOCVSSTTHKCLIAEAWCSVRDLPALQELALRSSMBEGVSVAHRIIPCDMPPT 360
Db 301 AVYLALNOCVSSTTHKCLIAEAWCSVRDLPALQELALRSSMBEGVSVAHRIIPCDMPPT 360

QY 361 LIIRNRTASFOGIVDRYGVGRYQVBNPAPYTIITFPFLFAVMFGDVHGLLMFLFALAM 420
Db 361 LIIRNRTASFOGIVDAVGVEYQVBNPAPYTIITFPFLFAVMFGDVHGLLMFLFALAM 420

QY 421 VLAENRPAVKAQNEINQWTFPRGRYLLLMGLMGLFSYTGFIYNECFSRATSIFFPSGWSVA 480
Db 421 VLAENRPAVKAQNEINQWTFPRGRYLLLMGLMGLFSYTGFIYNECFSRATSIFFPSGWSVA 480


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Q64F87 HUMAN
ID Q64F87_HUMAN PRELIMINARY; PRT; 218 AA.
AC Q64F87
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE T-cell immune regulator 1 transcript variant 4 (Fragment).
GN Name=TCIRG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Galbladder;
RX PubMed=15809087; DOI=10.1016/j.bbrc.2005.03.065;
RA Smirnova A.S., Morgun A., Shulzhenko N., Silva I.D.,
RA Gerbase-Delima M.;
RT "Identification of new alternative splice events in the TCIRG1 gene in
different human tissues";
RL Biochem. Biophys. Res. Commun. 330:943-949(2005).
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CC -----
DR EMBL; AY708388; AAU20795.1; -; mRNA.
DR Ensembl; ENSG00000110719; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR002490; V_ATPase_sub116.
DR PANTHER; PTHR11629; V_ATPase_sub116.
DR Pfam; PF01496; V_ATPase_I; 1.
DR NON_TER 218
SQ SEQUENCE 218 AA; 24383 MW; 55F80AB2B2A79DBD CRC64;

Query Match 18.6%; Score 153; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-147;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 RCELEKFTTFLQEEVRRAGLVLPKGLPAPPDRDLRIQETTERLAQELRDVRGNQ 116
DB 57 RCELEKFTTFLQEEVRRAGLVLPKGLPAPPDRDLRIQETTERLAQELRDVRGNQ 116

QY 117 ALRAQLHQLHAALVLRQHEPQLAAHTDGSERTELLQAPGGPHQDLRVNFVAGAVEP 176
DB 117 ALRAQLHQLHAALVLRQHEPQLAAHTDGSERTELLQAPGGPHQDLRVNFVAGAVEP 176

QY 177 HKAPALERLLWRACRGFLIASFRELEQPLEHPV 209
DB 177 HKAPALERLLWRACRGFLIASFRELEQPLEHPV 209

RESULT 4
Q6QBN6 HUMAN
ID Q6QBN6_HUMAN PRELIMINARY; PRT; 60 AA.
AC Q6QBN6
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE T-cell immune regulator 1 transcript variant 6 (Fragment).
GN Name=TCIRG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Tonsil;
RX PubMed=15809087; DOI=10.1016/j.bbrc.2005.03.065;
RA Smirnova A.S., Morgun A., Shulzhenko N., Silva I.D.,
RA Gerbase-Delima M.;
RT "Identification of new alternative splice events in the TCIRG1 gene in
different human tissues";
RL Biochem. Biophys. Res. Commun. 330:943-949(2005).
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CC -----
DR EMBL; AY548967; AAS59834.1; -; mRNA.
DR Ensembl; ENSG00000110719; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR002490; V_ATPase_sub116.
DR PANTHER; PTHR11629; V_ATPase_sub116.
DR Pfam; PF01496; V_ATPase_I; 1.
DR NON_TER 125
SQ SEQUENCE 125 AA; 14272 MW; C7AA604E66F54444 CRC64;

Query Match 7.1%; Score 58; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.7e-50;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 RCELEKFTTFLQEEVRRAGLVLPKGLPAPPDRDLRIQETTERLAQELRDVRGN 114
DB 57 RCELEKFTTFLQEEVRRAGLVLPKGLPAPPDRDLRIQETTERLAQELRDVRGN 114

RESULT 6
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RT "Identification of new alternative splice events in the TCIRG1 gene in
different human tissues";
RL Biochem. Biophys. Res. Commun. 330:943-949(2005).
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DR EMBL; AY548969; AAS59836.1; -; mRNA.
DR Ensembl; ENSG00000110719; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR002490; V_ATPase_sub116.
DR PANTHER; PTHR11629; V_ATPase_sub116.
DR Pfam; PF01496; V_ATPase_I; 1.
DR NON_TER 1
SQ SEQUENCE 60 AA; 6545 MW; 5009E0C221BD4E96 CRC64;

Query Match 7.3%; Score 60; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.8e-52;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 459 FYINECFSRATSIIPSGWSVAAMANQSGWSDAFLAQHTMLTLDPNVTGVFLGPPGIDP 518
DB 1 FYINECFSRATSIIPSGWSVAAMANQSGWSDAFLAQHTMLTLDPNVTGVFLGPPGIDP 60

RESULT 5
Q6QBN8 HUMAN
ID Q6QBN8_HUMAN PRELIMINARY; PRT; 125 AA.
AC Q6QBN8
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE T-cell immune regulator 1 transcript variant 4 (Fragment).
GN Name=TCIRG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Tonsil;
RX PubMed=15809087; DOI=10.1016/j.bbrc.2005.03.065;
RA Smirnova A.S., Morgun A., Shulzhenko N., Silva I.D.,
RA Gerbase-Delima M.;
RT "Identification of new alternative splice events in the TCIRG1 gene in
different human tissues";
RL Biochem. Biophys. Res. Commun. 330:943-949(2005).
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CC -----
DR EMBL; AY548967; AAS59834.1; -; mRNA.
DR Ensembl; ENSG00000110719; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR002490; V_ATPase_sub116.
DR PANTHER; PTHR11629; V_ATPase_sub116.
DR Pfam; PF01496; V_ATPase_I; 1.
DR NON_TER 125
SQ SEQUENCE 125 AA; 14272 MW; C7AA604E66F54444 CRC64;

Query Match 7.1%; Score 58; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.7e-50;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 RCELEKFTTFLQEEVRRAGLVLPKGLPAPPDRDLRIQETTERLAQELRDVRGN 114
DB 57 RCELEKFTTFLQEEVRRAGLVLPKGLPAPPDRDLRIQETTERLAQELRDVRGN 114
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Q8TCH1_HUMAN
ID Q8TCH1_HUMAN PRELIMINARY; PRT; 61 AA.
AC Q8TCH1;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE T-cell immune regulator 1 transcript variant 3 (Fragment).
GN Name=TCIRG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC NCBI_TaxID=9606;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Uterine cervix;
RC PubMed=15809087; DOI=10.1016/j.bbrc.2005.03.065;
RX Smirnova A.S., Morgun A., Shulzhenko N., Silva I.D.,
RA Gerbase-DeLima M.;
RT "Identification of new alternative splice events in the TCIRG1 gene in
RT different human tissues";
RL Biochem. Biophys. Res. Commun. 330:943-949 (2005).
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CC -----
CC EMBL; AF497545; AAM18704.1; ; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR002490; V_ATPase_sub116.
DR PANTHER; PTHR11629; V_ATPase_sub116; 1.
DR Pfam; PF01496; V_ATPase_1; 1.
FT NON_TER 1
SQ SEQUENCE 61 AA; 6805 MW; B5F91060BFB3D01 CRC64;

Query Match 5.6%; Score 46; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 4.2e-38;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 699 DDEEAEELVPSEVLHQAIHTIEFCLGCVSNTASYLRWLWLSLAHA 744
DB 1 DDEEAEELVPSEVLHQAIHTIEFCLGCVSNTASYLRWLWLSLAHA 46

RESULT 7
Q9CTA9_MOUSE
ID Q9CTA9_MOUSE PRELIMINARY; PRT; 490 AA.
AC Q9CTA9;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE 18-day embryo whole body cDNA. RIKEN full-length enriched library.
DE clone:1110034K16 product:ATPASE, H+ TRANSPORTING, LYSOSOMAL 1, full
DE insert sequence. (Fragment).
GN Name=rcirg1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
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RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
Bajic V.B., Brenner S.E., Batalov S., Forrest A.E., Zavolan M.,
Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kummerfeld S.K.,
Kutano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
Nilsen R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
Schombach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
Tamajima K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki K., Akashira N.,
Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimomiya N.,
Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563 (2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome";
RL Science 309:1564-1566 (2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
Kanal A., Kawaji H., Kawasawa Y., Redierski R.M., King B.U.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maggioni D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou C.A., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wellie C.,
RA Wilning L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RT Nature 420:563-573 (2002)."
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saio R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690 (2001)."
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000)."
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RT Genome Res. 10:1757-1771 (2000)."
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saio R., Saio R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBSJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AK004094; BAB231166.1; -; mRNA.
DR Ensembl; ENSMUSG0000001750; Mus musculus.
DR MGI; MGI:1350931; Tcirlg.
DR GO; GO:0016021; C: integral to membrane; RCA.
DR GO; GO:0005886; C: plasma membrane; IDA.
DR GO; GO:0008553; F: hydrogen-exporting ATPase activity, phospho. .; RCA.
DR GO; GO:0006818; P: hydrogen transport; RCA.
DR InterPro; IPR002490; V_ATPase_sub116.
DR PANTHER; PTHR11629; V_ATPase_sub116; 1.
DR Pfam; PF01496; V_ATPase_1; 1.
FT NON_TER 1
SQ SEQUENCE 490 AA; 54595 MW; 896B7F036A47542A CRC64;
Query Match 4.9%; Score 40; DB 2; Length 490;
Best Local Similarity 100.0%; Pred. No. 3.7e-31; Mismatches 0; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 783 TVALLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPP 822
DB 444 TVALLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPP 483
RESULT 8
QJHFS_MOUSE
ID QJHFS_MOUSE PRELIMINARY; PRT; 834 AA.
AC QJHFS_MOUSE
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE A3 subunit of vacuolar-adenosine triphosphatase (Osteoclast-specific
DE 116-kDa V-ATPase subunit).
GN Name=Tcirlg; Synonym=Oc116;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20187595; PubMed=10722719; DOI=10.1074/jbc.275.12.8760;
RA Toyomura T., Oka T., Yamaguchi C., Wada Y., Futai M.;
RT "Three subunit a isoforms of mouse vacuolar H+-ATPase. Preferential
RT expression of the a3 isoform during osteoclast differentiation.";
RL J. Biol. Chem. 275:8760-8765 (2000)."
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Sv;
RX MEDLINE=20173225; PubMed=10709991; DOI=10.1016/S8756-3282(99)00278-1;
RA Scimeca J.-C., Franchi A., Trojani C., Parrinello H., Grosgeorge J.,
RA Robert C., Jallion O., Poirier C., Gaudray P., Carle G.F.;
RT "The gene encoding the mouse homologue of the human osteoclast-
RT specific 116-kDa V-ATPase subunit bears a deletion in osteoclastotic
RT (oc/oc) mutants.";
RL Bone 26:207-213 (2000)."
RN [3]
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CC -----
CC EMBL; AB022322; BAA93006.1; -; mRNA.
DR EMBL; AF188702; AAF37193.1; -; Genomic DNA.
DR Ensembl; ENSMUSG0000001750; Mus musculus.
DR MGI; MGI:1350931; Tcirlg.
DR GO; GO:0016021; C: integral to membrane; RCA.
DR GO; GO:0005886; C: plasma membrane; IDA.
DR GO; GO:0008553; F: hydrogen-exporting ATPase activity, phospho. .; RCA.
DR GO; GO:0006818; P: hydrogen transport; RCA.
DR InterPro; IPR002490; V_ATPase_sub116.

DR PANTHER: PTHR11629; V_ATPase_sub116; 1.
DR Pfam: PF01496; V_ATPase_I; 1.
SQ SEQUENCE 834 AA; 93460 MW; E95ECD70C26367C0 CRC64;

Query Match 4.9%; Score 40; DB 2; Length 834;
Best Local Similarity 100.0%; Pred. No. 5.8e-31;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 783 TVALLVMEGLSFLHALRLHWVEFQNKFGYSGTGKLSPPF 822
DB 788 TVALLVMEGLSFLHALRLHWVEFQNKFGYSGTGKLSPPF 827

RESULT 9

Q9JL12_MOUSE
ID Q9JL12_MOUSE PRELIMINARY; PRT; 834 AA.
AC Q9JL12;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Vacuolar proton-translocating ATPase 100 kDa subunit isoform a3.
GN Name=rcirg1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RG NIH MGC Project;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RG NIH MGC Project;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.

[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RG NIH MGC Project;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.

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CC EMBL; AF218253; AAP5922.1; -; mRNA.
CC Ensembl; ENSMUSG0000001750; Mus musculus.
CC MGI; MGI:1350931; Tcirlg1.
CC GO; GO:0016021; C:integral to membrane; RCA.
CC GO; GO:0005886; C:plasma membrane; IDA.
CC GO; GO:000553; P:hydrogen-exporting ATPase activity, phospho. .; RCA.
CC InterPro; IPR002490; V_ATPase_sub116.
CC PANTHER; PTHR11629; V_ATPase_I; 1.
CC Pfam; PF01496; V_ATPase_I; 1.
SQ SEQUENCE 834 AA; 93506 MW; EB8E42B45163004F CRC64;

Query Match 4.9%; Score 40; DB 2; Length 834;
Best Local Similarity 100.0%; Pred. No. 5.8e-31;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 783 TVALLVMEGLSFLHALRLHWVEFQNKFGYSGTGKLSPPF 822
DB 788 TVALLVMEGLSFLHALRLHWVEFQNKFGYSGTGKLSPPF 827

RESULT 10

Q9JW06_MOUSE
ID Q9JW06_MOUSE PRELIMINARY; PRT; 834 AA.
AC Q9JW06;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-MAR-2006, entry version 20.
DE T-cell, immune regulator 1.
GN Name=rcirg1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N, and NMRI; TISSUE=Mammary tumor. C3, and Mammary tumor.
RC WAP-Tag model. 5 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RG NIH MGC Project;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RG NIH MGC Project;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.

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CC EMBL; BC006761; AA06761.1; -; mRNA.
CC EMBL; BC085234; AA085234.1; -; mRNA.
CC Ensembl; ENSMUSG0000001750; Mus musculus.
CC MGI; MGI:1350931; Tcirlg1.
CC GO; GO:0016021; C:integral to membrane; RCA.
CC GO; GO:0005886; C:plasma membrane; IDA.
CC GO; GO:000553; P:hydrogen-exporting ATPase activity, phospho. .; RCA.
CC GO; GO:0005818; P:hydrogen transport; RCA.
CC InterPro; IPR002490; V_ATPase_sub116.
CC PANTHER; PTHR11629; V_ATPase_I; 1.
CC Pfam; PF01496; V_ATPase_I; 1.
SQ SEQUENCE 834 AA; 93448 MW; 87D2C37911EBF172 CRC64;

Query Match 4.9%; Score 40; DB 2; Length 834;
Best Local Similarity 100.0%; Pred. No. 5.8e-31;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 783 TVALLVMEGLSFLHALRLHWVEFQNKFGYSGTGKLSPPF 822
DB 788 TVALLVMEGLSFLHALRLHWVEFQNKFGYSGTGKLSPPF 827

RESULT 11

Q2I6B0_RAT
ID Q2I6B0_RAT PRELIMINARY; PRT; 834 AA.
AC Q2I6B0;
DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, sequence version 1.
DT 07-MAR-2006, entry version 1.
DE V-H-ATPase subunit a3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Kiscar;
RA Guyon S., Amar M., Fossier P., Morel N.;
RT "Neurons coexpress three different v-ATPase subunit a isoforms.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; DQ286426; ABB91445.1; -; mRNA.
SQ SEQUENCE 834 AA; 93168 MW; 2E0DCFF9EED3979B CRC64;

Query Match 4.9%; Score 40; DB 2; Length 834;
Best Local Similarity 100.0%; Pred. No. 5.8e-31;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 783 TVALLVMEGLSAPFLHALRHVWFQNKFSYGTGYKLSPP 822
DB 788 TVALLVMEGLSAPFLHALRHVWFQNKFSYGTGYKLSPP 827
|||||

RESULT 12
Q6P735 RAT PRELIMINARY; PRT; 420 AA.
AC Q6P735
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Tcigr1 protein.
GN Name=Tcigr1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RG NIH MGC Project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC061859; AAH61859.1; -; mRNA.
DR Ensembl; ENSRNOG00000017220; Rattus norvegicus.

DR RGD; 735136; Tcigr1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR002490; V_ATPase_sub116.
DR PANTHER; PTHR11629; V_ATPase_sub116; 1.
DR Pfam; PF01496; V_ATPase_I; 1.
SQ SEQUENCE 420 AA; 46956 MW; 1D3E094160F1ABD0 CRC64;

Query Match 4.6%; Score 38; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 3.6e-29;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 EVNPAPYTIITPPFLFAVMFGDVGHGLLMFLPALAMVL 422
DB 247 EVNPAPYTIITPPFLFAVMFGDVGHGLLMFLPALAMVL 284
|||||

RESULT 13
Q6QBN7 HUMAN PRELIMINARY; PRT; 45 AA.
AC Q6QBN7
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE T-cell immune regulator 1 transcript variant 5 (Fragment).
GN Name=Tcigr1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX PubMed=15809087; DOI=10.1016/j.jbbrc.2005.03.065;
RA Smirnova A.S., Morgun A., Shulzhenko N., Silva I.D.,
RA Gerbase-Delima M.;
RT "Identification of new alternative splice events in the TCIRG1 gene in
different human tissues.";
RL Biochem. Biophys. Res. Commun. 330:943-949 (2005).
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CC -----
DR EMBL; AY548968; AAS59835.1; -; mRNA.
DR Ensembl; ENSG00000110719; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR002490; V_ATPase_sub116.
DR PANTHER; PTHR11629; V_ATPase_sub116; 1.
DR Pfam; PF01496; V_ATPase_I; 1.
FT NON_TER 1
SQ SEQUENCE 45 AA; 5125 MW; 08E1883DECB81C70 CRC64;

Query Match 4.3%; Score 35; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 6.4e-27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 453 FSIYTGFIYNECFRSRATSIFFPSGWSVAAMANSQGW 487
DB 10 FSIYTGFIYNECFRSRATSIFFPSGWSVAAMANSQGW 44
|||||

RESULT 14
Q7ZVM7 BRARE PRELIMINARY; PRT; 822 AA.
AC Q7ZVM7
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Zgc155891.
GN ORFName=zgc155891;
OS Brachydanio rerio (zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=AB; TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=AB; TISSUE=Whole body;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; BC045484; AAH45484.1; -; mRNA.
 DR Ensembl; ENSDARG0000035711; Danio rerio.
 DR ZFIN; ZDB-GENE-040426-2022; zgc:55891.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015992; P:proton transport; IEA.
 DR InterPro; IPR002490; V_ATPase_sub116.
 DR PANTHER; PTHR11629; V_ATPase_sub116; 1.
 DR Pfam; PF01496; V_ATPase_I; 1.
 SQ SEQUENCE 822 AA; 93476 MW; 9432428966111755 CRC64;
 Query Match 4.1%; Score 34; DB 2; Length 822;
 Best Local Similarity 100.0%; Pred. No. 8.3e-25;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 786 ILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKL 819
 DB 776 ILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKL 809
 RESULT 15
 Q6PA83 XENLA
 ID Q6PA83 XENLA PRELIMINARY; PRT; 846 AA.
 AC Q6PA83;
 DT 05-JUL-2004, integrated into UniprotKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE MGC68661 protein.
 GN Name=MGC68661;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.D., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative."
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA Klein S., Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; BC060417; AAH60417.1; -; mRNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0015992; P:proton transport; IEA.
 DR InterPro; IPR002490; V_ATPase_sub116.
 DR PANTHER; PTHR11629; V_ATPase_sub116; 1.
 DR Pfam; PF01496; V_ATPase_I; 1.
 SQ SEQUENCE 846 AA; 97025 MW; DFCBABA4953780759 CRC64;
 Query Match 3.9%; Score 32; DB 2; Length 846;
 Best Local Similarity 100.0%; Pred. No. 9.7e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 783 TVAILVMEGLSAFLHALRLHWVEFQNKFSYSG 814
 DB 795 TVAILVMEGLSAFLHALRLHWVEFQNKFSYSG 826

Search completed: June 29, 2006, 13:22:03
 Job time : 309 secs

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Db 61 LEKTTFFLOEEVRRAGLVLPKPGRLPAPPPRDLRLIQEETERLAQELRDVRGNQALRA 120
QY 121 QLHQQLHAAVLRQGHQPQAAAAHTDASERTPLQAPGGPHQDLRVNFVAGAVEPHKAP 180
Db 121 QLHQQLHAAVLRQGHQPQAAAAHTDASERTPLQAPGGPHQDLRVNFVAGAVEPHKAP 180
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Db 181 ALERLLWRACRGFLTASPRELEQPLEHPVTGEPATWMTFLISYWGEOIQKIRK1TDCPH 240
QY 241 CHVFPFLOEEVRRAGLVLPKPGRLPAPPPRDLRLIQEETERLAQELRDVRGNQALRA 300
Db 241 CHVFPFLOEEVRRAGLVLPKPGRLPAPPPRDLRLIQEETERLAQELRDVRGNQALRA 300
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QY 361 LIRNRTFASFGQIVDRYGVGRYQEVNPAPYTIITFPFLFAYMFGDVGHGLMFLPALAM 420
Db 361 LIRNRTFASFGQIVDRYGVGRYQEVNPAPYTIITFPFLFAYMFGDVGHGLMFLPALAM 420
QY 421 VLAENRPAVKAQAQNEIWOTFFRGRYLLLMGLFSYITGFIYNECFSRATSIFPSCWSVAA 480
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QY 481 MANQSGWSDAFIAQHTMTLTDPNVTGVLGPPYFGIDPIWLSLAANHLSFLNSFKMKMSVI 540
Db 481 MANQSGWSDAFIAQHTMTLTDPNVTGVLGPPYFGIDPIWLSLAANHLSFLNSFKMKMSVI 540
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Db 541 LGVHMAFGVVLGVFNHVFQGRHLLLETLPELTFLGLFGYLVFLVIYKWLVCWAARA 600
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Db 601 ASPSLIHFINFLFSPNSRLLYPROEVQATLVIALAMVPIILLGTPLHLHRHR 660
QY 721 EFCLGCVSNTASYLRMLSLAQAQLSEVLWAMVNRIGLGLGREVGVAAVLVPFAAFA 780
Db 721 EFCLGCVSNTASYLRMLSLAQAQLSEVLWAMVNRIGLGLGREVGVAAVLVPFAAFA 780
QY 781 VMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPPF 822
Db 781 VMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPPF 822

RESULT 2

US-09-618-304B-2
; Sequence 2, Application US/09618304B
; Patent No. 677537

GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; APPLICANT: Li, Yi-Ping
; TITLE OF INVENTION: Osteoclast Proton Pump Subunit
; FILE REFERENCE: 1564.1006-001
; CURRENT APPLICATION NUMBER: US/09/618,304B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 08/605,378
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-618-304B-2

Query Match 100.0%; Score 822; DB 2; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSFSPSEVALVOLFLPTAAAYTCVSRUGELGLVFEFRDLNASVSAFORRVVDVWRCEE 60
Db 1 MGSFSPSEVALVOLFLPTAAAYTCVSRUGELGLVFEFRDLNASVSAFORRVVDVWRCEE 60
QY 61 LEKTTFFLOEEVRRAGLVLPKPGRLPAPPPRDLRLIQEETERLAQELRDVRGNQALRA 120
Db 61 LEKTTFFLOEEVRRAGLVLPKPGRLPAPPPRDLRLIQEETERLAQELRDVRGNQALRA 120
QY 121 QLHQQLHAAVLRQGHQPQAAAAHTDASERTPLQAPGGPHQDLRVNFVAGAVEPHKAP 180
Db 121 QLHQQLHAAVLRQGHQPQAAAAHTDASERTPLQAPGGPHQDLRVNFVAGAVEPHKAP 180
QY 181 ALERLLWRACRGFLTASPRELEQPLEHPVTGEPATWMTFLISYWGEOIQKIRK1TDCPH 240
Db 181 ALERLLWRACRGFLTASPRELEQPLEHPVTGEPATWMTFLISYWGEOIQKIRK1TDCPH 240
QY 241 CHVFPFLOEEVRRAGLVLPKPGRLPAPPPRDLRLIQEETERLAQELRDVRGNQALRA 300
Db 241 CHVFPFLOEEVRRAGLVLPKPGRLPAPPPRDLRLIQEETERLAQELRDVRGNQALRA 300
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Db 301 AVYALNQCSTVTHKCLIAEAWCSVRDLPALQOALRDSSMEEGVSAVAHRIPCRDMPPT 360
QY 361 LIRNRTFASFGQIVDRYGVGRYQEVNPAPYTIITFPFLFAYMFGDVGHGLMFLPALAM 420
Db 361 LIRNRTFASFGQIVDRYGVGRYQEVNPAPYTIITFPFLFAYMFGDVGHGLMFLPALAM 420
QY 421 VLAENRPAVKAQAQNEIWOTFFRGRYLLLMGLFSYITGFIYNECFSRATSIFPSCWSVAA 480
Db 421 VLAENRPAVKAQAQNEIWOTFFRGRYLLLMGLFSYITGFIYNECFSRATSIFPSCWSVAA 480
QY 481 MANQSGWSDAFIAQHTMTLTDPNVTGVLGPPYFGIDPIWLSLAANHLSFLNSFKMKMSVI 540
Db 481 MANQSGWSDAFIAQHTMTLTDPNVTGVLGPPYFGIDPIWLSLAANHLSFLNSFKMKMSVI 540
QY 541 LGVHMAFGVVLGVFNHVFQGRHLLLETLPELTFLGLFGYLVFLVIYKWLVCWAARA 600
Db 541 LGVHMAFGVVLGVFNHVFQGRHLLLETLPELTFLGLFGYLVFLVIYKWLVCWAARA 600
QY 601 ASPSLIHFINFLFSPNSRLLYPROEVQATLVIALAMVPIILLGTPLHLHRHR 660
Db 601 ASPSLIHFINFLFSPNSRLLYPROEVQATLVIALAMVPIILLGTPLHLHRHR 660
QY 661 RLRRPADROENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLHQAIHTI 720
Db 661 RLRRPADROENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLHQAIHTI 720
QY 721 EFCLGCVSNTASYLRMLSLAQAQLSEVLWAMVNRIGLGLGREVGVAAVLVPFAAFA 780
Db 721 EFCLGCVSNTASYLRMLSLAQAQLSEVLWAMVNRIGLGLGREVGVAAVLVPFAAFA 780
QY 781 VMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPPF 822
Db 781 VMTVAILLVMEGLSAFLHALRLHWVEFQNKFSYGTGYKLSPPF 822

RESULT 3

US-09-949-016-8846
; Sequence 8846, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8846
; LENGTH: 849
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8846

Query Match 66.3%; Score 545; DB 2; Length 849;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 765; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 57 RCELEKTTFFLOEVRAGLVLPKGRPLPAPPDRLLRIQETTERLAQELRDVRGNQ 116
DB 76 RCELEKTTFFLOEVRAGLVLPKGRPLPAPPDRLLRIQETTERLAQELRDVRGNQ 135

QY 117 ALRAQLHQLHAAVLRLQGHPEPQLAAHTDGCASERTPLQAPGPHODLRVNFVAGAVEP 176
DB 136 ALRAQLHQLHAAVLRLQGHPEPQLAAHTDGCASERTPLQAPGPHODLRVNFVAGAVEP 195

QY 177 HKPALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGQIGQIKIRKIT 236
DB 196 HKPALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGQIGQIKIRKIT 255

QY 237 DCFCHVFPFLQOEERLALQLOOQSOEVLGETERFLSQVLGRVQLLPPGQVQV 296
DB 256 DCFCHVFPFLQOEERLALQLOOQSOEVLGETERFLSQVLGRVQLLPPGQVQV 315

QY 297 HKMKAVYALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDSMEGVSAAVHRIFCRD 356
DB 316 HKMKAVYALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDSMEGVSAAVHRIFCRD 375

QY 357 MPPTLIRTNRTASFGQIVDYGVRGYQEVNPAPTYITITPPFLFVAVMFGDVGHGLMLFLF 416
DB 376 MPPTLIRTNRTASFGQIVDYGVRGYQEVNPAPTYITITPPFLFVAVMFGDVGHGLMLFLF 435

QY 417 ALAMVLAENRPAKAAQNEIWQTFRRGRYLLLLMGLFSIYTGFIYNECFSRATSIFFPSGW 476
DB 436 ALAMVLAENRPAKAAQNEIWQTFRRGRYLLLLMGLFSIYTGFIYNECFSRATSIFFPSGW 495

QY 477 SVAAMANQSGWSDAFIAQHTMTLTDNPNVTGVFLGYPFGIDPIWLSLAANHLFLNSPKMK 536
DB 496 SVAAMANQSGWSDAFIAQHTMTLTDNPNVTGVFLGYPFGIDPIWLSLAANHLFLNSPKMK 555

QY 537 MSVILGVVHMAFGVNLGVFNHVFQGRHRLLETLPELTFLGLFGYLVFLVIYKMLVCW 596
DB 556 MSVILGVVHMAFGVNLGVFNHVFQGRHRLLETLPELTFLGLFGYLVFLVIYKMLVCW 615

QY 597 ARAAAS-PSLIIHFINNLFSSHSPSNRLLYPROEVVQATLVIALAMVPIILLGTPLHLL 655
DB 616 ARAAASPSLIIHFINNLFSSHSPSNRLLYPROEVVQATLVIALAMVPIILLGTPLHLL 675

QY 656 HRHRRRLRRPADQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLHMQ 715
DB 676 HRHRRRLRRPADQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLHMQ 735

QY 716 AIHTIEFCGCVSNTASYLRWALSALAHQSEVLWAMVMRIIGLGLREVGVAAVLVPI 775
DB 736 AIHTIEFCGCVSNTASYLRWALSALAHQSEVLWAMVMRIIGLGLREVGVAAVLVPI 795

QY 776 FAFAVMTVAILLMEGLSFLHALRLHWVEFQNKFSYGTGYKLSPP 822
DB 796 FAFAVMTVAILLMEGLSFLHALRLHWVEFQNKFSYGTGYKLSPP 842
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RESULT 4

US-09-949-016-8847

; Sequence 8847, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8847
; LENGTH: 849
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8847

Query Match 66.3%; Score 545; DB 2; Length 849;
Best Local Similarity 99.7%; Pred. No. 0;

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QY 57 RCELEKTTFFLOEVRAGLVLPKGRPLPAPPDRLLRIQETTERLAQELRDVRGNQ 116
DB 76 RCELEKTTFFLOEVRAGLVLPKGRPLPAPPDRLLRIQETTERLAQELRDVRGNQ 135

QY 117 ALRAQLHQLHAAVLRLQGHPEPQLAAHTDGCASERTPLQAPGPHODLRVNFVAGAVEP 176
DB 136 ALRAQLHQLHAAVLRLQGHPEPQLAAHTDGCASERTPLQAPGPHODLRVNFVAGAVEP 195

QY 177 HKPALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGQIGQIKIRKIT 236
DB 196 HKPALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGQIGQIKIRKIT 255

QY 237 DCFCHVFPFLQOEERLALQLOOQSOEVLGETERFLSQVLGRVQLLPPGQVQV 296
DB 256 DCFCHVFPFLQOEERLALQLOOQSOEVLGETERFLSQVLGRVQLLPPGQVQV 315

QY 297 HKMKAVYALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDSMEGVSAAVHRIFCRD 356
DB 316 HKMKAVYALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDSMEGVSAAVHRIFCRD 375

QY 357 MPPTLIRTNRTASFGQIVDYGVRGYQEVNPAPTYITITPPFLFVAVMFGDVGHGLMLFLF 416
DB 376 MPPTLIRTNRTASFGQIVDYGVRGYQEVNPAPTYITITPPFLFVAVMFGDVGHGLMLFLF 435

QY 417 ALAMVLAENRPAKAAQNEIWQTFRRGRYLLLLMGLFSIYTGFIYNECFSRATSIFFPSGW 476
DB 436 ALAMVLAENRPAKAAQNEIWQTFRRGRYLLLLMGLFSIYTGFIYNECFSRATSIFFPSGW 495

QY 477 SVAAMANQSGWSDAFIAQHTMTLTDNPNVTGVFLGYPFGIDPIWLSLAANHLFLNSPKMK 536
DB 496 SVAAMANQSGWSDAFIAQHTMTLTDNPNVTGVFLGYPFGIDPIWLSLAANHLFLNSPKMK 555

QY 537 MSVILGVVHMAFGVNLGVFNHVFQGRHRLLETLPELTFLGLFGYLVFLVIYKMLVCW 596
DB 556 MSVILGVVHMAFGVNLGVFNHVFQGRHRLLETLPELTFLGLFGYLVFLVIYKMLVCW 615

QY 597 ARAAAS-PSLIIHFINNLFSSHSPSNRLLYPROEVVQATLVIALAMVPIILLGTPLHLL 655
DB 616 ARAAASPSLIIHFINNLFSSHSPSNRLLYPROEVVQATLVIALAMVPIILLGTPLHLL 675

QY 656 HRHRRRLRRPADQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLHMQ 715
DB 676 HRHRRRLRRPADQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAEELVPSEVLHMQ 735

QY 716 AIHTIEFCGCVSNTASYLRWALSALAHQSEVLWAMVMRIIGLGLREVGVAAVLVPI 775
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Db 736 A|H|T|E|F|C|L|G|C|V|S|N|T|A|S|Y|L|R|W|A|L|S|L|A|H|A|Q|L|S|V|L|W|A|V|M|R|I|G|L|G|L|G|G|V|A|A|V|L|V|P|I 795
QY 776 F|A|A|F|A|V|T|V|A|I|L|L|V|W|E|G|L|S|A|F|L|H|A|L|R|L|H|W|V|E|F|Q|N|K|F|S|G|T|G|Y|K|L|S|P|F 822
Db 796 F|A|A|F|A|V|T|V|A|I|L|L|V|W|E|G|L|S|A|F|L|H|A|L|R|L|H|W|V|E|F|Q|N|K|F|S|G|T|G|Y|K|L|S|P|F 842

RESULT 5
US-09-949-016-8275
; Sequence 8275, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8275
; LENGTH: 853
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8275

Query Match 66.3%; Score 545; DB 2; Length 853;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 765; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 57 R|C|E|E|L|E|K|T|F|T|Q|E|E|V|R|R|A|G|L|V|L|P|P|K|G|R|L|P|A|P|P|P|R|D|L|L|R|I|O|E|T|E|R|L|A|Q|E|L|R|D|V|R|G|N|Q 116
Db 80 R|C|E|E|L|E|K|T|F|T|Q|E|E|V|R|R|A|G|L|V|L|P|P|K|G|R|L|P|A|P|P|P|R|D|L|L|R|I|O|E|T|E|R|L|A|Q|E|L|R|D|V|R|G|N|Q 139
QY 117 A|L|R|A|Q|L|H|Q|L|H|A|V|L|R|Q|H|E|P|Q|L|A|A|H|T|D|G|A|S|E|R|T|P|L|Q|A|P|G|G|H|Q|D|L|R|V|N|F|V|A|G|A|V|E|P 176
Db 140 A|L|R|A|Q|L|H|Q|L|H|A|V|L|R|Q|H|E|P|Q|L|A|A|H|T|D|G|A|S|E|R|T|P|L|Q|A|P|G|G|H|Q|D|L|R|V|N|F|V|A|G|A|V|E|P 199
QY 177 H|K|A|P|A|L|E|R|L|W|R|A|C|R|G|F|L|A|S|P|R|E|L|E|Q|P|L|E|H|P|V|T|G|E|P|A|T|W|T|F|L|S|Y|W|G|E|Q|I|G|O|K|I|R|K|I|T 236
Db 200 H|K|A|P|A|L|E|R|L|W|R|A|C|R|G|F|L|A|S|P|R|E|L|E|Q|P|L|E|H|P|V|T|G|E|P|A|T|W|T|F|L|S|Y|W|G|E|Q|I|G|O|K|I|R|K|I|T 259
QY 237 D|C|F|H|C|H|V|P|P|F|L|Q|E|E|R|A|L|G|A|L|Q|L|Q|O|Q|S|O|E|L|Q|E|V|L|G|E|T|E|R|F|L|S|Q|V|L|G|R|V|L|Q|L|P|P|Q|Q|V 296
Db 260 D|C|F|H|C|H|V|P|P|F|L|Q|E|E|R|A|L|G|A|L|Q|L|Q|O|Q|S|O|E|L|Q|E|V|L|G|E|T|E|R|F|L|S|Q|V|L|G|R|V|L|Q|L|P|P|Q|Q|V 319
QY 297 H|K|A|V|Y|L|A|N|C|S|V|T|H|K|L|I|A|E|A|W|C|S|V|R|D|L|P|A|Q|E|R|D|S|S|M|E|E|G|V|S|A|V|A|H|R|I|P|C|R|D 356
Db 320 H|K|A|V|Y|L|A|N|C|S|V|T|H|K|L|I|A|E|A|W|C|S|V|R|D|L|P|A|Q|E|R|D|S|S|M|E|E|G|V|S|A|V|A|H|R|I|P|C|R|D 379
QY 357 M|P|T|L|I|R|N|R|F|T|A|S|F|Q|I|V|D|A|V|G|V|G|R|Y|Q|E|V|N|P|A|P|Y|T|I|T|F|P|F|A|V|M|F|G|D|V|G|H|L|M|F|L|F 416
Db 380 M|P|T|L|I|R|N|R|F|T|A|S|F|Q|I|V|D|A|V|G|V|G|R|Y|Q|E|V|N|P|A|P|Y|T|I|T|F|P|F|A|V|M|F|G|D|V|G|H|L|M|F|L|F 439
QY 417 A|L|A|V|L|A|E|R|N|R|P|A|V|K|A|Q|N|E|I|W|T|F|F|R|G|R|Y|L|L|L|M|G|L|F|S|Y|T|G|I|Y|N|E|C|F|S|R|A|T|S|I|P|P|S|G|W 476
Db 440 A|L|A|V|L|A|E|R|N|R|P|A|V|K|A|Q|N|E|I|W|T|F|F|R|G|R|Y|L|L|L|M|G|L|F|S|Y|T|G|I|Y|N|E|C|F|S|R|A|T|S|I|P|P|S|G|W 499
QY 477 S|V|A|A|N|Q|S|G|W|S|D|A|F|L|A|Q|H|T|L|T|D|N|V|T|G|V|L|P|G|P|Y|P|F|G|I|D|P|I|W|S|L|A|A|N|H|L|S|F|L|N|S|F|K|N|K 536
Db 500 S|V|A|A|N|Q|S|G|W|S|D|A|F|L|A|Q|H|T|L|T|D|N|V|T|G|V|L|P|G|P|Y|P|F|G|I|D|P|I|W|S|L|A|A|N|H|L|S|F|L|N|S|F|K|N|K 559
QY 537 M|S|V|I|L|G|V|H|H|A|F|G|V|L|G|V|N|H|V|H|F|G|Q|R|H|L|L|L|T|E|L|P|L|T|F|L|G|L|F|G|Y|L|V|F|L|Y|K|W|L|C|V|W 596
Db 560 M|S|V|I|L|G|V|H|H|A|F|G|V|L|G|V|N|H|V|H|F|G|Q|R|H|L|L|L|T|E|L|P|L|T|F|L|G|L|F|G|Y|L|V|F|L|Y|K|W|L|C|V|W 619
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QY 597 A|A|R|A|S|-P|S|I|H|I|N|F|I|N|M|F|L|F|S|H|S|P|N|R|L|Y|P|R|O|E|V|V|Q|A|T|L|V|V|L|A|A|V|P|I|L|L|G|T|P|L|H|L 655
Db 620 A|A|R|A|S|A|P|S|I|H|I|N|F|I|N|M|F|L|F|S|H|S|P|N|R|L|Y|P|R|O|E|V|V|Q|A|T|L|V|V|L|A|A|V|P|I|L|L|G|T|P|L|H|L 679
QY 656 H|R|R|R|R|R|R|R|P|A|D|R|O|E|N|K|A|G|L|D|L|P|D|A|S|V|N|G|S|S|D|E|E|K|A|G|L|D|D|E|E|A|E|L|V|P|S|E|V|L|H|Q 715
Db 680 H|R|R|R|R|R|R|R|P|A|D|R|O|E|N|K|A|G|L|D|L|P|D|A|S|V|N|G|S|S|D|E|E|K|A|G|L|D|D|E|E|A|E|L|V|P|S|E|V|L|H|Q 739
QY 716 A|H|T|E|F|C|L|G|C|V|S|N|T|A|S|Y|L|R|W|A|L|S|L|A|H|A|Q|L|S|V|L|W|A|V|M|R|I|G|L|G|L|G|G|V|A|A|V|L|V|P|I 775
Db 740 A|H|T|E|F|C|L|G|C|V|S|N|T|A|S|Y|L|R|W|A|L|S|L|A|H|A|Q|L|S|V|L|W|A|V|M|R|I|G|L|G|L|G|G|V|A|A|V|L|V|P|I 799
QY 776 F|A|A|F|A|V|T|V|A|I|L|L|V|W|E|G|L|S|A|F|L|H|A|L|R|L|H|W|V|E|F|Q|N|K|F|S|G|T|G|Y|K|L|S|P|F 822
Db 800 F|A|A|F|A|V|T|V|A|I|L|L|V|W|E|G|L|S|A|F|L|H|A|L|R|L|H|W|V|E|F|Q|N|K|F|S|G|T|G|Y|K|L|S|P|F 846

RESULT 6
US-09-949-016-8276
; Sequence 8276, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8276
; LENGTH: 853
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8276

Query Match 66.3%; Score 545; DB 2; Length 853;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 765; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 57 R|C|E|E|L|E|K|T|F|T|Q|E|E|V|R|R|A|G|L|V|L|P|P|K|G|R|L|P|A|P|P|P|R|D|L|L|R|I|O|E|T|E|R|L|A|Q|E|L|R|D|V|R|G|N|Q 116
Db 80 R|C|E|E|L|E|K|T|F|T|Q|E|E|V|R|R|A|G|L|V|L|P|P|K|G|R|L|P|A|P|P|P|R|D|L|L|R|I|O|E|T|E|R|L|A|Q|E|L|R|D|V|R|G|N|Q 139
QY 117 A|L|R|A|Q|L|H|Q|L|H|A|V|L|R|Q|H|E|P|Q|L|A|A|H|T|D|G|A|S|E|R|T|P|L|Q|A|P|G|G|H|Q|D|L|R|V|N|F|V|A|G|A|V|E|P 176
Db 140 A|L|R|A|Q|L|H|Q|L|H|A|V|L|R|Q|H|E|P|Q|L|A|A|H|T|D|G|A|S|E|R|T|P|L|Q|A|P|G|G|H|Q|D|L|R|V|N|F|V|A|G|A|V|E|P 199
QY 177 H|K|A|P|A|L|E|R|L|W|R|A|C|R|G|F|L|A|S|P|R|E|L|E|Q|P|L|E|H|P|V|T|G|E|P|A|T|W|T|F|L|S|Y|W|G|E|Q|I|G|O|K|I|R|K|I|T 236
Db 200 H|K|A|P|A|L|E|R|L|W|R|A|C|R|G|F|L|A|S|P|R|E|L|E|Q|P|L|E|H|P|V|T|G|E|P|A|T|W|T|F|L|S|Y|W|G|E|Q|I|G|O|K|I|R|K|I|T 259
QY 237 D|C|F|H|C|H|V|P|P|F|L|Q|E|E|R|A|L|G|A|L|Q|L|Q|O|Q|S|O|E|L|Q|E|V|L|G|E|T|E|R|F|L|S|Q|V|L|G|R|V|L|Q|L|P|P|Q|Q|V 296
Db 260 D|C|F|H|C|H|V|P|P|F|L|Q|E|E|R|A|L|G|A|L|Q|L|Q|O|Q|S|O|E|L|Q|E|V|L|G|E|T|E|R|F|L|S|Q|V|L|G|R|V|L|Q|L|P|P|Q|Q|V 319
QY 297 H|K|A|V|Y|L|A|N|C|S|V|T|H|K|L|I|A|E|A|W|C|S|V|R|D|L|P|A|Q|E|R|D|S|S|M|E|E|G|V|S|A|V|A|H|R|I|P|C|R|D 356
Db 320 H|K|A|V|Y|L|A|N|C|S|V|T|H|K|L|I|A|E|A|W|C|S|V|R|D|L|P|A|Q|E|R|D|S|S|M|E|E|G|V|S|A|V|A|H|R|I|P|C|R|D 379
QY 357 M|P|T|L|I|R|N|R|F|T|A|S|F|Q|I|V|D|A|V|G|V|G|R|Y|Q|E|V|N|P|A|P|Y|T|I|T|F|P|F|A|V|M|F|G|D|V|G|H|L|M|F|L|F 416
Db 380 M|P|T|L|I|R|N|R|F|T|A|S|F|Q|I|V|D|A|V|G|V|G|R|Y|Q|E|V|N|P|A|P|Y|T|I|T|F|P|F|A|V|M|F|G|D|V|G|H|L|M|F|L|F 439
QY 417 A|L|A|V|L|A|E|R|N|R|P|A|V|K|A|Q|N|E|I|W|T|F|F|R|G|R|Y|L|L|L|M|G|L|F|S|Y|T|G|I|Y|N|E|C|F|S|R|A|T|S|I|P|P|S|G|W 476
Db 440 A|L|A|V|L|A|E|R|N|R|P|A|V|K|A|Q|N|E|I|W|T|F|F|R|G|R|Y|L|L|L|M|G|L|F|S|Y|T|G|I|Y|N|E|C|F|S|R|A|T|S|I|P|P|S|G|W 499
```

Qy	477	SVAAMANGSWSDAFLAQHTMLTLPDPNVGTGVLPGYPFGIDPWSLAANHLSFLNSFKMK	536
Db	500	SVAAMANGSWSDAFLAQHTMLTLPDPNVGTGVLPGYPFGIDPWSLAANHLSFLNSFKMK	559
Qy	537	MSVILGVVHMAFGVVLGVFNHVHFGQRHRLLETLPELTFLGLFGYLVFLVIYKWLQW	596
Db	560	MSVILGVVHMAFGVVLGVFNHVHFGQRHRLLETLPELTFLGLFGYLVFLVIYKWLQW	619
Qy	597	AARAAS-PSILITHFINMFLFSHSPSNRLLYPQEVVQATLVVLALAMWPIILGLTGPLHL	655
Db	620	AARAASPSILITHFINMFLFSHSPSNRLLYPQEVVQATLVVLALAMWPIILGLTGPLHL	679
Qy	656	HRHRRRLRRPADROEENKAGLLDLPDASVNGSWSDDEEKAGGLDDEEAELVPSEVLMHQ	715
Db	680	HRHRRRLRRPADROEENKAGLLDLPDASVNGSWSDDEEKAGGLDDEEAELVPSEVLMHQ	739
Qy	716	AIHTIEPCGVSNTASYLRLWALSAHAQAQSEVLWAMVMRIGLGLGREGVAAVVLVPI	775
Db	740	AIHTIEFCGVSNTASYLRLWALSAHAQAQSEVLWAMVMRIGLGLGREGVAAVVLVPI	799
Qy	776	FAAFVMTVAILLWMEGLSAFLHAILRHWFVEFQNKFGYKLSPP	822
Db	800	FAAFVMTVAILLWMEGLSAFLHAILRHWFVEFQNKFGYKLSPP	846

RESULT 7

```

US-09-949-016-7201
; Sequence 7201, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE OF INVENTION: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7201
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7201

```

Query Match	52.7%	Score 433;	DB 2;	Length 750;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 653;	Conservative	0;	Mismatches	1;
Indels	1.1;	Gaps	1;	

Qy	169	FVAGNPFHKAPALERLLWRACRGFLIASFRELQPLEHPVTGSPATWMTFLISYWGSGQI	228
Db	89	FVAGNPFHKAPALERLLWRACRGFLIASFRELQPLEHPVTGSPATWMTFLISYWGSGQI	148
Qy	229	GQIKRITDCFCHVFPPFLOQEEARLGAQLQOQSQELQVLGETERFSLQVLGRVLQL	288
Db	149	GQIKRITDCFCHVFPPFLOQEEARLGAQLQOQSQELQVLGETERFSLQVLGRVLQL	208
Qy	289	LPQGQOVQHKMKAVYLAALNQCQSVSTHKCLITAEAWCSVRDLPAQLEALRDSMEEGVSAY	348
Db	209	LPQGQOVQHKMKAVYLAALNQCQSVSTHKCLITAEAWCSVRDLPAQLEALRDSMEEGVSAY	268
Qy	349	AHRIPCDMPPTLIRTNRPASFGQIVDRYGVGVQEVNRPAYTIITPPPLFAMWFGDVG	408
Db	269	AHRIPCDMPPTLIRTNRPASFGQIVDAGVGRIQEVNRPAYTIITPPPLFAMWFGDVG	328
Qy	409	HGLLMFLFALAMVLAENRPVAKAQNBIQTQTFPRGRVLLLLMGFLFSYITGTIYNECFPSRA	468

329	DB	HGLLMFIFALAMVLAEHRPAKAAQONETWQTFFRGRYFLLLLMGUFLSYITGYINECPSRA	388
469	QY	TSIPFGSWVAAMANQSGWSDAFIAQHTMLTLDPNVTGVFLGPYPFGIDPIWSLAANHLS	528
389	DB	TSIPFGSWVAAMANQSGWSDAFIAQHTMLTLDPNVTGVFLGPYPFGIDPIWSLAANHLS	448
529	QY	FLNSFKMKMSVILGVWMAFGVNLGVFNHVFHQBRHRLLETLBELTFLGLGFLGYLVLV	588
449	DB	FLNSFKMKMSVILGVWMAFGVNLGVFNHVFHQBRHRLLETLBELTFLGLGFLGYLVLV	508
589	QY	IYKWLCVWAARAAS - PSTLIHFIMFLFSPHSPSNRLLYPROEVQOATLVILAMVPTLL	647
509	DB	IYKWLCVWAARAASAPSTLIHFIMFLFSPHSPSNRLLYPROEVQOATLVILAMVPTLL	568
648	QY	LGTEPLHLHLHRRLRRPADROENKAGLLDLPDASVNGWSDBEEKAGGLDDEEEABL	707
569	DB	LGTEPLHLHLHRRLRRPADROENKAGLLDLPDASVNGWSDBEEKAGGLDDEEEABL	628
708	QY	PSEVLHQAIHTIEFCLGCVSNTASYLRLWALS LAHAQLSEVLWAMVMRIGLGLGREYGV	767
629	DB	PSEVLHQAIHTIEFCLGCVSNTASYLRLWALS LAHAQLSEVLWAMVMRIGLGLGREYGV	688
768	QY	AAVULVDFIAFAVMTVAILLVMGLSAPFLHALRLHWVFONKPYSGTGKYLSPF	822
689	DB	AAVULVDFIAFAVMTVAILLVMGLSAPFLHALRLHWVFONKPYSGTGKYLSPF	743

RESULT 8

```

US-09-949-016-7202
; Sequence 7202, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7202
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7202

```

Query Match 52.7%; Score 433; DB 2; Length 750;
Best Local Similarity 99.7%; Pred. No. 0;

Accession	Conservative	Residues	1	Gaps
Qy	169	FVAGAVEPHKPALEKILLWRACRGFLIASPRELEQPLEHPVTGEPATWMTFLISYWGQEI	228	
Db	89	FVAGAVEPHKPALEKILLWRACRGFLIASPRELEQPLEHPVTGEPATWMTFLISYWGQEI	148	
Qy	229	GQKIRKITDCHFCHVPFFLQEEEARLQALQQLQQSQEQLQEVLTGETERFLSQVLGRVLQ	288	
Db	149	GQKIRKITDCHFCHVPFFLQEEEARLQALQQLQQSQEQLQEVLTGETERFLSQVLGRVLQ	208	
Qy	289	LPFGQVQVHKMKAVYLALNQCSYSTTHKCLIAEAWCSVRDLPALQALRDSSMEEGVSAY	348	
Db	209	LPFGQVQVHKMKAVYLALNQCSYSTTHKCLIAEAWCSVRDLPALQALRDSSMEEGVSAY	268	
Qy	349	AHRIPCRDMPTTLIRNRTFASQGIYDVGVRQYQVNPAPYTIITFPFLFAVMGVDVG	408	
Db	269	AHRIPCRDMPTTLIRNRTFASQGIYDVGVRQYQVNPAPYTIITFPFLFAVMGVDVG	328	
Qy	409	HGLMLFLFALAMVLAENRPVAKAAQNEIWQTFPRGRYLLLLMGLFSIYTGFIYNECFRSA	468	

```
Db 329 HGLLMLFALAMVLAENRRAVKAQNEIQTFPRGRYLLLLMGLFSIYTGFIYNECFSA 388
QY 469 TSIPSGWSVAAMANQSGWSDAPLAQHTMLTLDPNVTGVFLGYPYPGIDPIWLSLAANHLS 528
Db 389 TSIPSGWSVAAMANQSGWSDAPLAQHTMLTLDPNVTGVFLGYPYPGIDPIWLSLAANHLS 448
QY 529 FLNSFKMKSVILGVVHMAFGVVLGVFNHVFHQRHRLLETLPELTLLGLFGYLVFLV 588
Db 449 FLNSFKMKSVILGVVHMAFGVVLGVFNHVFHQRHRLLETLPELTLLGLFGYLVFLV 508
QY 589 IYKMLCVMAARAAS-PSIIHIFNMELFSGHSPSNRLLYPRQEVQVQATLVVLALAMVPILL 647
Db 509 IYKMLCVMAARAASPSIIHIFNMELFSGHSPSNRLLYPRQEVQVQATLVVLALAMVPILL 568
QY 648 LGTPLLHLHRRRLRRRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELV 707
Db 569 LGTPLLHLHRRRLRRRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDEEAELV 628
QY 708 PSEVLHQAIHTIEFCCLGCVSNTASVLRWLWLSLAHAQISEVLWAMVMRIGLIGREVCV 767
Db 629 PSEVLHQAIHTIEFCCLGCVSNTASVLRWLWLSLAHAQISEVLWAMVMRIGLIGREVCV 688
QY 768 AAVLVPIFAAFVMTVAILLVMEGLSAFLHALRHLHWVEFQNKFSYGTGYKLSPPF 822
Db 689 AAVLVPIFAAFVMTVAILLVMEGLSAFLHALRHLHWVEFQNKFSYGTGYKLSPPF 743
```

RESULT 9

```
US-09-618-304B-9
; Sequence 9, Application US/09618304B
; Patent No. 6777537
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; TITLE OF INVENTION: Osteoclast Proton Pump Subunit
; FILE REFERENCE: 1564.1006-001
; CURRENT APPLICATION NUMBER: US/09/618,304B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 08/605,378
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-618-304B-9
```

```
Query Match 4.0%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 764 EYGVAAVLVPIFAAFVMTVAILLVMEGLSAF 796
Db 1 EYGVAAVLVPIFAAFVMTVAILLVMEGLSAF 33
```

RESULT 10

```
US-09-618-304B-4
; Sequence 4, Application US/09618304B
; Patent No. 6777537
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; TITLE OF INVENTION: Osteoclast Proton Pump Subunit
; FILE REFERENCE: 1564.1006-001
; CURRENT APPLICATION NUMBER: US/09/618,304B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 08/605,378
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 4
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-618-304B-4
```

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Query Match 3.9%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.9e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 391 YTIITFFFLFAVMFGDVGHGLMLFLPALAMVL 422
Db 1 YTIITFFFLFAVMFGDVGHGLMLFLPALAMVL 32
```

RESULT 11

```
US-09-618-304B-7
; Sequence 7, Application US/09618304B
; Patent No. 6777537
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; TITLE OF INVENTION: Osteoclast Proton Pump Subunit
; FILE REFERENCE: 1564.1006-001
; CURRENT APPLICATION NUMBER: US/09/618,304B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 08/605,378
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-618-304B-7
```

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Query Match 3.6%; Score 30; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 571 LPFLTLLGLFGYLVFLVIYKWLVCVMAARA 600
Db 1 LPFLTLLGLFGYLVFLVIYKWLVCVMAARA 30
```

RESULT 12

```
US-09-618-304B-5
; Sequence 5, Application US/09618304B
; Patent No. 6777537
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; TITLE OF INVENTION: Osteoclast Proton Pump Subunit
; FILE REFERENCE: 1564.1006-001
; CURRENT APPLICATION NUMBER: US/09/618,304B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 08/605,378
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-618-304B-5
```

```
Query Match 3.2%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 438 QTFPRGRYLLMLGLFSIYTGFIYNE 463
Db 1 QTFPRGRYLLMLGLFSIYTGFIYNE 26
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RESULT 13
US-10-094-749-2211
; Sequence 2211, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2211
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2211

Query Match 2.9%; Score 24; DB 2; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 728 SNTASYRLRLWALSIAHAQLSEVLW 751
Db 409 SNTASYRLRLWALSIAHAQLSEVLW 432

RESULT 14
US-09-618-304B-3
; Sequence 3, Application US/09618304B
; Patent No. 6777537
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; APPLICANT: Li, Yi-Ping
; TITLE OF INVENTION: Osteoclast Proton Pump Subunit
; FILE REFERENCE: 1564.1006-001
; CURRENT APPLICATION NUMBER: US/09/618,304B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 08/605,378
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 847
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
; FEATURE:
; NAME/KEY: VARIANT

; LOCATION: (1)...(847)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-618-304B-3
Query Match 2.9%; Score 24; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 2.1e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 728 SNTASYRLRLWALSIAHAQLSEVLW 751
Db 741 SNTASYRLRLWALSIAHAQLSEVLW 764
RESULT 15
US-09-618-304B-8
; Sequence 8, Application US/09618304B
; Patent No. 6777537
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; APPLICANT: Li, Yi-Ping
; TITLE OF INVENTION: Osteoclast Proton Pump Subunit
; FILE REFERENCE: 1564.1006-001
; CURRENT APPLICATION NUMBER: US/09/618,304B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 08/605,378
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-618-304B-8

Query Match 2.8%; Score 23; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.5e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 632 QATLVVLALAMVPILLGTPLHL 654
Db 1 QATLVVLALAMVPILLGTPLHL 23

Search completed: June 29, 2006, 13:23:53
Job time : 54 secs

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GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: June 29, 2006, 13:23:09 ; Search time 188 Seconds
 (without alignments)
 2025.333 Million cell updates/sec
 Title: US-10-783-519-2
 Perfect score: 822
 Sequence: 1 MGSMPRSEEVALLVQLFLPTA.....HWVEFQNKFGYGTGYKLSPF 822
 Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0
 Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096646

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pap:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pap:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pap:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pap:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	822	100.0	822	5	US-10-783-519-2
2	385	46.8	614	4	US-10-145-012-2
3	385	46.8	614	6	US-11-126-866-2
4	385	46.8	614	6	US-11-126-841A-2
5	325	39.5	614	4	US-10-145-012-13
6	325	39.5	614	5	US-10-489-725-5
7	325	39.5	614	6	US-11-126-866-13
8	325	39.5	614	6	US-11-126-841A-13
9	291	35.4	643	4	US-10-264-049-2656
10	33	4.0	33	5	US-10-783-519-9
11	32	3.9	32	5	US-10-783-519-4
12	30	3.6	30	5	US-10-783-519-7
13	29	3.5	29	5	US-10-489-725-7
14	26	3.2	26	5	US-10-783-519-5
15	24	2.9	24	5	US-10-489-725-9
16	24	2.9	513	4	US-10-094-749-2211
17	24	2.9	558	5	US-10-450-763-39739
18	24	2.9	821	4	US-10-017-161-2144
19	24	2.9	821	4	US-10-292-798-1790
20	24	2.9	841	5	US-10-874-706-20
21	24	2.9	847	5	US-10-783-519-3
22	23	2.8	23	5	US-10-783-519-8
23	22	2.7	814	6	US-11-097-143-36642
24	22	2.7	834	6	US-11-097-143-41499
25	22	2.7	834	6	US-11-097-143-41700
26	22	2.7	844	6	US-11-097-143-41496
27	22	2.7	873	4	US-10-369-493-6070

RESULT 1
 US-10-783-519-2
 ; Sequence 2, Application US/10783519
 ; Publication No. US2005064448A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stashenko, Philip
 ; APPLICANT: Li, Yi-Ping
 ; TITLE OF INVENTION: Osteoclast Proton Pump Subunit
 ; FILE REFERENCE: 1564.1006-001
 ; CURRENT APPLICATION NUMBER: US/10783,519
 ; CURRENT FILING DATE: 2004-02-20
 ; PRIOR APPLICATION NUMBER: US/09/618,304
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 08/605,378
 ; PRIOR FILING DATE: 1996-02-22
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 822
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ;
 US-10-783-519-2

ALIGNMENTS

Query Match 100.0%; Score 822; DB 5; Length 822;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGSMPRSEEVALLVQLFLPTAAAYTCVSRGELGLVFRDLNASVSFAQRRFVVDVWRCCE	60
Db	1	MGSMPRSEEVALLVQLFLPTAAAYTCVSRGELGLVFRDLNASVSFAQRRFVVDVWRCCE	60
Qy	61	LEKTFTLQEEVRRAGLVLPKPKRLLPAPPPRDLRIQETTERLAQLRDLVRGNOQALRA	120
Db	61	LEKTFTLQEEVRRAGLVLPKPKRLLPAPPPRDLRIQETTERLAQLRDLVRGNOQALRA	120
Qy	121	QLHQLQHLAAVLKQGHPEPOLAAHTDGAERTPLQAPGGPHODLRVNFVAGAVEPHKAP	180
Db	121	QLHQLQHLAAVLKQGHPEPOLAAHTDGAERTPLQAPGGPHODLRVNFVAGAVEPHKAP	180
Qy	181	ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEGIQKIRKITDCFH	240
Db	181	ALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGEGIQKIRKITDCFH	240
Qy	241	CHVFPFLQEEARLGAQLQQLQOQSQELQVGLGTERFLSQVGLRVLLPFGQVQVHKM	300
Db	241	CHVFPFLQEEARLGAQLQQLQOQSQELQVGLGTERFLSQVGLRVLLPFGQVQVHKM	300
Qy	301	AVYLAALNQCSVSTTHKCLIAEAWCSVRDLPALQEARLSSMEEGVSAVAHRIPCRDMPPT	360
Db	301	AVYLAALNQCSVSTTHKCLIAEAWCSVRDLPALQEARLSSMEEGVSAVAHRIPCRDMPPT	360

QY 361 LIIRNRFTASFOGIVDRYGVGRYQEVNPAPYITITIPFELFAMVFGDVGHGLLMLFALAM 420
DB 361 LIIRNRFTASFOGIVDRYGVGRYQEVNPAPYITITIPFELFAMVFGDVGHGLLMLFALAM 420
QY 421 VLAENRPVAKAAQNEIWTQFFRGRYLLMLGLFSIYTGFIYNECFSRATSIIPSGWSVAA 480
DB 421 VLAENRPVAKAAQNEIWTQFFRGRYLLMLGLFSIYTGFIYNECFSRATSIIPSGWSVAA 480
QY 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGPYPFGDPIWLSAANHLSPNSFKMKSIVI 540
DB 481 MANQSGWSDAFLAQHTMLTLDPNVTGVFLGPYPFGDPIWLSAANHLSPNSFKMKSIVI 540
QY 541 LGVVMHAFGVVGVNHFHFGQHRRLLETLPELTLLGLFGLVFLVYKMLCWAARA 600
DB 541 LGVVMHAFGVVGVNHFHFGQHRRLLETLPELTLLGLFGLVFLVYKMLCWAARA 600
QY 601 ASPSTLIHFINFLPSHSPSNRLLYPRQEVQATLVVLAAMVPIILLGLTPLHLRHR 660
DB 601 ASPSTLIHFINFLPSHSPSNRLLYPRQEVQATLVVLAAMVPIILLGLTPLHLRHR 660
QY 661 RLRRPADROENKAGLLDLPDASVNGWSDEEKAGGLDDEBAELVPSEVLHQAIHTI 720
DB 661 RLRRPADROENKAGLLDLPDASVNGWSDEEKAGGLDDEBAELVPSEVLHQAIHTI 720
QY 721 EFCLGCVSNTASYLRWLSLAHAQLSEVLWAMVNRIGLGRGVAAVVLVPIFAAFA 780
DB 721 EFCLGCVSNTASYLRWLSLAHAQLSEVLWAMVNRIGLGRGVAAVVLVPIFAAFA 780
QY 781 VMTVAILLVMEGLSAFLHALRHWVEFQNKFSYSGTGKLSPP 822
DB 781 VMTVAILLVMEGLSAFLHALRHWVEFQNKFSYSGTGKLSPP 822

RESULT 2

US-10-145-012-2
; Sequence 2, Application US/10145012
; Publication No. US20030124614A1
; GENERAL INFORMATION:
; APPLICANT: UTU et al.
; TITLE OF INVENTION: T-CELL MEMBRANE PROTEIN (TIRC7), PEPTIDES AND ANTIBODIES DERIVED
; FILE REFERENCE: 4400-0105P
; CURRENT APPLICATION NUMBER: US/10/145,012
; CURRENT FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-012-2

Query Match 46.8%; Score 385; DB 4; Length 614;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 605; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 217 MTFLISYNGEQIGQKIRKITDCFHCHVFPFLOQEEARLQALQOQSQSELQEVLETGER 276
DB 1 MTFLISYNGEQIGQKIRKITDCFHCHVFPFLOQEEARLQALQOQSQSELQEVLETGER 60
QY 277 FLSQVLRVQLQLPPQGVQVHKMAVYLAALNOCVSTTHKCLIAEAWCSVRDLPALQAL 336
DB 61 FLSQVLRVQLQLPPQGVQVHKMAVYLAALNOCVSTTHKCLIAEAWCSVRDLPALQAL 120
QY 337 RDSSMEEGVSAVAHRIPCDMPPTLIRNFTASFGIVDRYGVGRYQEVNPAPYITITF 396
DB 121 RDSSMEEGVSAVAHRIPCDMPPTLIRNFTASFGIVDRYGVGRYQEVNPAPYITITF 180
QY 397 PFLPAMFGDVGHGLLMLFALAMVLAENRPVAKAAQNEIWTQFFRGRYLLMLGLFSIY 456
DB 181 PFLPAMFGDVGHGLLMLFALAMVLAENRPVAKAAQNEIWTQFFRGRYLLMLGLFSIY 240

QY 457 TGFYIYNECFSRATSIIPSGWSVAAMANQSGWSDAFLAQHTMLTLDPNVTGVFLGPYPFGI 516
DB 241 TGFYIYNECFSRATSIIPSGWSVAAMANQSGWSDAFLAQHTMLTLDPNVTGVFLGPYPFGI 300
QY 517 DPINSLAANHLSPNSFKMKSIVIILGVVHMAFGVVLGVFNHVFHFGQHRRLLETLPELTF 576
DB 301 DPINSLAANHLSPNSFKMKSIVIILGVVHMAFGVVLGVFNHVFHFGQHRRLLETLPELTF 360
QY 577 LLGLFGYLVFLVYKMLCWAARAAS-PSILIHFINFLPSHSPSNRLLYPRQEVQATL 635
DB 361 LLGLFGYLVFLVYKMLCWAARAASPSILIHFINFLPSHSPSNRLLYPRQEVQATL 420
QY 636 VVLAAMVPIILLGLTPLHLRHRRLRRPADROENKAGLLDLPDASVNGWSDEEKA 695
DB 421 VVLAAMVPIILLGLTPLHLRHRRLRRPADROENKAGLLDLPDASVNGWSDEEKA 480
QY 696 GGLDDEBAELVPSEVLHQAIHTIEFCLGCVSNTASYLRWLSLAHAQLSEVLWAMV 755
DB 481 GGLDDEBAELVPSEVLHQAIHTIEFCLGCVSNTASYLRWLSLAHAQLSEVLWAMV 540
QY 756 RIGLGRGVAAVVLVPIFAAFAVMTVAILLVMEGLSAFLHALRHWVEFQNKFSYSGT 815
DB 541 RIGLGRGVAAVVLVPIFAAFAVMTVAILLVMEGLSAFLHALRHWVEFQNKFSYSGT 600
QY 816 GYKLSPP 822
DB 601 GYKLSPP 607

RESULT 3

US-11-126-866-2
; Sequence 2, Application US/11126866
; Publication No. US20050220789A1
; GENERAL INFORMATION:
; APPLICANT: UTU, et al., NALAN
; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS
; FILE REFERENCE: 1472/71099-ZA/JPM/AG
; CURRENT APPLICATION NUMBER: US/11/126,866
; CURRENT FILING DATE: 2005-05-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 2
; LENGTH: 614
; TYPE: PRT
; ORGANISM: human
US-11-126-866-2

Query Match 46.8%; Score 385; DB 6; Length 614;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 605; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 217 MTFLISYNGEQIGQKIRKITDCFHCHVFPFLOQEEARLQALQOQSQSELQEVLETGER 276
DB 1 MTFLISYNGEQIGQKIRKITDCFHCHVFPFLOQEEARLQALQOQSQSELQEVLETGER 60
QY 277 FLSQVLRVQLQLPPQGVQVHKMAVYLAALNOCVSTTHKCLIAEAWCSVRDLPALQAL 336
DB 61 FLSQVLRVQLQLPPQGVQVHKMAVYLAALNOCVSTTHKCLIAEAWCSVRDLPALQAL 120
QY 337 RDSSMEEGVSAVAHRIPCDMPPTLIRNFTASFGIVDRYGVGRYQEVNPAPYITITF 396
DB 121 RDSSMEEGVSAVAHRIPCDMPPTLIRNFTASFGIVDAVGGRYQEVNPAPYITITF 180
QY 397 PFLPAMFGDVGHGLLMLFALAMVLAENRPVAKAAQNEIWTQFFRGRYLLMLGLFSIY 456
DB 181 PFLPAMFGDVGHGLLMLFALAMVLAENRPVAKAAQNEIWTQFFRGRYLLMLGLFSIY 240
QY 457 TGFYIYNECFSRATSIIPSGWSVAAMANQSGWSDAFLAQHTMLTLDPNVTGVFLGPYPFGI 516
DB 241 TGFYIYNECFSRATSIIPSGWSVAAMANQSGWSDAFLAQHTMLTLDPNVTGVFLGPYPFGI 300
QY 517 DPINSLAANHLSPNSFKMKSIVIILGVVHMAFGVVLGVFNHVFHFGQHRRLLETLPELTF 576

Db 301 DPTWLSAANHLVSFNSFKMNSVILGVVHNAFVGVVGVVHFGQRHRLLETLPELT 360
QY 577 LLGLFGYLVFLVIYKMLCVWAARAAS-PSILIHFINMFLFSHSPSNRLLYPROEVQATL 635
Db 361 LLGLFGYLVFLVIYKMLCVWAARAASAPSIILIHFINMFLFSHSPSNRLLYPROEVQATL 420
QY 636 VVLALAMVPILLGLTPLHLHRRHRRRLRRPADQREENKAGLLDLPDASVNGWSDEKA 695
Db 421 VVLALAMVPILLGLTPLHLHRRHRRRLRRPADQREENKAGLLDLPDASVNGWSDEKA 480
QY 696 GGLDDEEAEELVPSEVLVMEGLSAFLHRLHLLHWHVEFQNKFSYSGT 755
Db 481 GGLDDEEAEELVPSEVLVMEGLSAFLHRLHLLHWHVEFQNKFSYSGT 540
QY 756 RIGLGLGREVGVAAVLVPIFAAFVAVMTVAILLVMEGLSAFLHRLHLLHWHVEFQNKFSYSGT 815
Db 481 GGLDDEEAEELVPSEVLVMEGLSAFLHRLHLLHWHVEFQNKFSYSGT 540
QY 816 GYKLSPP 822
Db 601 GYKLSPP 607

RESULT 4

US-11-126-841A-2

; Sequence 2, Application US/11126841A

; Publication No. US20050271659A1

; GENERAL INFORMATION:

; APPLICANT: UTU, et al., NALAN

; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS TO

; FILE REFERENCE: 1472/71099-ZB/JPW/AG

; CURRENT FILING DATE: 2005-05-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: Patentin version 3.3

; SEQ ID NO 2

; LENGTH: 614

; TYPE: PRT

; ORGANISM: human

US-11-126-841A-2

Query Match 46.8%; Score 385; DB 6; Length 614;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 605; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 217 MTLISVWGSGIQGKIRKIDCFCHVFPFLQOEAEALGALQLOQOQSELOEVLGETER 276
Db 1 MTLISVWGSGIQGKIRKIDCFCHVFPFLQOEAEALGALQLOQOQSELOEVLGETER 60
QY 277 FLSQVLGRVLQLLPPGVQVHKMKAIVYALNQCQSVSTTHKCLIAEAWCSVRDLPALQEAL 336
Db 61 FLSQVLGRVLQLLPPGVQVHKMKAIVYALNQCQSVSTTHKCLIAEAWCSVRDLPALQEAL 120
QY 337 RDSMEEGVSAVHRIPCRDMPPTLIRTNFTASFGQIVDRYGVGRYQEVNPAITYITF 396
Db 121 RDSMEEGVSAVHRIPCRDMPPTLIRTNFTASFGQIVDRYGVGRYQEVNPAITYITF 180
QY 397 PFLFVAFMGDVGHGLMFLFALAMVLAENRPAVKAQNEIWOTFFRGYLLILMLGLFSY 456
Db 181 PFLFVAFMGDVGHGLMFLFALAMVLAENRPAVKAQNEIWOTFFRGYLLILMLGLFSY 240
QY 457 TGFYINCEFSRATSIFFSGWSVAAMANQSGWSDAFLAQHTMTLTDPNVTGVFLGPYFPGI 516
Db 241 TGFYINCEFSRATSIFFSGWSVAAMANQSGWSDAFLAQHTMTLTDPNVTGVFLGPYFPGI 300
QY 517 DPTWLSAANHLVSFNSFKMNSVILGVVHNAFVGVVGVVHFGQRHRLLETLPELT 576
Db 301 DPTWLSAANHLVSFNSFKMNSVILGVVHNAFVGVVGVVHFGQRHRLLETLPELT 360
QY 577 LLGLFGYLVFLVIYKMLCVWAARAAS-PSILIHFINMFLFSHSPSNRLLYPROEVQATL 635

Db 361 LLGLFGYLVFLVIYKMLCVWAARAASAPSIILIHFINMFLFSHSPSNRLLYPROEVQATL 420
QY 636 VVLALAMVPILLGLTPLHLHRRHRRRLRRPADQREENKAGLLDLPDASVNGWSDEKA 695
Db 421 VVLALAMVPILLGLTPLHLHRRHRRRLRRPADQREENKAGLLDLPDASVNGWSDEKA 480
QY 696 GGLDDEEAEELVPSEVLVMEGLSAFLHRLHLLHWHVEFQNKFSYSGT 755
Db 481 GGLDDEEAEELVPSEVLVMEGLSAFLHRLHLLHWHVEFQNKFSYSGT 540
QY 756 RIGLGLGREVGVAAVLVPIFAAFVAVMTVAILLVMEGLSAFLHRLHLLHWHVEFQNKFSYSGT 815
Db 541 RIGLGLGREVGVAAVLVPIFAAFVAVMTVAILLVMEGLSAFLHRLHLLHWHVEFQNKFSYSGT 600
QY 816 GYKLSPP 822
Db 601 GYKLSPP 607

RESULT 5

US-10-145-012-13

; Sequence 13, Application US/10145012

; Publication No. US20030124614A1

; GENERAL INFORMATION:

; APPLICANT: UTU et al.

; TITLE OF INVENTION: T-CELL MEMBRANE PROTEIN (TIRC7), PEPTIDES AND ANTIBODIES DERIVED

; FILE REFERENCE: 4400-0105P

; CURRENT APPLICATION NUMBER: US/10/145,012

; CURRENT FILING DATE: 2002-05-13

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 13

; LENGTH: 614

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-145-012-13

Query Match 39.5%; Score 325; DB 4; Length 614;
Best Local Similarity 99.8%; Pred. No. 2.7e-295;
Matches 445; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 378 YGVGRYQEVNPAITYITTFPFLFAMVFGDVGHGLMFLFALAMVLAENRPAVKAQNEIW 437
Db 162 YGVGRYQEVNPAITYITTFPFLFAMVFGDVGHGLMFLFALAMVLAENRPAVKAQNEIW 221
QY 438 QTFEFGRYLLMLGLFSIYTGFIYNECFSRATSIFFSGWSVAAMANQSGWSDAFLAQHTM 497
Db 222 QTFEFGRYLLMLGLFSIYTGFIYNECFSRATSIFFSGWSVAAMANQSGWSDAFLAQHTM 281
QY 498 LTLDPNVTGVFLGPYFPGIDPIWLSAANHLVSFNSFKMNSVILGVVHNAFVGVVGVVFNH 557
Db 282 LTLDPNVTGVFLGPYFPGIDPIWLSAANHLVSFNSFKMNSVILGVVHNAFVGVVGVVFNH 341
QY 558 VHFQGRHRLLETLPELTFLGLFGYLVFLVIYKMLCVWAARAAS-PSILIHFINMFLFS 616
Db 342 VHFQGRHRLLETLPELTFLGLFGYLVFLVIYKMLCVWAARAASAPSIILIHFINMFLFS 401
QY 617 HSPSNRLLYPROEVQATLVVLALAMVPILLGLTPLHLHRRHRRRLRRPADQREENKAG 676
Db 402 HSPSNRLLYPROEVQATLVVLALAMVPILLGLTPLHLHRRHRRRLRRPADQREENKAG 461
QY 677 LLDPDASVNGWSDEKAGGLDDEEAEELVPSEVLVMEGLSAFLHRLHLLHWHVEFQNKFSYSGT 736
Db 462 LLDPDASVNGWSDEKAGGLDDEEAEELVPSEVLVMEGLSAFLHRLHLLHWHVEFQNKFSYSGT 521
QY 737 WALSLAHAQLSEVLVWAMVNRIGLGLGREVGVAAVLVPIFAAFVAVMTVAILLVMEGLSAF 796
Db 522 WALSLAHAQLSEVLVWAMVNRIGLGLGREVGVAAVLVPIFAAFVAVMTVAILLVMEGLSAF 581
QY 797 LHALRLHWHVEFQNKFSYSGTGYKLSPP 822
Db 582 LHALRLHWHVEFQNKFSYSGTGYKLSPP 607

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RESULT 6
US-10-489-725-5
; Sequence 5, Application US/10489725
; Publication No. US20050048067A1
; GENERAL INFORMATION:
; APPLICANT: Utku, et al., Nalan
; TITLE OF INVENTION: Peptides capable of modulating immune response
; FILE REFERENCE: GE19A46/P-WO
; CURRENT APPLICATION NUMBER: US/10/489,725
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/322,896
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/322,895
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-725-5

Query Match      39.5%; Score 325; DB 5; Length 614;
Best Local Similarity 99.8%; Pred. No. 2.7e-295;
Matches 445; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 378 YGVGRYQEVNPAPYITITPPFLFAVMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIW 437
DB 162 YGVGRYQEVNPAPYITITPPFLFAVMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIW 221
QY 438 QTFFRGYLLLMGLFSIYTGFIYNECFSRATSIFFSGWSVAAMANQSCWSDAFLAQHTM 497
DB 222 QTFFRGYLLLMGLFSIYTGFIYNECFSRATSIFFSGWSVAAMANQSCWSDAFLAQHTM 281
QY 498 LTLDPNVTGVFLGPPYFGIDPIWSLAANHLSPFNSFKMKSIVILGVVHMAFGVVLGVFNH 557
DB 282 LTLDPNVTGVFLGPPYFGIDPIWSLAANHLSPFNSFKMKSIVILGVVHMAFGVVLGVFNH 341
QY 558 VHFQGRHRLLELTPELTFLGLFGYLVFLVIYKMLCVWAARAAS-PSILIHFINNPLFS 616
DB 342 VHFQGRHRLLELTPELTFLGLFGYLVFLVIYKMLCVWAARAASAPSILIHFINNPLFS 401
QY 617 HSPSNRLLYPROEVVQATLVVLALAMVPILLGTPLHLHRRHRRRLRRPADRQENKAG 676
DB 402 HSPSNRLLYPROEVVQATLVVLALAMVPILLGTPLHLHRRHRRRLRRPADRQENKAG 461
QY 677 LLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLMHQAIHTIEFCLGCVSNTASYLRL 736
DB 462 LLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLMHQAIHTIEFCLGCVSNTASYLRL 521
QY 737 WALSLAHAQLSEVLWAMVNRIGLIGRGVGVAAVLPVIFAFAVMTVAILLVMEGLSAP 796
DB 522 WALSLAHAQLSEVLWAMVNRIGLIGRGVGVAAVLPVIFAFAVMTVAILLVMEGLSAP 581
QY 797 LHALLRHVVEFQNKFSYGTGYKLSPP 822
DB 582 LHALLRHVVEFQNKFSYGTGYKLSPP 607

RESULT 7
US-11-126-866-13
; Sequence 13, Application US/11126866
; Publication No. US20050220789A1
; GENERAL INFORMATION:
; APPLICANT: Utku, et al., Nalan
; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS TO
; FILE REFERENCE: 1472/71099-2A/JPW/AG
; CURRENT APPLICATION NUMBER: US/11/126,866
; CURRENT FILING DATE: 2005-05-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-126-866-13

Query Match      39.5%; Score 325; DB 6; Length 614;
Best Local Similarity 99.8%; Pred. No. 2.7e-295;
Matches 445; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 378 YGVGRYQEVNPAPYITITPPFLFAVMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIW 437
DB 162 YGVGRYQEVNPAPYITITPPFLFAVMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIW 221
QY 438 QTFFRGYLLLMGLFSIYTGFIYNECFSRATSIFFSGWSVAAMANQSCWSDAFLAQHTM 497
DB 222 QTFFRGYLLLMGLFSIYTGFIYNECFSRATSIFFSGWSVAAMANQSCWSDAFLAQHTM 281
QY 498 LTLDPNVTGVFLGPPYFGIDPIWSLAANHLSPFNSFKMKSIVILGVVHMAFGVVLGVFNH 557
DB 282 LTLDPNVTGVFLGPPYFGIDPIWSLAANHLSPFNSFKMKSIVILGVVHMAFGVVLGVFNH 341
QY 558 VHFQGRHRLLELTPELTFLGLFGYLVFLVIYKMLCVWAARAAS-PSILIHFINNPLFS 616
DB 342 VHFQGRHRLLELTPELTFLGLFGYLVFLVIYKMLCVWAARAASAPSILIHFINNPLFS 401
QY 617 HSPSNRLLYPROEVVQATLVVLALAMVPILLGTPLHLHRRHRRRLRRPADRQENKAG 676
DB 402 HSPSNRLLYPROEVVQATLVVLALAMVPILLGTPLHLHRRHRRRLRRPADRQENKAG 461
QY 677 LLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLMHQAIHTIEFCLGCVSNTASYLRL 736
DB 462 LLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLMHQAIHTIEFCLGCVSNTASYLRL 521
QY 737 WALSLAHAQLSEVLWAMVNRIGLIGRGVGVAAVLPVIFAFAVMTVAILLVMEGLSAP 796
DB 522 WALSLAHAQLSEVLWAMVNRIGLIGRGVGVAAVLPVIFAFAVMTVAILLVMEGLSAP 581
QY 797 LHALLRHVVEFQNKFSYGTGYKLSPP 822
DB 582 LHALLRHVVEFQNKFSYGTGYKLSPP 607

RESULT 8
US-11-126-841A-13
; Sequence 13, Application US/11126841A
; Publication No. US20050271659A1
; GENERAL INFORMATION:
; APPLICANT: Utku, et al., Nalan
; TITLE OF INVENTION: METHODS OF TREATMENT USING AN ANTIBODY THAT SPECIFICALLY BINDS TO
; FILE REFERENCE: 1472/71099-2B/JPW/AG
; CURRENT APPLICATION NUMBER: US/11/126,841A
; CURRENT FILING DATE: 2005-05-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-126-841A-13

Query Match      39.5%; Score 325; DB 6; Length 614;
Best Local Similarity 99.8%; Pred. No. 2.7e-295;
Matches 445; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 378 YGVGRYQEVNPAPYITITPPFLFAVMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIW 437
DB 162 YGVGRYQEVNPAPYITITPPFLFAVMFGDVGHGLLMFLPALAMVLAENRPAVKAQNEIW 221
QY 438 QTFFRGYLLLMGLFSIYTGFIYNECFSRATSIFFSGWSVAAMANQSCWSDAFLAQHTM 497
DB 222 QTFFRGYLLLMGLFSIYTGFIYNECFSRATSIFFSGWSVAAMANQSCWSDAFLAQHTM 281
QY 498 LTLDPNVTGVFLGPPYFGIDPIWSLAANHLSPFNSFKMKSIVILGVVHMAFGVVLGVFNH 557
DB 282 LTLDPNVTGVFLGPPYFGIDPIWSLAANHLSPFNSFKMKSIVILGVVHMAFGVVLGVFNH 341
QY 558 VHFQGRHRLLELTPELTFLGLFGYLVFLVIYKMLCVWAARAAS-PSILIHFINNPLFS 616
DB 342 VHFQGRHRLLELTPELTFLGLFGYLVFLVIYKMLCVWAARAASAPSILIHFINNPLFS 401
QY 617 HSPSNRLLYPROEVVQATLVVLALAMVPILLGTPLHLHRRHRRRLRRPADRQENKAG 676
DB 402 HSPSNRLLYPROEVVQATLVVLALAMVPILLGTPLHLHRRHRRRLRRPADRQENKAG 461
QY 677 LLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLMHQAIHTIEFCLGCVSNTASYLRL 736
DB 462 LLDLPDASVNGWSSDEEKAGGLDDEEAELVPSEVLMHQAIHTIEFCLGCVSNTASYLRL 521
QY 737 WALSLAHAQLSEVLWAMVNRIGLIGRGVGVAAVLPVIFAFAVMTVAILLVMEGLSAP 796
DB 522 WALSLAHAQLSEVLWAMVNRIGLIGRGVGVAAVLPVIFAFAVMTVAILLVMEGLSAP 581
QY 797 LHALLRHVVEFQNKFSYGTGYKLSPP 822
DB 582 LHALLRHVVEFQNKFSYGTGYKLSPP 607
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Db 162 YGVRGYQEVNPAVYTIITFPFLFAVMFGDVGHGILLMFLFALAMVLAENRPAVKAQNEIW 221
QY 438 QTFPRGRYLLLMGLFSIYTGFIYNECFSRATSIPTPSGWSVAAMANQSGWSDAFLAQHTM 497
Db 222 QTFPRGRYLLLMGLFSIYTGFIYNECFSRATSIPTPSGWSVAAMANQSGWSDAFLAQHTM 281
QY 498 LTLDPNVTGVFLGYPVPGIDPIWLSAANHLFSFKMKMSVILGVVHMAFGVVLGVFNH 557
Db 282 LTLDPNVTGVFLGYPVPGIDPIWLSAANHLFSFKMKMSVILGVVHMAFGVVLGVFNH 341
QY 558 VHFQORHRLLETLPELTFLGLGFLYVFLVIYKWLVCWMAAAS-PSILHFINMFLFS 616
Db 342 VHFQORHRLLETLPELTFLGLGFLYVFLVIYKWLVCWMAAAS-PSILHFINMFLFS 401
QY 617 HSPENRLLYPRQEVVQATLVIALAMPILLGTHPLHLHRRRRLRRPADROENKAG 676
Db 402 HSPENRLLYPRQEVVQATLVIALAMPILLGTHPLHLHRRRRLRRPADROENKAG 461
QY 677 LLDLPDASVNGWSSDEEKAGGLDDEBAELVPSVLMHQATHTEFCIGCVSNTASYRL 736
Db 462 LLDLPDASVNGWSSDEEKAGGLDDEBAELVPSVLMHQATHTEFCIGCVSNTASYRL 521
QY 737 WALSLAQAQLSEVLWAMVMRIGLGLGREVGVAAYVLPVIFAFAFVMTVAILLVMEGLSAP 796
Db 522 WALSLAQAQLSEVLWAMVMRIGLGLGREVGVAAYVLPVIFAFAFVMTVAILLVMEGLSAP 581
QY 797 LHALRLHWVEFONKFYSGTGKLSPP 822
Db 582 LHALRLHWVEFONKFYSGTGKLSPP 607

RESULT 9

US-10-264-049-2656
; Sequence 2656, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birtse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAI33PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2656
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (77)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (318)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (598)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-2656

Query Match 35.4%; Score 291; DB 4; Length 643;
Best Local Similarity 99.6%; Pred. No. 2.2e-263;
Matches 491; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 110 DVRGNQQAQLHQLHQAHLVLRQGHPEPOLAAHTDGASERTPLLOAQPGGHQDLRVNF 169
Db 78 DVRGNQQAQLHQLHQAHLVLRQGHPEPOLAAHTDGASERTPLLOAQPGGHQDLRVNF 137

QY 170 VAGAVEPHKAPALBRLLWRACRGFLIASPRELEQPLEHPVTGEBPATWMTFLISWGEQIG 229
Db 138 VAGAVEPHKAPALBRLLWRACRGFLIASPRELEQPLEHPVTGEBPATWMTFLISWGEQIG 197
QY 230 QKIRKIIDTCFCHVFPFLQOEAEARLGALQOLQOQSQOELOEVLGETERFSLQVLRVLOLL 289
Db 198 QKIRKIIDTCFCHVFPFLQOEAEARLGALQOLQOQSQOELOEVLGETERFSLQVLRVLOLL 257
QY 290 PPGQVQVHKMAVYLAALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDSMSEGSVA 349
Db 258 PPGQVQVHKMAVYLAALNQCSTVTHKCLIAEAWCSVRDLPALQEARLDSMSEGSVA 317
QY 350 HRIPCRDMPPTLIRTNRTASFOGIVDRYGVGRVQEVNPAVYTIITFPFLFAVMFGDVGH 409
Db 318 XRIPCRDMPPTLIRTNRTASFOGIVDAYGVGRVQEVNPAVYTIITFPFLFAVMFGDVGH 377
QY 410 GLIMFLFALAMVLAENRPAVKAQNEIWQTFPRGRYLLLMGLFSIYTGFIYNECFSRAT 469
Db 378 GLIMFLFALAMVLAENRPAVKAQNEIWQTFPRGRYLLLMGLFSIYTGFIYNECFSRAT 437
QY 470 SIFPSGWSVAAMANQSGWSDAFLAQHTMTLDPNVTGVFLGYPVPGIDPIWLSAANHLSP 529
Db 438 SIFPSGWSVAAMANQSGWSDAFLAQHTMTLDPNVTGVFLGYPVPGIDPIWLSAANHLSP 497
QY 530 LNSFKMKMSVILGVVHMAFGVVLGVFNHVFHQHRLILLETLPETLFLGLGFLYVFLVI 589
Db 498 LNSFKMKMSVILGVVHMAFGVVLGVFNHVFHQHRLILLETLPETLFLGLGFLYVFLVI 557
QY 590 YKWLVCWMAAAS 602
Db 558 YKWLVCWMAAAS 570

RESULT 10

US-10-783-519-9
; Sequence 9, Application US/10783519
; Publication No. US20050064448A1
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; TITLE OF INVENTION: Osteoclast Proton Pump Subunit
; FILE REFERENCE: 1564.1006-001
; CURRENT APPLICATION NUMBER: US/10/783,519
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/618,304
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 08/605,378
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-519-9

Query Match 4.0%; Score 33; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 764 EVGVAAVVLVPIFAAFVMTVAILLVMEGLSAP 796
Db 1 EVGVAAVVLVPIFAAFVMTVAILLVMEGLSAP 33

RESULT 11

US-10-783-519-4
; Sequence 4, Application US/10783519
; Publication No. US2005006448A1
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; TITLE OF INVENTION: Osteoclast Proton Pump Subunit

FILE REFERENCE: 1564.1006-001
CURRENT APPLICATION NUMBER: US/10/783,519
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: US/09/618,304
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 08/605,378
PRIOR FILING DATE: 1996-02-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 32
TYPE: PRT
ORGANISM: Homo sapiens
US-10-783-519-4

Query Match 3.9%; Score 32; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.9e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 YTIITPFLFAMVFGDVGHGLLMFLFALANVL 422
Db 1 YTIITPFLFAMVFGDVGHGLLMFLFALANVL 32

RESULT 12

US-10-783-519-7
Sequence 7, Application US/10783519
Publication No. US20050064448A1
GENERAL INFORMATION:
APPLICANT: Stashenko, Philip
APPLICANT: Li, Yi-Ping
TITLE OF INVENTION: Osteoclast Proton Pump Subunit
FILE REFERENCE: 1564.1006-001
CURRENT APPLICATION NUMBER: US/10/783,519
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: US/09/618,304
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 08/605,378
PRIOR FILING DATE: 1996-02-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
US-10-783-519-7

Query Match 3.6%; Score 30; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 7e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 571 LPBLTFLGLFGYLVFLVIYKWLVCWAARA 600
Db 1 LPBLTFLGLFGYLVFLVIYKWLVCWAARA 30

RESULT 13

US-10-489-725-7
Sequence 7, Application US/10489725
Publication No. US20050048067A1
GENERAL INFORMATION:
APPLICANT: Utaku, Nalan
TITLE OF INVENTION: Peptides capable of modulating immune response
CURRENT APPLICATION NUMBER: US/10/489,725
CURRENT FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: 60/322,896
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/322,895
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7

LENGTH: 29
TYPE: PRT
ORGANISM: Homo sapiens
US-10-489-725-7

Query Match 3.5%; Score 29; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.9e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 664 RRPADQENKAGLLDLPDASVNGWSSDE 692
Db 1 RRPADQENKAGLLDLPDASVNGWSSDE 29

RESULT 14

US-10-783-519-5
Sequence 5, Application US/10783519
Publication No. US20050064448A1
GENERAL INFORMATION:
APPLICANT: Stashenko, Philip
APPLICANT: Li, Yi-Ping
TITLE OF INVENTION: Osteoclast Proton Pump Subunit
FILE REFERENCE: 1564.1006-001
CURRENT APPLICATION NUMBER: US/10/783,519
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: US/09/618,304
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 08/605,378
PRIOR FILING DATE: 1996-02-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 26
TYPE: PRT
ORGANISM: Homo sapiens
US-10-783-519-5

Query Match 3.2%; Score 26; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 QTFFRGYLLLMGLFSIYTGFIYNE 463
Db 1 QTFFRGYLLLMGLFSIYTGFIYNE 26

RESULT 15

US-10-489-725-9
Sequence 9, Application US/10489725
Publication No. US20050048067A1
GENERAL INFORMATION:
APPLICANT: Utaku, Nalan
TITLE OF INVENTION: Peptides capable of modulating immune response
CURRENT APPLICATION NUMBER: US/10/489,725
CURRENT FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: 60/322,896
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/322,895
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
US-10-489-725-9

Query Match 2.9%; Score 24; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 679 DLPDASVNGWSSDEEKAGLDDEE 702

Db 1 DLPDASVNGWSDEERKAGGLDDEE 24

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(without alignments)
924.542 Million cell updates/sec

Title: US-10-783-519-2

Perfect score: 822

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Post-processing: Listing first 45 summaries

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- 3: /EMC_Celerra_SID33/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SID33/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SID33/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SID33/prodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SID33/prodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SID33/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	545	66.3	830	6	US-10-511-937-2474
2	20	2.4	43	6	US-10-449-902-29221
3	20	2.4	271	6	US-10-953-349-18081
4	20	2.4	273	6	US-10-953-349-18080
5	20	2.4	314	6	US-10-953-349-18079
6	20	2.4	820	6	US-10-449-902-54048
7	17	2.1	357	6	US-10-449-902-29928
8	17	2.1	489	6	US-10-449-902-52773
9	17	2.1	818	6	US-10-449-902-47207
10	17	2.1	818	6	US-10-449-902-53444
11	17	2.1	923	6	US-10-449-902-41603
12	8	1.0	98	6	US-10-449-902-50960
13	8	1.0	136	6	US-10-953-349-32586
14	8	1.0	301	6	US-10-449-902-32058
15	8	1.0	335	6	US-10-449-902-33155
16	8	1.0	444	6	US-10-449-902-31385
17	8	1.0	518	6	US-10-449-902-31736
18	8	1.0	623	6	US-10-449-902-50362
19	8	1.0	678	6	US-10-449-902-55991
20	8	1.0	777	6	US-10-449-902-46537
21	8	1.0	777	6	US-10-449-902-56066
22	7	0.9	106	6	US-10-953-349-28780
23	7	0.9	117	6	US-10-953-349-28801
24	7	0.9	120	6	US-10-449-902-49220
25	7	0.9	149	6	US-10-953-349-18110

26	7	0.9	153	6	US-10-953-349-35214	Sequence 35214, A
27	7	0.9	161	6	US-10-953-349-27011	Sequence 27011, A
28	7	0.9	167	6	US-10-449-902-43929	Sequence 43929, A
29	7	0.9	168	6	US-10-449-902-49250	Sequence 49250, A
30	7	0.9	170	6	US-10-505-928-861	Sequence 861, App
31	7	0.9	176	7	US-11-293-697-3250	Sequence 3250, Ap
32	7	0.9	182	6	US-10-449-902-54303	Sequence 54303, A
33	7	0.9	187	6	US-10-953-349-49621	Sequence 49621, A
34	7	0.9	189	6	US-10-953-349-32783	Sequence 32783, A
35	7	0.9	190	6	US-10-953-349-25429	Sequence 25429, A
36	7	0.9	193	6	US-10-449-902-49436	Sequence 49436, A
37	7	0.9	210	7	US-11-075-398-7	Sequence 7, Appli
38	7	0.9	212	6	US-10-449-902-39836	Sequence 39836, A
39	7	0.9	216	6	US-10-953-349-25897	Sequence 25897, A
40	7	0.9	220	6	US-10-449-902-45122	Sequence 45122, A
41	7	0.9	223	6	US-10-449-902-50795	Sequence 50795, A
42	7	0.9	226	6	US-10-953-349-31843	Sequence 31843, A
43	7	0.9	245	6	US-10-449-902-51856	Sequence 51856, A
44	7	0.9	257	6	US-10-953-349-31818	Sequence 31818, A
45	7	0.9	262	6	US-10-449-902-31992	Sequence 31992, A

ALIGNMENTS

RESULT 1

US-10-511-937-2474
; Sequence 2474, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2474
; LENGTH: 830
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2474

Query Match 66.3%; Score 545; DB 6; Length 830;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 765; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY	57	RCELEKTTFLQEEVRRAGLVLPKGRLPAPPKRLRIQETERLAQELRDVRNQ	116
DB	57	RCELEKTTFLQEEVRRAGLVLPKGRLPAPPKRLRIQETERLAQELRDVRNQ	116
QY	117	ALRAQLHQLHQAALVROGHEPQAAHTDGAERTFLQAPGGPHODLRVNFAGAVEP	176
DB	117	ALRAQLHQLHQAALVROGHEPQAAHTDGAERTFLQAPGGPHODLRVNFAGAVEP	176
QY	177	HKAPALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGQIGQIKIRIT	236
DB	177	HKAPALERLLWRACRGFLIASFRELEQPLEHPVTGEPATWMTFLISYWGQIGQIKIRIT	236

QY 237 DCFHCHVFPFLOEQEALGALQOQSOBELQVLGETERFLSQVLGRVLQLLPPGQVQV 296
Db 237 DCFHCHVFPFLOEQEALGALQOQSOBELQVLGETERFLSQVLGRVLQLLPPGQVQV 296
QY 297 HKMKAVYLLNQCSVSTTHKCLIAEAWCSVRDLPALQELRDSMEEGVSAVAHRIPCRD 356
Db 297 HKMKAVYLLNQCSVSTTHKCLIAEAWCSVRDLPALQELRDSMEEGVSAVAHRIPCRD 356
QY 357 MPPTLLTRNRTFASFOGIVDRGVGVQVNPAPYTIITFPFLFAMFGDVGHLLMFLF 416
Db 357 MPPTLLTRNRTFASFOGIVDAVGGRYQEVNPAPYTIITFPFLFAMFGDVGHLLMFLF 416
QY 417 ALAMVLAENRAPKAAQNEIWQTFPRGRYLLIMGLFSIYTGFIYNECFSRATSIPPSGW 476
Db 417 ALAMVLAENRAPKAAQNEIWQTFPRGRYLLIMGLFSIYTGFIYNECFSRATSIPPSGW 476
QY 477 SVAAANQSGWSDAFIAQHTMTLTLDPNVTGVFLGPPGIDPTIWSLAANHLSFLNSFKMK 536
Db 477 SVAAANQSGWSDAFIAQHTMTLTLDPNVTGVFLGPPGIDPTIWSLAANHLSFLNSFKMK 536
QY 537 MSVILGVVHMGVVLGVFNHVFQGRHRLLETLPELTLFLLGCLGYLVFLVIYKWLVM 596
Db 537 MSVILGVVHMGVVLGVFNHVFQGRHRLLETLPELTLFLLGCLGYLVFLVIYKWLVM 596
QY 597 AARAAS-PSILIHFINMFLFSHPNSRLLYPROEVVQATLVVLAMVPIILLIGTPLHLL 655
Db 597 AARAASPSILIHFINMFLFSHPNSRLLYPROEVVQATLVVLAMVPIILLIGTPLHLL 656
QY 656 HRHRRRLRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDBEEAELVPSEVLMHQ 715
Db 657 HRHRRRLRRPADRQENKAGLLDLPDASVNGWSSDEEKAGGLDDBEEAELVPSEVLMHQ 716
QY 716 ALHTTEFCGCVSNTASYLRLWALSIAHAQLSEVLWAMVMRIGLGRGVGVAANVLP 775
Db 717 ALHTTEFCGCVSNTASYLRLWALSIAHAQLSEVLWAMVMRIGLGRGVGVAANVLP 776
QY 776 FAFAVMTVAILLVMBGLSAFLHALRLHWVEFQNKFSYGTGYKLSPF 822
Db 777 FAFAVMTVAILLVMBGLSAFLHALRLHWVEFQNKFSYGTGYKLSPF 823

RESULT 2

US-10-449-902-29221
; Sequence 29221, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Research.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29221
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-29221

Query Match 2.4%; Score 20; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 5.2e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 793 LSAPFLHALRLHWVEFQNKFY 812
Db 4 LSAPFLHALRLHWVEFQNKFY 23

RESULT 3

US-10-953-349-18081
; Sequence 18081, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18081
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18081

Query Match 2.4%; Score 20; DB 6; Length 271;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 793 LSAPFLHALRLHWVEFQNKFY 812
Db 233 LSAPFLHALRLHWVEFQNKFY 252

RESULT 4

US-10-953-349-18080
; Sequence 18080, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18080
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18080

Query Match 2.4%; Score 20; DB 6; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 793 LSAPFLHALRLHWVEFQNKFY 812
Db 235 LSAPFLHALRLHWVEFQNKFY 254

RESULT 5

US-10-953-349-18079
; Sequence 18079, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18079
; LENGTH: 314

; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18079

Query Match 2.4%; Score 20; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 793 LSAPFLHALRLHWVFQNKFY 812
Db 276 LSAPFLHALRLHWVFQNKFY 295
|||||

RESULT 6
US-10-449-902-54048
; Sequence 54048, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54048
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54048

Query Match 2.4%; Score 20; DB 6; Length 820;
Best Local Similarity 100.0%; Pred. No. 6.8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 793 LSAPFLHALRLHWVFQNKFY 812
Db 781 LSAPFLHALRLHWVFQNKFY 800
|||||

RESULT 7
US-10-449-902-29928
; Sequence 29928, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29928
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-29928

Query Match 2.1%; Score 17; DB 6; Length 357;

Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 727 VSNTASYRLRLWALS LAH 743
Db 257 VSNTASYRLRLWALS LAH 273
|||||

RESULT 8
US-10-449-902-52773
; Sequence 52773, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52773
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-52773

Query Match 2.1%; Score 17; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 727 VSNTASYRLRLWALS LAH 743
Db 389 VSNTASYRLRLWALS LAH 405
|||||

RESULT 9
US-10-449-902-47207
; Sequence 47207, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47207
; LENGTH: 818
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47207

Query Match 2.1%; Score 17; DB 6; Length 818;
Best Local Similarity 100.0%; Pred. No. 5.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 727 VSNTASYRLRLWALS LAH 743
|||||

Db 718 VNTASYLRRLWALSLAH 734

RESULT 10

US-10-449-902-53444
; Sequence 53444, Application US/10449902
; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 53444

; LENGTH: 818

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-53444

Query Match 2.1%; Score 17; DB 6; Length 818;

Best Local Similarity 100.0%; Pred. No. 5.2e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 VNTASYLRRLWALSLAH 743

|||||

Db 718 VNTASYLRRLWALSLAH 734

RESULT 11

US-10-449-902-41603
; Sequence 41603, Application US/10449902
; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 41603

; LENGTH: 923

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-41603

Query Match 2.1%; Score 17; DB 6; Length 923;

Best Local Similarity 100.0%; Pred. No. 5.8e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 VNTASYLRRLWALSLAH 743

|||||

Db 824 VNTASYLRRLWALSLAH 840

RESULT 12

US-10-449-902-50960

; Sequence 50960, Application US/10449902
; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 50960

; LENGTH: 98

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-50960

Query Match

Best Local Similarity 1.0%; Score 8; DB 6; Length 98;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 659 RRRRLRRRP 666

|||||

Db 52 RRRRLRRRP 59

RESULT 13

US-10-953-349-32586
; Sequence 32586, Application US/10953349
; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: ENCODED THERBY

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 32586

; LENGTH: 136

; TYPE: PRT

; ORGANISM: Triticum aestivum

US-10-953-349-32586

Query Match

Best Local Similarity 1.0%; Score 8; DB 6; Length 136;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 AARAAASPS 604

|||||

Db 71 AARAAASPS 78

RESULT 14

US-10-449-902-32058
; Sequence 32058, Application US/10449902
; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32058
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-32058

Query Match 1.0%; Score 8; DB 6; Length 301;
Best Local Similarity 100.0%; Pred. No. 9.9; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 654 LLHRHRR 661
| | | | |
DB 13 LLHRHRR 20

RESULT 15

US-10-449-902-33155
; Sequence 33155, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A020511-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33155
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-33155

Query Match 1.0%; Score 8; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 11; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 654 LLHRHRR 661
| | | | |
DB 13 LLHRHRR 20

Search completed: June 29, 2006, 13:27:33
Job time : 22 secs

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